

Table 70: Comparative Sequences relating to SAG 1280

ATACCTTTATTGAGTTTGAAACCTTGAATTTGATTTCTTTTGTGGATGAGGCTCATC
 ACTTCAAGAATATCCGTCCAATCACTGGACTTGGGAATGTAGCTGGAATCACCACACAA
 CTTCTAAAAAGAACGTTGGATATGGAGATGAAGGTGAGACAGTACAGGCAGAGCATGGAG
 ATAGAAATGTCGTTTTCGCGACAGGAACACCAAGTTTCTAACTCTATTAGTGAACCTTTCA
 CCATGATGGATTACATTTCAACCTGATGTCTTGGAACGATACCTGGTATCAAATTTTGACT
 CCTGGGTTGGGGCTTTTGGGAATATCGAAACTCCATGGAAGTACCCCGACAGGAGATA
 AGTACCAACCCAGAAACCGTTCAAGAAATTTGTCAACCTTCCTGAACTCATGCGAATCT
 ACAAGGAACTGCCGATATTAGACCTCAGACATGCTTGATTTACCAGTACCGGAAGCTA
 AGATTATTGCGGTGGAAGCGAGTTAACGCAAGCTCAGAAATCTATTGGAAGAGCTGG
 TAAAGCGTTGACAGCGTATCAAGTCAGGTAGTGTGATCCAAGTAGAGATAACATGCTTA
 AAATCACAGGAGAAGCCGAAACTAGCTATTGATATGCGGTTGATTGACCCCTACTTACT
 CCTTATCGGATTAATCAGAAATCCTTCAAGTAGTTCGATAATGTCGAGCGGATTACCGTG
 ATGGAGCTGGAGACAAGCCACTCAGATGATTTCTCAGATATTGGAACCCCTAAAAGTA
 AGGAAGAAGGGTTTGATGTCTACAATGAACCTTAAGGACTTGTTTGTGCGATCGAGGGATAC
 CAAAAGAGAAATTTGCTTCCATGATGCCAATCTGATGAGAAGAAAACTCTCTGT
 CAGCAAGGTCAATAGTGGAGAAAGTACGGATTCTCATGGCTTCTACGGAAAAAGGGGAA
 CAGGATTAACCTCCATCTCGCATGAAAGCTGTCCACTATTAGACGTTCCCTGGAGGC
 CCTCAGACATTTGTCAGCGAAATGGACGACTAATTCGACAAGGAAACATGCACCGAGG
 TAGATATTATCACTAATATTACTAAAGGGAGCTTTGACAATTACCTCTGGCAGACGCGAG
 AGAATAAGCTAAAGTATATCACCCAGATAATGACCTCAAAGATCCTGTGAGATCAGCTG
 AAGACATTGATGAACAAACCATGACCGCTCAGACTTAAAGGCATTGGCAACTGGGAACC
 CTTATCTCAAACCTCAAATGGAGTTGGAAAAATGAACCTGACAGTTTATAGAGAACTCAA
 GAGCCTTTAATCGCTCCAAAGACGAGTATCGCCATACCATTTCTATAGCGAGAAGCACC
 TCCTTATTATGGAAGAACCGTTGAGTCAATATGATAAAGATATTGCCCAATCTTTGGCAA
 CCAAGTCGCAAGATTTTGTGATGCGATTGACAATCAAGCAATGGATAATCGTGCTGAAG
 TGGGGACTATCTGCGAAACTCATTACCTATAACCGCTCAGAGACCAAGGAAGTCAGGA
 CACTTGGCAGCTTTAGAGGATTTGATTTAAAAATGACTACACGAGGTGCTAGTGAGCCCT
 TACCAGAAACCATTTCTTAAATGATTGATGGTATGATACAGTATCTGTCGCCCTTGATT
 TGAATACAGACCTGGGAACCATTCACCGATTAGTAATGCCATTGACCATATTATAGATG
 ACCAAGAAAAGACGCAAGAGCTGGTAAAGGATTTAAAGATAAGCTACAGGTAGCCAAAG
 TAGAAGTTGATAAAGTCTTTCCAAAGGAAGAGGACTATCAGCTTGTAAGGCTAAGTATG
 ATGTTTATGCTCCCTTGGTTGAAAAGAGAGCAGAGATTGAAGAGATAGATGCAGCTTTGG
 CCAAGTTTAGTGAAGATACAAACCCCAAGGAAGCAACAAATAGCATTGCGAGATA

SEQ ID. NO. 7002

STRAIN H36B

GGAGGGAAAAATGAATCAAGAAGTCTTACTACAAATGAT
 GAGAGCCACTATTCCTCGTGATAGAGCCCTTGCTTGAGGCATTTTATATT
 ACCAAGCAGAGCATTTTGATGAGGAGTGGGATAGTCTTATTCATCAGTTT
 ATGACCAATAGGCAAGAAATAAATAAGTCTGTTCAAGTACTTCACTTTGA
 GACAGATGTTTCAGCTTTTGTCCAGGCTAGTCTTATGATAGTCTCATG
 ATCTATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACTA
 GATAAATATCGCCGCTCGAAAAAACTTGGTGATAGAAGTGGCCTTGT
 CAATCTGGCCACTCGTTTCAATATTGGATTCCAATGGACACTACCAAA
 CCATATCGCCGATTCACTCTTACAAAAGAGTAGGGAGCTAATTTGGTC
 AATGTGTATCGTGTGGCTAATAATTAGCGGATCGTATTAGTCGAGATAT
 TGAACAGTTTCTCTAACTTACGAGCCTGAGCTTGAACTAGAGCTGATG
 AAAGTGTCTAGAAAAATGAAGAACTGTGATGAGCACAAAAAAGTGT
 CATCAAGCAATATCTTTGGAAGAGAGGGCTCTCTGTTATTGCTAGTTT
 GGATGTAGATTGTTCTCAACTAGATGTTCAAAATAGGAAAAACAGTCATC
 TGCCAGCTTATGAAGAGTTATCCTTACGACGTAATTTGAGATTCTAACA
 TATTTTGACCAAAATCGAAATGAACGTTCCAAAGTCCCAAGTTTATAGC
 AGGTGATTTTGACACAGAGATGGAAATGACACAGTCTTTGATGGCGAGG
 AATTACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGA
 ACGCTGACTACAGTCAAGAAAAAGGAATTAGAAAAAATGGACAAGCCAT
 TAGGATAGAAAAATCAAGAAAAATGACTCAGCTA₈GkATTGrTTTATCTC
 AGTTTGACCCAGACCGAGTCGGTATTTTATTGkATGCAGCAGGTGCTyT
 CGTTTawAwAATGCAGACCTTGCTTCACTAGGTGGTTATCCAAAGCCTC
 GGTAACTCAACTAGCCCTTGCGACAGAACTACTCCAAATGGGACTAAGTC
 ATGAAAAGGTTGAATTTTCTTTGGTAGCCAGCTTCCATGAAGAGCTG
 CGACAAGTTGCCTACGCCCTTTTACACCAAGAACTCAGCAGAGAAGATGC
 GGAGCAATTTGAAAAAGATAAAGGTAATCAGCCAGATTAACTCTCAGAG
 ATTGGAAAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAGTAGTTGATGAA
 GAATTCGCGGAAAATCCACTGGTTGAGAGATATTGGACACTTATCCTCT
 GGGGTCAATTGGTTTCTATAAGGGACAGGACTTTGAGGTGATGTCGCTCA
 GCGATGCTCGATGAACGGTTTGATTGCGATTGAGTTAGTCAATGACTTT
 TCGGATATCATTGAACAAAATCCAGTTCTTTATGTGAGGACCTGGGAAGA
 AGTCAGTCAGGCACTTCATCAGCCAAAGGCAGAACCAAAACAGAGTTAG
 AAGAAGCGGACCAAGAATTAAACCTATTCTCATTTCTGGAAGAGGAGCTA
 GTTCAGAGTATTGGACTATTGGAAACAGATGATTAGAAAAATGGTCATAA
 CGATACTGATCTTGAAGAAAACAGATAATCAAATTCCTGAAGAGGAAGTCG
 TCGAAACAATTCAGAGATTCCAGTAAACGGACTTTTATTTTCAGAAAGAT
 TTGACGGACTTTTATCCTAAGACTGCTAGAGATAAGTTGAGACAAACAT
 TGTGGCCATTGTTTGGTAAAAATCTAGAAGTAGAGCACCGCAATGCTT
 CACCAAGTGAACAAGAACTCCTTGCAAGTATGATGGCTGGGGTGGACTA
 GCCAATGAATTTTGTGACTATAATCCAAATTTTCTAAGGAACGAGA
 AGAAGTGAAGAGCTAGTCACAGATAAAGAGTATTGCGATATGAACAGT
 CCTCCCTGACAGCCTATTACACAGACCCATCCCTGATCCGTGAGATGTGG
 GATAAGTTGGAAGAGATGGCTTTACAGGTGGCAAAATCCTAGATCCTTC
 CATGGGAACAGGGAATTTCTTTGCGGCTATGCCAAAACACTTAAGAGAAA
 AGAGTGAGTTGATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCC
 AAACACCTTCATCCCAATAGTCATATTGAATTAAGGGATTTGAGACGGT
 GGCTTTTAAACGCAATAGTTTGGATTGGTGATTCAAATGTGCCCTTTG

Table 70: Comparative Sequences relating to SAG 1280

CCAATATACGAATTGCGGATAATAGGTACGATAGGCCCTTACATGATTTCAT
 GACTACTTTGTCAAAAAGTCACTTGATTGCTTCATGATGGTGGACAAAGT
 AGCGATTATCTCTTCCACAGGAACATATGGATAAGCGAACAGAAAACATCT
 TACAAGATATTCTGAGACAACCTGAATTTCTTGGTGGGGTTCGACTGCCT
 GACTCTGCCCTTAAGGCCATTGACAGGAACGAGTGTCAACACGGATATGTT
 ATTCTTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCT
 TTTGAGGTTCATTCGCTATGACAAGGATAGTCGCATTTGGCTCAATCCT
 TATTTTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTGAG
 GAATTTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGA
 TTGCAAGTGTGAAACAGCTCTAAATCACGTTAAGGCCCAAGAGAGATT
 GATAGAAATGAGGTCACTTAACCCAGATGTGTTGACCAACAAGTCAA
 TGATACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTGAGTACAGTT
 TTGGTTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTGGA
 GTCGGAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

SEQ ID. NO. 7003

STRAIN 18RS21

GnAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGA
 GCCACTATTCTCGTGATAGAGCCTTGCTTGAGGCATTTTATATTACCA
 AGCAGAGCATTTTGATGAGGAGTGGGATAGTCTTATTTCATCAGTTTATGA
 CCAATAGGCAAGAAAATAAATAGTCTGTTCAAGTACTTCACTTTGAGACA
 GATGTTTCAGCTTTTGTCCAGGCTAGTCTTATGATACTGCTCATGATCT
 ATTGACCTTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACCTAGATA
 AACTATCGCCGCTGAAAAAACTTGGTGATAGAAGTGGCCTTGTTCAT
 CTGGCCACTCGTTTCAATTTATGGATTCCAATGGACACTACCAACCAT
 ATCGCCGATTCACCTTACAAAAGAGTAGGGGAGCTAATTTGGTCAATG
 TGTATCGTGTGGCTAATAATTTAGCGGATCGTATTAGTCGAGATATTGAA
 CAGTTTCTCTTAACCTTACGAGCCTGAGCTTGAAACTAGAGCTGATGAAAC
 TGTCTAGAAAAATGAAGAACTGTTGATGAGCACAACAAAGTGTTCATC
 AAGCAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTGCTAGTTTGGAT
 GTAGATTTGTCTCACTAGATGTTCAAATAGGAAAAACAGTCATCTGCC
 AGCTTATGAAGAGTTTCTTACGAGCTAAATTTGAGATTCTAACATATT
 TTGACCAAAATCGAAATGAACGTTCCAAAGTCCCAAGTTTGTAGCAGGTT
 GATTTTGACACAGAGATGGAATGACACCAAGTCTTGTATGGCGAGGAATT
 ACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGAACGC
 TGACTACAGTcGAAGAAAAGGAATTAGAAAAAATTTGGACAAGCCATTAGG
 ATAGAAAAATCAAGAAAAATGACTCAGCTAGGGATTGATTTATCTCAGTT
 TGACCCAGACCGAGTCCGTTATTTTATGGATGACAGCGGTCTTTTCGTT
 TAAAAAATGACAGCCTTGCTTTACTAGGTGGTTATCCCAAAGCCTCGGTA
 ACTCAACTAGCCCTTGCAGACAGAACTACTCCAATGGGACTAAGTCATGA
 AAAGGTTGAATTTTCTTGTAGCCAGCTTTCATTGAAGAGCTGCGAC
 AAGTTGCCCTACGCCCTTTTACACCAAGAACTCAGCAGAGAAGATGCGGAG
 CAATTTGAAAAAGATAAAGGTAATCAGCCAGATTAACTCTCAGAGATTG
 GAAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAGTAGTTGATGAAGAAT
 TCGCGGAAAATCCACTGGTTCAAGAGATTTGGACACTTATCTCTGGGG
 TCATTGGTTTCTTATAAGGGACAGGACTTTGAGGTCAATGTCGGTCAGCGA
 TGCTCGATTGAACGGTTTGATTTCGATTGAGTTAGTCAATGACTTTTCG
 ATATCATTGAACAAAATCCAGTTCTTATGAGGACCTGGGAAGAAAGTC
 AGTCAGGCACTTCATCAGCCAAAGGCAGAACCAACACAGAGTTAGAAGA
 AGCGGACCAAGAATTAAACCTATTCTCATTCTGGAAGAGGAGCCAGTTC
 AGAGTATTGGACTATTGGAACCAAGATGATTGAGAAAATGGTTCATAACGAT
 ACTGATCTTGAAGAAACAGATAATCAAATTCCTGAAGAGGAAGTCTGCGA
 AACAAATCCAGAGATTCCAGTAACGGACTTTTATTTTCCAGAAGATTGA
 CGGACTTTTATCTAAGACTGCTAGAGATAAGTTGAGACAAACATTGTG
 GCCATTCTGTTGGTAAAAATCTAGAAGTAGAGCACCAGCAATGCTTCACC
 AAGTGAAACAAGAACTCCTTGCCAAGTATGTAGGCTGGGGTGGACTAGCCA
 ATGAAATTTTGTGATGACTATATCCAAAATTTTCTAAGGAACAGAGAAGAA
 CTGAAGAGCCTAGTCAAGATAAAGAGTATTCCGATATGAACAGTCCCTC
 CCTGACAGCCTATTACACAGACCCATCCCTGATCCGTGAGATGTGGGATA
 AGTTGGAAGAGATGGCTTTACAGGTGGCAAAATCTTAGATCCTTCCATG
 GGAACAGGGAATTTCTTGGCGCTATGCCAAAACACTTAAGAGAAAAGAG
 TGAGTTGATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCCAAAC
 ACCTTTCATCCCAATAGTCATATTGAAATTAAGGGATTGAGACGGTGGCT
 TTTAACGACAATAGTTTGATTGGTGATTTCAAATGTGCCCTTTTGCCAA
 TATACGAATTGCGGATAATAGGTACGATAGGCCCTTACATGATTTCATGACT
 ACTTTGTCAAAAAGTCACTTGATTGCTTTCATGATGGTGGACAAGTAGCG
 ATTATCTCTTCCACAGGAACATATGATAAGCGAACAGAAAACATCTTACA
 AGATATTCTGAGACAACCTGAATTTCTTGGTGGGGTTCGACTGCCCTGACT
 CTGCCCTTAAGGCCATTGACAGGAACGAGTGTCAACACGGATATGTTATT
 TTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCTTTTC
 AGGTTCCATTTCGCTATGACAAGGATAGTCGCATTTGGCTCAATCTTATT
 TTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTGAGGAAT
 TTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGATGTC
 AAGTGTGAAACAGCTCTAAATCACGTTAAGGCCCAAGAGAGATTGATA
 GAAATGAGGTCACTTAACCCAGATGTGTTGACCAACAAGTCAATGAT
 ACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTGAGTACAGTTTGG
 TTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTGAGTGC
 GAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa31161.2{*} June 20, 2002 10:41 ..

Table 70: Comparative Sequences relating to SAG 1280

| | | | | | |
|-------------------------|-------------|------------|-------------|-------------|------------|
| msa31161.2{327dnt_2603} | GgAGGGAAAA | TGAATCAAGA | AGTCTTACTA | CAAATGATGA | GAGCCACTAT |
| msa31161.2{327d_18RS21} | GnAGGGAAAA | TGAATCAAGA | AGTCTTACTA | CAAATGATGA | GAGCCACTAT |
| msa31161.2{327dnt_H36B} | GgAGGGAAAA | TGAATCAAGA | AGTCTTACTA | CAAATGATGA | GAGCCACTAT |
| Consensus | *-***** | ***** | ***** | ***** | ***** |
| | 51 | | | | 100 |
| msa31161.2{327dnt_2603} | TCCTCGTGAT | AGAGCCTTGC | TTGAGGCATT | TTTATATTAC | CAAGCAGAGC |
| msa31161.2{327d_18RS21} | TCCTCGTGAT | AGAGCCTTGC | TTGAGGCATT | TTTATATTAC | CAAGCAGAGC |
| msa31161.2{327dnt_H36B} | TCCTCGTGAT | AGAGCCTTGC | TTGAGGCATT | TTTATATTAC | CAAGCAGAGC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 101 | | | | 150 |
| msa31161.2{327dnt_2603} | ATTTTGATGA | GGAGTGGGAT | AGTCTTATTC | ATCAGTTTAT | GACCAATAGG |
| msa31161.2{327d_18RS21} | ATTTTGATGA | GGAGTGGGAT | AGTCTTATTC | ATCAGTTTAT | GACCAATAGG |
| msa31161.2{327dnt_H36B} | ATTTTGATGA | GGAGTGGGAT | AGTCTTATTC | ATCAGTTTAT | GACCAATAGG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 151 | | | | 200 |
| msa31161.2{327dnt_2603} | CAAGAAATAA | ATAAGTCTGT | TCAAGTACTT | CACITTTGAGA | CAGATGTTTC |
| msa31161.2{327d_18RS21} | CAAGAAATAA | ATAAGTCTGT | TCAAGTACTT | CACITTTGAGA | CAGATGTTTC |
| msa31161.2{327dnt_H36B} | CAAGAAATAA | ATAAGTCTGT | TCAAGTACTT | CACITTTGAGA | CAGATGTTTC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 201 | | | | 250 |
| msa31161.2{327dnt_2603} | AGCITTTGTC | CAGGCTAGTC | CTTATGATAC | TGCTCATGAT | CTATTGACCT |
| msa31161.2{327d_18RS21} | AGCITTTGTC | CAGGCTAGTC | CTTATGATAC | TGCTCATGAT | CTATTGACCT |
| msa31161.2{327dnt_H36B} | AGCITTTGTC | CAGGCTAGTC | CTTATGATAC | TGCTCATGAT | CTATTGACCT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 251 | | | | 300 |
| msa31161.2{327dnt_2603} | ATACACAAGT | TTTCGGCCAA | AGTGGTCTTC | AAAACTAGA | TAAACTATCG |
| msa31161.2{327d_18RS21} | ATACACAAGT | TTTCGGCCAA | AGTGGTCTTC | AAAACTAGA | TAAACTATCG |
| msa31161.2{327dnt_H36B} | ATACACAAGT | TTTCGGCCAA | AGTGGTCTTC | AAAACTAGA | TAAACTATCG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 301 | | | | 350 |
| msa31161.2{327dnt_2603} | CCGTCCTGAAA | AAAACCTGGT | GATAGAAGTG | GCCTTGTTCA | ATCTGGCCAC |
| msa31161.2{327d_18RS21} | CCGTCCTGAAA | AAAACCTGGT | GATAGAAGTG | GCCTTGTTCA | ATCTGGCCAC |
| msa31161.2{327dnt_H36B} | CCGTCCTGAAA | AAAACCTGGT | GATAGAAGTG | GCCTTGTTCA | ATCTGGCCAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 351 | | | | 400 |
| msa31161.2{327dnt_2603} | TCGTTTTCAA | TTATTGGATT | CCAATGGACA | CTACCAAACC | ATATCGCCGG |
| msa31161.2{327d_18RS21} | TCGTTTTCAA | TTATTGGATT | CCAATGGACA | CTACCAAACC | ATATCGCCGG |
| msa31161.2{327dnt_H36B} | TCGTTTTCAA | TTATTGGATT | CCAATGGACA | CTACCAAACC | ATATCGCCGG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 401 | | | | 450 |
| msa31161.2{327dnt_2603} | ATTCACCTCT | ACAAAAGAGT | AGGGGAGCTA | ATTGGGTCAA | TGTGTATCGT |
| msa31161.2{327d_18RS21} | ATTCACCTCT | ACAAAAGAGT | AGGGGAGCTA | ATTGGGTCAA | TGTGTATCGT |
| msa31161.2{327dnt_H36B} | ATTCACCTCT | ACAAAAGAGT | AGGGGAGCTA | ATTGGGTCAA | TGTGTATCGT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 451 | | | | 500 |
| msa31161.2{327dnt_2603} | GTGGCTAATA | ATTTAGCGGA | TCGTATTAGT | CGAGATATTG | AACAGTTTCT |
| msa31161.2{327d_18RS21} | GTGGCTAATA | ATTTAGCGGA | TCGTATTAGT | CGAGATATTG | AACAGTTTCT |
| msa31161.2{327dnt_H36B} | GTGGCTAATA | ATTTAGCGGA | TCGTATTAGT | CGAGATATTG | AACAGTTTCT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 501 | | | | 550 |
| msa31161.2{327dnt_2603} | CTTAACCTTAC | GAGCCTGAGC | TTGAAACTAG | AGCTGATGAA | ACTGTTCTAG |
| msa31161.2{327d_18RS21} | CTTAACCTTAC | GAGCCTGAGC | TTGAAACTAG | AGCTGATGAA | ACTGTTCTAG |
| msa31161.2{327dnt_H36B} | CTTAACCTTAC | GAGCCTGAGC | TTGAAACTAG | AGCTGATGAA | ACTGTTCTAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 551 | | | | 600 |
| msa31161.2{327dnt_2603} | AAAATGAAGA | AACTGTTGAT | GAGCACAAAA | CAAGTGTTC | TCAAGCAATA |
| msa31161.2{327d_18RS21} | AAAATGAAGA | AACTGTTGAT | GAGCACAAAA | CAAGTGTTC | TCAAGCAATA |
| msa31161.2{327dnt_H36B} | AAAATGAAGA | AACTGTTGAT | GAGCACAAAA | CAAGTGTTC | TCAAGCAATA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 601 | | | | 650 |
| msa31161.2{327dnt_2603} | TCITTTTCGAG | AAGAGGGCTC | TCITGGTTATT | GCTAGTTTGG | ATGTAGATT |
| msa31161.2{327d_18RS21} | TCITTTTCGAG | AAGAGGGCTC | TCITGGTTATT | GCTAGTTTGG | ATGTAGATT |
| msa31161.2{327dnt_H36B} | TCITTTTCGAG | AAGAGGGCTC | TCITGGTTATT | GCTAGTTTGG | ATGTAGATT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 651 | | | | 700 |
| msa31161.2{327dnt_2603} | GTCTCAACTA | GATGTTCAAA | TAGGAAAAAC | CAGTCATCTG | CCAGCTTATG |
| msa31161.2{327d_18RS21} | GTCTCAACTA | GATGTTCAAA | TAGGAAAAAC | CAGTCATCTG | CCAGCTTATG |
| msa31161.2{327dnt_H36B} | GTCTCAACTA | GATGTTCAAA | TAGGAAAAAC | CAGTCATCTG | CCAGCTTATG |
| Consensus | ***** | ***** | ***** | ***** | ***** |

Table 70: Comparative Sequences relating to SAG 1280

| | | | | | | |
|-------------------------|-------------|------------|------------|------------|------------|------|
| msa31161.2{327dNt_2603} | 701 | | | | | 750 |
| | AAGAGTTATC | CTTACGACGT | AAATTTGAGA | TTCTAACATA | TTTTGACCAA | |
| | AAGAGTTATC | CTTACGACGT | AAATTTGAGA | TTCTAACATA | TTTTGACCAA | |
| | AAGAGTTATC | CTTACGACGT | AAATTTGAGA | TTCTAACATA | TTTTGACCAA | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 751 | | | | | 800 |
| | ATTTCGAAATG | AACGTTCCAA | AGTCCCAAGT | TTTAGACGAG | GTGATTTTGA | |
| | ATTTCGAAATG | AACGTTCCAA | AGTCCCAAGT | TTTAGACGAG | GTGATTTTGA | |
| | ATTTCGAAATG | AACGTTCCAA | AGTCCCAAGT | TTTAGACGAG | GTGATTTTGA | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 801 | | | | | 850 |
| | CACAGAGATG | GAAATGACAC | CAGTCTTTGA | TGGCGAGGAA | TTACTTACTT | |
| | CACAGAGATG | GAAATGACAC | CAGTCTTTGA | TGGCGAGGAA | TTACTTACTT | |
| | CACAGAGATG | GAAATGACAC | CAGTCTTTGA | TGGCGAGGAA | TTACTTACTT | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 851 | | | | | 900 |
| | ATCTCGAAGC | TGATGGCAGT | CCCTATGAGC | TGAAACGAAC | GCTGACTACA | |
| | ATCTCGAAGC | TGATGGCAGT | CCCTATGAGC | TGAAACGAAC | GCTGACTACA | |
| | ATCTCGAAGC | TGATGGCAGT | CCCTATGAGC | TGAAACGAAC | GCTGACTACA | |
| msa31161.2{327dNt_2603} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 901 | | | | | 950 |
| | GTCGAAGAAA | AGGAATTAGA | AAAAATTGGA | CAAGCCATTA | GGATAGAAAA | |
| | GTCGAAGAAA | AGGAATTAGA | AAAAATTGGA | CAAGCCATTA | GGATAGAAAA | |
| | GTCGAAGAAA | AGGAATTAGA | AAAAATTGGA | CAAGCCATTA | GGATAGAAAA | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 951 | | | | | 1000 |
| | TCAAGAAAAA | TTGACTCAGC | TAAGGATTGa | TTTATCTCAG | TTTGACCCAG | |
| | TCAAGAAAAA | TTGACTCAGC | TAAGGATTGa | TTTATCTCAG | TTTGACCCAG | |
| | TCAAGAAAAA | TTGACTCAGC | TAAGGATTGr | TTTATCTCAG | TTTGACCCAG | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 1001 | | | | | 1050 |
| | ACCGAGTCGG | TATTTTATTG | gATGCAGCAG | GTCGTtTCG | TTTAaAaAAT | |
| | ACCGAGTCGG | TATTTTATTG | gATGCAGCAG | GTCGTtTCG | TTTAaAaAAT | |
| | ACCGAGTCGG | TATTTTATTG | kATGCAGCAG | GTCGTyyTCG | TTTAwAwAAT | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 1051 | | | | | 1100 |
| | GCAGACCTTG | CTTtACTAGG | TGGTTATCCC | AAAGCCTCGG | TAACCTCACT | |
| | GCAGACCTTG | CTTtACTAGG | TGGTTATCCC | AAAGCCTCGG | TAACCTCACT | |
| | GCAGACCTTG | CTTtACTAGG | TGGTTATCCC | AAAGCCTCGG | TAACCTCACT | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 1101 | | | | | 1150 |
| | AGCCCTTGCG | ACAGAACTAC | TCCAAATGGG | ACTAAGTCAT | GAAAAGGTTG | |
| | AGCCCTTGCG | ACAGAACTAC | TCCAAATGGG | ACTAAGTCAT | GAAAAGGTTG | |
| | AGCCCTTGCG | ACAGAACTAC | TCCAAATGGG | ACTAAGTCAT | GAAAAGGTTG | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 1151 | | | | | 1200 |
| | AAATTTTCTT | TGGTAGCCAG | CTTCCATTG | AAGAGCTGCG | ACAAGTTGCC | |
| | AAATTTTCTT | TGGTAGCCAG | CTTCCATTG | AAGAGCTGCG | ACAAGTTGCC | |
| | AAATTTTCTT | TGGTAGCCAG | CTTCCATTG | AAGAGCTGCG | ACAAGTTGCC | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 1201 | | | | | 1250 |
| | TACGCCTTTT | TatACCAAGA | ACTCAGCAGA | GAAGATGCGG | AGCAATTTGA | |
| | TACGCCTTTT | TacACCAAGA | ACTCAGCAGA | GAAGATGCGG | AGCAATTTGA | |
| | TACGCCTTTT | TacACCAAGA | ACTCAGCAGA | GAAGATGCGG | AGCAATTTGA | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 1251 | | | | | 1300 |
| | AAAAGATAAA | GGTAATCAGC | CAGATTTAAC | TCTCAGAGAT | TGGAAAAGCA | |
| | AAAAGATAAA | GGTAATCAGC | CAGATTTAAC | TCTCAGAGAT | TGGAAAAGCA | |
| | AAAAGATAAA | GGTAATCAGC | CAGATTTAAC | TCTCAGAGAT | TGGAAAAGCA | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 1301 | | | | | 1350 |
| | AGCTAGAGAA | AGCTGAGGGA | AAAGAAGTAG | TTGATGAAGA | ATTTCGCGAA | |
| | AGCTAGAGAA | AGCTGAGGGA | AAAGAAGTAG | TTGATGAAGA | ATTTCGCGAA | |
| | AGCTAGAGAA | AGCTGAGGGA | AAAGAAGTAG | TTGATGAAGA | ATTTCGCGAA | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |
| msa31161.2{327dNt_2603} | 1351 | | | | | 1400 |
| | AATCCACTGG | TTCAGAGAGT | ATTGGACACT | TATCCTCTGG | GGTCATTGGT | |
| | AATCCACTGG | TTCAGAGAGT | ATTGGACACT | TATCCTCTGG | GGTCATTGGT | |
| | AATCCACTGG | TTCAGAGAGT | ATTGGACACT | TATCCTCTGG | GGTCATTGGT | |
| msa31161.2{327d_18RS21} | Consensus | ***** | ***** | ***** | ***** | |

Table 70: Comparative Sequences relating to SAG 1280

| | | | | | | |
|-------------------------|-----------|------------|-------------|------------|------------|------------|
| msa31161.2{327dNt_2603} | 1401 | TTCTTATAAG | GGACAGGACT | TTGAGGTCAT | GTCGGTCAGC | GATGCTCGAT |
| | | TTCTTATAAG | GGACAGGACT | TTGAGGTCAT | GTCGGTCAGC | GATGCTCGAT |
| | | TTCTTATAAG | GGACAGGACT | TTGAGGTCAT | GTCGGTCAGC | GATGCTCGAT |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327d_18RS21} | 1451 | TGAACGGTTT | GATTTCGGATT | GAGTTAGTCA | ATGACTTTTC | GGATATCATT |
| | | TGAACGGTTT | GATTTCGGATT | GAGTTAGTCA | ATGACTTTTC | GGATATCATT |
| | | TGAACGGTTT | GATTTCGGATT | GAGTTAGTCA | ATGACTTTTC | GGATATCATT |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327dNT_H36B} | 1501 | GAACAAAATC | CAGTTCCTTA | TGTGAGGACC | TGGGAAGAAG | TCAGTCAGGC |
| | | GAACAAAATC | CAGTTCCTTA | TGTGAGGACC | TGGGAAGAAG | TCAGTCAGGC |
| | | GAACAAAATC | CAGTTCCTTA | TGTGAGGACC | TGGGAAGAAG | TCAGTCAGGC |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327dNt_2603} | 1551 | ACTTCATCAG | CCAAAGGCAG | AACCACAAAC | AGAGTTAGAA | GAAGCGGACC |
| | | ACTTCATCAG | CCAAAGGCAG | AACCACAAAC | AGAGTTAGAA | GAAGCGGACC |
| | | ACTTCATCAG | CCAAAGGCAG | AACCACAAAC | AGAGTTAGAA | GAAGCGGACC |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327d_18RS21} | 1601 | AAGAATTAAA | CCTATTCTCA | TTTCTGGAAG | AGGAGCAGT | TCAGAGTATT |
| | | AAGAATTAAA | CCTATTCTCA | TTTCTGGAAG | AGGAGCAGT | TCAGAGTATT |
| | | AAGAATTAAA | CCTATTCTCA | TTTCTGGAAG | AGGAGCAGT | TCAGAGTATT |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327dNT_H36B} | 1651 | GGACTATTGG | AACCAGATGA | TTCAGAAAAT | GGTCATAACG | ATACTGATCT |
| | | GGACTATTGG | AACCAGATGA | TTCAGAAAAT | GGTCATAACG | ATACTGATCT |
| | | GGACTATTGG | AACCAGATGA | TTCAGAAAAT | GGTCATAACG | ATACTGATCT |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327dNt_2603} | 1701 | TGAAGAAACA | GATAATCAAA | TTCTGAAGA | GGAAGTCGTC | GAAACAATTC |
| | | TGAAGAAACA | GATAATCAAA | TTCTGAAGA | GGAAGTCGTC | GAAACAATTC |
| | | TGAAGAAACA | GATAATCAAA | TTCTGAAGA | GGAAGTCGTC | GAAACAATTC |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327d_18RS21} | 1751 | CAGAGATTCC | AGTAACGGAC | TTTTATTTTC | CAGAAGATTT | GACGGACTTT |
| | | CAGAGATTCC | AGTAACGGAC | TTTTATTTTC | CAGAAGATTT | GACGGACTTT |
| | | CAGAGATTCC | AGTAACGGAC | TTTTATTTTC | CAGAAGATTT | GACGGACTTT |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327dNT_H36B} | 1801 | TATCCTAAGA | CTGCTAGAGA | TAAGGTTGAG | ACAAACATTG | TGGCCATTTC |
| | | TATCCTAAGA | CTGCTAGAGA | TAAGGTTGAG | ACAAACATTG | TGGCCATTTC |
| | | TATCCTAAGA | CTGCTAGAGA | TAAGGTTGAG | ACAAACATTG | TGGCCATTTC |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327dNt_2603} | 1851 | TTTGGTAAAA | AATCTAGAAG | TAGAGCACCG | CAATGCTTCA | CCAAGTGAAC |
| | | TTTGGTAAAA | AATCTAGAAG | TAGAGCACCG | CAATGCTTCA | CCAAGTGAAC |
| | | TTTGGTAAAA | AATCTAGAAG | TAGAGCACCG | CAATGCTTCA | CCAAGTGAAC |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327d_18RS21} | 1901 | AAGAACTCCT | TGCCAAGTAT | GTAGGCTGGG | GTGGACTAGC | CAATGAATTT |
| | | AAGAACTCCT | TGCCAAGTAT | GTAGGCTGGG | GTGGACTAGC | CAATGAATTT |
| | | AAGAACTCCT | TGCCAAGTAT | GTAGGCTGGG | GTGGACTAGC | CAATGAATTT |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327dNT_H36B} | 1951 | TTTGATGACT | ATAATCCAAA | ATTTTCTAAG | GAACGAGAAG | AACTGAAGAG |
| | | TTTGATGACT | ATAATCCAAA | ATTTTCTAAG | GAACGAGAAG | AACTGAAGAG |
| | | TTTGATGACT | ATAATCCAAA | ATTTTCTAAG | GAACGAGAAG | AACTGAAGAG |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327dNt_2603} | 2001 | CCTAGTCACA | GATAAAGAGT | ATTCGGATAT | GAAACAGTCC | TCCCTGACAG |
| | | CCTAGTCACA | GATAAAGAGT | ATTCGGATAT | GAAACAGTCC | TCCCTGACAG |
| | | CCTAGTCACA | GATAAAGAGT | ATTCGGATAT | GAAACAGTCC | TCCCTGACAG |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327d_18RS21} | 2051 | CCTATTACAC | AGACCCATCC | CTGATCCGTC | AGATGTGGGA | TAAGTTGGAA |
| | | CCTATTACAC | AGACCCATCC | CTGATCCGTC | AGATGTGGGA | TAAGTTGGAA |
| | | CCTATTACAC | AGACCCATCC | CTGATCCGTC | AGATGTGGGA | TAAGTTGGAA |
| | Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31161.2{327dNT_H36B} | 2100 | CCTATTACAC | AGACCCATCC | CTGATCCGTC | AGATGTGGGA | TAAGTTGGAA |
| | | CCTATTACAC | AGACCCATCC | CTGATCCGTC | AGATGTGGGA | TAAGTTGGAA |
| | | CCTATTACAC | AGACCCATCC | CTGATCCGTC | AGATGTGGGA | TAAGTTGGAA |
| | Consensus | ***** | ***** | ***** | ***** | ***** |

Table 70: Comparative Sequences relating to SAG 1280

| | | | | | |
|-------------------------|------------|------------|------------|------------|------------|
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2101 | | | | 2150 |
| msa31161.2{327dNt_2603} | AGAGATGGCT | TTACAGGTGG | CAAAATCCTA | GATCCTTCCA | TGGGAACAGG |
| msa31161.2{327d_18RS21} | AGAGATGGCT | TTACAGGTGG | CAAAATCCTA | GATCCTTCCA | TGGGAACAGG |
| msa31161.2{327dNT_H36B} | AGAGATGGCT | TTACAGGTGG | CAAAATCCTA | GATCCTTCCA | TGGGAACAGG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2151 | | | | 2200 |
| msa31161.2{327dNt_2603} | GAATTTCTTT | GCGGCTATGC | CAAAACACTT | AAGAGAAAAG | AGTGAGTTGT |
| msa31161.2{327d_18RS21} | GAATTTCTTT | GCGGCTATGC | CAAAACACTT | AAGAGAAAAG | AGTGAGTTGT |
| msa31161.2{327dNT_H36B} | GAATTTCTTT | GCGGCTATGC | CAAAACACTT | AAGAGAAAAG | AGTGAGTTGT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2201 | | | | 2250 |
| msa31161.2{327dNt_2603} | ATGGCGTAGA | GTTAGATACT | ATTACAGGAG | CTATTGCCAA | ACACCTTCAT |
| msa31161.2{327d_18RS21} | ATGGCGTAGA | GTTAGATACT | ATTACAGGAG | CTATTGCCAA | ACACCTTCAT |
| msa31161.2{327dNT_H36B} | ATGGCGTAGA | GTTAGATACT | ATTACAGGAG | CTATTGCCAA | ACACCTTCAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2251 | | | | 2300 |
| msa31161.2{327dNt_2603} | CCCAATAGTC | ATATTGAAAT | TAAGGGATTT | GAGACGGTGG | CTTTTAACGA |
| msa31161.2{327d_18RS21} | CCCAATAGTC | ATATTGAAAT | TAAGGGATTT | GAGACGGTGG | CTTTTAACGA |
| msa31161.2{327dNT_H36B} | CCCAATAGTC | ATATTGAAAT | TAAGGGATTT | GAGACGGTGG | CTTTTAACGA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2301 | | | | 2350 |
| msa31161.2{327dNt_2603} | CAATAGTTTT | GATTTGGTGA | TTTCAAATGT | GCCCTTTGCC | AATATACGAA |
| msa31161.2{327d_18RS21} | CAATAGTTTT | GATTTGGTGA | TTTCAAATGT | GCCCTTTGCC | AATATACGAA |
| msa31161.2{327dNT_H36B} | CAATAGTTTT | GATTTGGTGA | TTTCAAATGT | GCCCTTTGCC | AATATACGAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2351 | | | | 2400 |
| msa31161.2{327dNt_2603} | TTGCGGATAA | TAGGTACGAT | AGGCCTTACA | TGATTCATGA | CTACTTTGTC |
| msa31161.2{327d_18RS21} | TTGCGGATAA | TAGGTACGAT | AGGCCTTACA | TGATTCATGA | CTACTTTGTC |
| msa31161.2{327dNT_H36B} | TTGCGGATAA | TAGGTACGAT | AGGCCTTACA | TGATTCATGA | CTACTTTGTC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2401 | | | | 2450 |
| msa31161.2{327dNt_2603} | AAAAAGTCAC | TTGATTGCT | TCATGATGGT | GGACAAGTAG | CGATTATCTC |
| msa31161.2{327d_18RS21} | AAAAAGTCAC | TTGATTGCT | TCATGATGGT | GGACAAGTAG | CGATTATCTC |
| msa31161.2{327dNT_H36B} | AAAAAGTCAC | TTGATTGCT | TCATGATGGT | GGACAAGTAG | CGATTATCTC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2451 | | | | 2500 |
| msa31161.2{327dNt_2603} | TTCCACAGGA | ACTATGGATA | AGCGAACAGA | AAACATCTTA | CAAGATATTC |
| msa31161.2{327d_18RS21} | TTCCACAGGA | ACTATGGATA | AGCGAACAGA | AAACATCTTA | CAAGATATTC |
| msa31161.2{327dNT_H36B} | TTCCACAGGA | ACTATGGATA | AGCGAACAGA | AAACATCTTA | CAAGATATTC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2501 | | | | 2550 |
| msa31161.2{327dNt_2603} | GTGAGACAAC | TGAATTTCTT | GGTGGGGTTC | GACTGCCTGA | CTCTGCCTTT |
| msa31161.2{327d_18RS21} | GTGAGACAAC | TGAATTTCTT | GGTGGGGTTC | GACTGCCTGA | CTCTGCCTTT |
| msa31161.2{327dNT_H36B} | GTGAGACAAC | TGAATTTCTT | GGTGGGGTTC | GACTGCCTGA | CTCTGCCTTT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2551 | | | | 2600 |
| msa31161.2{327dNt_2603} | AAGGCCATTG | CAGGAACGAG | TGTCACAACG | GATATGTTAT | TCITCCAGAA |
| msa31161.2{327d_18RS21} | AAGGCCATTG | CAGGAACGAG | TGTCACAACG | GATATGTTAT | TCITCCAGAA |
| msa31161.2{327dNT_H36B} | AAGGCCATTG | CAGGAACGAG | TGTCACAACG | GATATGTTAT | TCITCCAGAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2601 | | | | 2650 |
| msa31161.2{327dNt_2603} | ACACTTAGAC | AAGGGATATG | TGGCAGACGA | TTTAGCCTTT | TCAGGTTCCA |
| msa31161.2{327d_18RS21} | ACACTTAGAC | AAGGGATATG | TGGCAGACGA | TTTAGCCTTT | TCAGGTTCCA |
| msa31161.2{327dNT_H36B} | ACACTTAGAC | AAGGGATATG | TGGCAGACGA | TTTAGCCTTT | TCAGGTTCCA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2651 | | | | 2700 |
| msa31161.2{327dNt_2603} | TTCGCTATGA | CAAGGATAGT | CGCATTTGGC | TCAATCCTTA | TTTTGATGGA |
| msa31161.2{327d_18RS21} | TTCGCTATGA | CAAGGATAGT | CGCATTTGGC | TCAATCCTTA | TTTTGATGGA |
| msa31161.2{327dNT_H36B} | TTCGCTATGA | CAAGGATAGT | CGCATTTGGC | TCAATCCTTA | TTTTGATGGA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2701 | | | | 2750 |
| msa31161.2{327dNt_2603} | GAATACAATA | GCCAGGTGCT | AGGAACCTAC | GAGGTCAGGA | ATTTTAACGG |
| msa31161.2{327d_18RS21} | GAATACAATA | GCCAGGTGCT | AGGAACCTAC | GAGGTCAGGA | ATTTTAACGG |
| msa31161.2{327dNT_H36B} | GAATACAATA | GCCAGGTGCT | AGGAACCTAC | GAGGTCAGGA | ATTTTAACGG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2751 | | | | 2800 |
| msa31161.2{327dNt_2603} | AGGAACACTT | TCTGTTAAGG | GGACTAGTGA | TGACTTGATT | GCAAGTGTG |
| msa31161.2{327d_18RS21} | AGGAACACTT | TCTGTTAAGG | GGACTAGTGA | TGACTTGATT | GCAAGTGTG |

Table 70: Comparative Sequences relating to SAG 1280

| | | | | | |
|-------------------------|------------|------------|------------|-------------|------------|
| msa31161.2{327dnt_H36B} | AGGAACACTT | TCTGTTAAGG | GGACTAGTGA | TGACTTGATT | GCAAGTGTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2801 | | | | 2850 |
| msa31161.2{327dnt_2603} | AAACAGCTCT | AAATCACGTT | AAGGCCCAA | GAGAGATTGA | TAGAAATGAG |
| msa31161.2{327d_18RS21} | AAACAGCTCT | AAATCACGTT | AAGGCCCAA | GAGAGATTGA | TAGAAATGAG |
| msa31161.2{327dnt_H36B} | AAACAGCTCT | AAATCACGTT | AAGGCCCAA | GAGAGATTGA | TAGAAATGAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2851 | | | | 2900 |
| msa31161.2{327dnt_2603} | GTCATCATT | ACCCAGATGT | GTTGACCAA | CAAGTCAATG | ATACCTCCAT |
| msa31161.2{327d_18RS21} | GTCATCATT | ACCCAGATGT | GTTGACCAA | CAAGTCAATG | ATACCTCCAT |
| msa31161.2{327dnt_H36B} | GTCATCATT | ACCCAGATGT | GTTGACCAA | CAAGTCAATG | ATACCTCCAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2901 | | | | 2950 |
| msa31161.2{327dnt_2603} | TCCAGCTGAA | ATGAGGGAAA | ATCTAGGTCA | GTACAGTTT | GGTTATCAGG |
| msa31161.2{327d_18RS21} | TCCAGCTGAA | ATGAGGGAAA | ATCTAGGTCA | GTACAGTTT | GGTTATCAGG |
| msa31161.2{327dnt_H36B} | TCCAGCTGAA | ATGAGGGAAA | ATCTAGGTCA | GTACAGTTT | GGTTATCAGG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 2951 | | | | 3000 |
| msa31161.2{327dnt_2603} | GGTCTACAGT | TTACTATCGA | GATAACAAAG | GCATTTCGAGT | CGGAACCAAG |
| msa31161.2{327d_18RS21} | GGTCTACAGT | TTACTATCGA | GATAACAAAG | GCATTTCGAGT | CGGAACCAAG |
| msa31161.2{327dnt_H36B} | GGTCTACAGT | TTACTATCGA | GATAACAAAG | GCATTTCGAGT | CGGAACCAAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 3001 | | | | 3033 |
| msa31161.2{327dnt_2603} | ACGGAAGAAA | TCAGTTACTA | TGTCGATGAA | GAG | |
| msa31161.2{327d_18RS21} | ACGGAAGAAA | TCAGTTACTA | TGTCGATGAA | GAG | |
| msa31161.2{327dnt_H36B} | ACGGAAGAAA | TCAGTTACTA | TGTCGATGAA | GAG | |
| Consensus | ***** | ***** | ***** | *** | |

SEQ ID. NO. 7004

STRAIN H36B frame: 1

GGKMNQEVLLQMMRATIPDRALLEAFLLYQAEHFDEWDLSLIHQFMTNRQEIINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSTVHQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHPAYEELSRLR
KFEILTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAIRIENQEKLTQLXIXLSQFDPDRVGILLXAGRXRLKNADLASLGYP
KASVTQLALATELLQMLSHKVEFFFGSLSIEELRQVAYAFHQLSREDAEQFEKDK
GNQPDLTLRDWKSKLEKAEKGVVDEEFAENPLVQVRVLDITYPLGSLVSYKGQDFEVM SVS
DARLNGLRIRIELVNDFSDI IEQNPVLYVRTWEEVSQALHQPKAEPQTELEADQELNLF
FLEELVQSIGLLEPDDSENGHNDTLEETDNIPEEEVETIPEIPVTDIFYFPEDLTDF
YPKTARDKVETINIVAIRLVKNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPSMG TG NFF
AAMPKHLREKSELYGVELDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVI SNVPFA
NIRIADNRYDRPYMIHDFVFKKSLDLLHDGGQVAIISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLKGYVADDLAFSGSIRYDKDSRIWLNPFYFDG
EYNSQVLGTIEVRNFGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVI INPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYVRDNGKIRVGTKTEEISYYVDEE

SEQ ID. NO. 7005

STRAIN 18RS21 frame: 1

GGKMNQEVLLQMMRATIPDRALLEAFLLYQAEHFDEWDLSLIHQFMTNRQEIINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSTVHQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHPAYEELSRLR
KFEILTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAIRIENQEKLTQLGIDLSQFDPDRVGILLDAAGFRFLKNADLALLGGYP
KASVTQLALATELLQMLSHKVEFFFGSLSIEELRQVAYAFHQLSREDAEQFEKDK
GNQPDLTLRDWKSKLEKAEKGVVDEEFAENPLVQVRVLDITYPLGSLVSYKGQDFEVM SVS
DARLNGLRIRIELVNDFSDI IEQNPVLYVRTWEEVSQALHQPKAEPQTELEADQELNLF
FLEEPVQSIGLLEPDDSENGHNDTLEETDNIPEEEVETIPEIPVTDIFYFPEDLTDF
YPKTARDKVETINIVAIRLVKNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPSMG TG NFF
AAMPKHLREKSELYGVELDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVI SNVPFA
NIRIADNRYDRPYMIHDFVFKKSLDLLHDGGQVAIISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLKGYVADDLAFSGSIRYDKDSRIWLNPFYFDG
EYNSQVLGTIEVRNFGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVI INPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYVRDNGKIRVGTKTEEISYYVDEE

SEQ ID. NO. 7006

STRAIN 2603 frame: 1

GGKMNQEVLLQMMRATIPDRALLEAFLLYQAEHFDEWDLSLIHQFMTNRQEIINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSTVHQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHPAYEELSRLR
KFEILTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAIRIENQEKLTQLGIDLSQFDPDRVGILLDAAGFRFLKNADLALLGGYP
KASVTQLALATELLQMLSHKVEFFFGSLSIEELRQVAYAFHQLSREDAEQFEKDK
GNQPDLTLRDWKSKLEKAEKGVVDEEFAENPLVQVRVLDITYPLGSLVSYKGQDFEVM SVS

Table 70: Comparative Sequences relating to SAG 1280

DARLNGLIRIELVNDFSDIIEQNPVLYVRTWEEVSQALHQPKEPQTELEBDAQELNLFSS
 FLEEEpVQSIGLLEPDDSENGHNDTDLEETDNQIPEEEVETIPEIPVTDFFPEDLTDF
 YPKTARDKVTNIVAIRLVNLEVEHRNASPEQELLAKYVGWGGLANEFFDDYNPKFSK
 EREELKSLVTDKEYSDMKQSSLTAYYTDPSLRIRQMWKLERDGTGGKILDPMSGTGNFF
 AAMPKHLREKSELYGVELDTITGAIKHLHPNSHIEIKGFETVAFNDNSFDLVISNVFFA
 NIRIADNRYDRPYMIHDYFVKSLDLLHDGGQVAIISSTGTMDKRTENILQDIRETTEFL
 GGVRLPDSAFKAIAGTSVTMDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPFYDG
 EYNSQVLGTYEVRNFGGTLVSVKGTSDDLIASVETALNHVKAPREIDRNEVINPDLVTK
 QVNDTSIPAEEMRENLGQYSPGYQGSTVYIRDNGKIRVGTKEEISYYVDEE

PRETTY of: /biotmp/msa23816.2{*} June 20, 2002 11:04 ..

| | | |
|-------------------------|---|-----|
| msa23816.2{327dnt_H36B} | 1 | 50 |
| msa23816.2{327dnt_2603} | gGKMNQEVLL QMMRATIPRD RALLEAFLLY QAEEHFDEEWD SLIHQFMNTR | |
| msa23816.2{327d_18RS21} | gGKMNQEVLL QMMRATIPRD RALLEAFLLY QAEEHFDEEWD SLIHQFMNTR | |
| Consensus | -***** | |
| msa23816.2{327dnt_H36B} | 51 | 100 |
| msa23816.2{327dnt_2603} | QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS | |
| msa23816.2{327d_18RS21} | QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS | |
| Consensus | ***** | |
| msa23816.2{327dnt_H36B} | 101 | 150 |
| msa23816.2{327dnt_2603} | PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RANLVNVYR | |
| msa23816.2{327d_18RS21} | PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RANLVNVYR | |
| Consensus | ***** | |
| msa23816.2{327dnt_H36B} | 151 | 200 |
| msa23816.2{327dnt_2603} | VANNLADRIS RDIEQFLITY EPELETRADE TVLENEETVD EHKTSVHQAI | |
| msa23816.2{327d_18RS21} | VANNLADRIS RDIEQFLITY EPELETRADE TVLENEETVD EHKTSVHQAI | |
| Consensus | ***** | |
| msa23816.2{327dnt_H36B} | 201 | 250 |
| msa23816.2{327dnt_2603} | SFREGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ | |
| msa23816.2{327d_18RS21} | SFREGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ | |
| Consensus | ***** | |
| msa23816.2{327dnt_H36B} | 251 | 300 |
| msa23816.2{327dnt_2603} | IRNERSKVPS FRRGDFDTEM EMTPVFDGEE LLTYLEADGS PYELKRTLIT | |
| msa23816.2{327d_18RS21} | IRNERSKVPS FRRGDFDTEM EMTPVFDGEE LLTYLEADGS PYELKRTLIT | |
| Consensus | ***** | |
| msa23816.2{327dnt_H36B} | 301 | 350 |
| msa23816.2{327dnt_2603} | VEEKELEKIG QAIRIENQEK LTQLxIxLSQ FDPDRVIGILL xAAGRrRLxN | |
| msa23816.2{327d_18RS21} | VEEKELEKIG QAIRIENQEK LTQLgIdLSQ FDPDRVIGILL dAAGRrRLkN | |
| Consensus | ***** | |
| msa23816.2{327dnt_H36B} | 351 | 400 |
| msa23816.2{327dnt_2603} | ADLAsLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA | |
| msa23816.2{327d_18RS21} | ADLAlLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA | |
| Consensus | ****-***** | |
| msa23816.2{327dnt_H36B} | 401 | 450 |
| msa23816.2{327dnt_2603} | YAFhQELSR EDAAEQFEKDK GNQPDLTlRD WSKLEKAEG KEVVDEEFAB | |
| msa23816.2{327d_18RS21} | YAFlyQELSR EDAAEQFEKDK GNQPDLTlRD WSKLEKAEG KEVVDEEFAB | |
| Consensus | ****-***** | |
| msa23816.2{327dnt_H36B} | 451 | 500 |
| msa23816.2{327dnt_2603} | NPLVQRVLDI YPLGSLVSYK QDQFEVMSVS DARLNGLIRI ELVNDFSDI | |
| msa23816.2{327d_18RS21} | NPLVQRVLDI YPLGSLVSYK QDQFEVMSVS DARLNGLIRI ELVNDFSDI | |
| Consensus | ***** | |
| msa23816.2{327dnt_H36B} | 501 | 550 |
| msa23816.2{327dnt_2603} | EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFSS FLEEEpVQSI | |
| msa23816.2{327d_18RS21} | EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFSS FLEEEpVQSI | |
| Consensus | ***** | |
| msa23816.2{327dnt_H36B} | 551 | 600 |
| msa23816.2{327dnt_2603} | GLLEPDDSEN GHNDTDLEET DNQIPEEEV ETIPEIPVTD FYFPEDLTDF | |
| msa23816.2{327d_18RS21} | GLLEPDDSEN GHNDTDLEET DNQIPEEEV ETIPEIPVTD FYFPEDLTDF | |
| Consensus | ***** | |

Table 70: Comparative Sequences relating to SAG 1280

| | | | | | |
|-------------------------|------------|------------|------------|------------|-------------|
| | 601 | | | | 650 |
| msa23816.2{327dNT_H36B} | YPKTARDKVE | TNIVAIRLVK | NLEVEHRNAS | PSEQELLAKY | VGWGGLANEF |
| msa23816.2{327dNT_2603} | YPKTARDKVE | TNIVAIRLVK | NLEVEHRNAS | PSEQELLAKY | VGWGGLANEF |
| msa23816.2{327d_18RS21} | YPKTARDKVE | TNIVAIRLVK | NLEVEHRNAS | PSEQELLAKY | VGWGGLANEF |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 651 | | | | 700 |
| msa23816.2{327dNT_H36B} | FDDYNPKFSK | EREELKSLVT | DKEYSDMKQS | SLTAYYTDPS | LIRQMWDKLE |
| msa23816.2{327dNT_2603} | FDDYNPKFSK | EREELKSLVT | DKEYSDMKQS | SLTAYYTDPS | LIRQMWDKLE |
| msa23816.2{327d_18RS21} | FDDYNPKFSK | EREELKSLVT | DKEYSDMKQS | SLTAYYTDPS | LIRQMWDKLE |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 701 | | | | 750 |
| msa23816.2{327dNT_H36B} | RDGFTGGKIL | DPSMGTGNFF | AAMPKHLREK | SELYGVELDT | ITGAIAKHLH |
| msa23816.2{327dNT_2603} | RDGFTGGKIL | DPSMGTGNFF | AAMPKHLREK | SELYGVELDT | ITGAIAKHLH |
| msa23816.2{327d_18RS21} | RDGFTGGKIL | DPSMGTGNFF | AAMPKHLREK | SELYGVELDT | ITGAIAKHLH |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 751 | | | | 800 |
| msa23816.2{327dNT_H36B} | PNSHIEIKGF | ETVAFNDNSF | DLVISNVPFA | NIRIADNRYD | RPYMIHDYFV |
| msa23816.2{327dNT_2603} | PNSHIEIKGF | ETVAFNDNSF | DLVISNVPFA | NIRIADNRYD | RPYMIHDYFV |
| msa23816.2{327d_18RS21} | PNSHIEIKGF | ETVAFNDNSF | DLVISNVPFA | NIRIADNRYD | RPYMIHDYFV |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 801 | | | | 850 |
| msa23816.2{327dNT_H36B} | KKSLDLLHDG | GQVAIISSTG | TMDKRTENIL | QDIRETTEFL | GGVRLPDSAF |
| msa23816.2{327dNT_2603} | KKSLDLLHDG | GQVAIISSTG | TMDKRTENIL | QDIRETTEFL | GGVRLPDSAF |
| msa23816.2{327d_18RS21} | KKSLDLLHDG | GQVAIISSTG | TMDKRTENIL | QDIRETTEFL | GGVRLPDSAF |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 851 | | | | 900 |
| msa23816.2{327dNT_H36B} | KAIAGTSVTT | DMLFFQKHL | KGYVADDLAF | SGSIRYDKDS | RIWLNPFYFDG |
| msa23816.2{327dNT_2603} | KAIAGTSVTT | DMLFFQKHL | KGYVADDLAF | SGSIRYDKDS | RIWLNPFYFDG |
| msa23816.2{327d_18RS21} | KAIAGTSVTT | DMLFFQKHL | KGYVADDLAF | SGSIRYDKDS | RIWLNPFYFDG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 901 | | | | 950 |
| msa23816.2{327dNT_H36B} | EYNSQVLGTY | EVRFNNGGTL | SVKGTSDDLI | ASVETALNHV | KAPREIDRNE |
| msa23816.2{327dNT_2603} | EYNSQVLGTY | EVRFNNGGTL | SVKGTSDDLI | ASVETALNHV | KAPREIDRNE |
| msa23816.2{327d_18RS21} | EYNSQVLGTY | EVRFNNGGTL | SVKGTSDDLI | ASVETALNHV | KAPREIDRNE |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 951 | | | | 1000 |
| msa23816.2{327dNT_H36B} | VIINPDVLTK | QVNDTSIPAE | MRENLGQYSF | GYQGSTVYYR | DNKGIRVGTK |
| msa23816.2{327dNT_2603} | VIINPDVLTK | QVNDTSIPAE | MRENLGQYSF | GYQGSTVYYR | DNKGIRVGTK |
| msa23816.2{327d_18RS21} | VIINPDVLTK | QVNDTSIPAE | MRENLGQYSF | GYQGSTVYYR | DNKGIRVGTK |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 1001 | 1011 | | | |
| msa23816.2{327dNT_H36B} | TEEISYYVDE | E | | | |
| msa23816.2{327dNT_2603} | TEEISYYVDE | E | | | |
| msa23816.2{327d_18RS21} | TEEISYYVDE | E | | | |
| Consensus | ***** | * | | | |

Table 71: Comparative Sequences relating to SAG1333

SEQ ID NO. 7101

STRAIN 2603

ATGAAAAAGAAAATTTATTTGAAAAGTAGTGTCTTGGTTTAGTCGCTGGGACTTCTATTT
 ATGTTCTCAAGCGTGTTCGCGGACCAAGTCCGCTGTCCTGATGGAAGTTAGGCGTCAATGACTTT
 CATGGTGCACCTTGACAATCTGGAACAGCAAAATATGCTGATGGAAGTTGCTAATGCT
 GGTACTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAACAACT
 AACCCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGTTGGAGCAAGTCCAGCC
 AACTCTGGGCTTCTTCAAGATGAACCAACTGTCAAAAATTTTAAATGCAATGAATGTTGAG
 TATGGCACATTGGGTAACCATGAATTTGATGAAGGGTTGGCAGAATATAATCGTATCGTT
 ACTGGTAAAGCCCCGCTCCAGATTCTAATATTATAATATTACGAAATCATACCCACAT
 GAAGCTGCAAAACAAAGAAATTTAGTGGCAAAATGTTATGATAAAGTTAAACAAACAAAT
 CCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCCTGTAATAACAAAGTGTGAAC
 GTTGGCTTTATCGGGATTGTCAACCAAGACATCCCAACCTTGTCTTACGTAAAAATTTAT
 GAACAATATGAATTTTAGATGAAGCTGAAACAATCGTTAAATACGCCAAAGAAATTACAA
 GCTAAAAATGTCAGAGCTATTGTAGTTCTCGCACATGTACCTGCAACAAGTAAAAATGAT
 ATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTGAAAAAT
 AGCGTAGATATTGTCTTGTCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAA
 ACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGTCTTA
 GATACTGATACACAAGATTTCATTGAGACCCCTTCAAGTAAAGTAATTGCAGTTGCTCCT
 GGTAAAAAAGCAGGTAGTCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTT
 AAACAAGTAACAGAAAGCAGCAAAATTTGGTACTGCGAGGTAAAGTGTATGATTACGCGTTCT
 GTTGATCAAGATAATGTTAGTCCGCTAGGCGACCTCATCAGAGGCTCAACTAGCAATT
 GCTCGAAAAAGCTGGCCAGATATCGATTTTGGCATGACAATAATGGTGGCAATTCTGCT
 GACTTACTCATCAAAACCATGATGGAACAATCACTGGGGAGCTGCACAAGCAGTTCAACCT
 TTTGGTAAATATCTTACAAGTCTGCGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAAC
 GAACAATACGACCAAAACAAATTTCTTCTTCAATAGCTGGTCTGCGATACACTTAC
 ACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAAGCTTATAAATCA
 AATGGTGAGGAAATCAATCTGATGCAAAATACAAATTAGTTATCAATGACTTTTTATTC
 GGTGGTGGTGTGATGGCTTTGCAAGCTTCAGAAATGCCAACTTTAGAGGCAATTAACCCC
 GATACAGAGGTATTATGGCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGC
 GTTCCAATAATAAACCTTAAATCTATGTCACTATGAAGATGGTTAATGAACTATTACA
 CAAAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGATCGACAAGGAAATATT
 GTAGCAACAAGAGATTGTATCAGACACTTTAAACCAACAAATCAAAATCTACAAAAATC
 AACCCGTAACTTCAAAATTCACAAAAACAATTAACCAATTTACAGCTATTAAACCTATG
 AGAAATTTATGGCAACCATCAAACTCCACTACTGTAAATCAAAACAATTACCAAAAAACA
 AACTCTGAATATGGACAATCATTCCTTATGTCTGTCTTGGTGTGGACTTATAGGAATT
 GCTTTAAATACAAAGAAAAAACATATGAAA

SEQ ID NO. 7102

STRAIN 090

AAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGAC
 AATACTGGAACAGCAAAATATGCTGACGGAAGTTACTAATGCTGGCAC
 TGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAAC
 AAATAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGGTT
 GGAGCAAGTCCAGCTAACTCAGGGCTTCTCAAGATGAACCAACCGTTAA
 AACATTTAATGCAATGAATGTTGAGTATGGCACTTAGGTAACCATGAAT
 TTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCCCT
 GCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAGC
 TGCAAAACAGAAATTTAGTGGCAACGTTATTGATAAAGTTAAACAAAC
 AAATCCCTTACAATTTGAAACCTTACGCTATTAAAAATATTCCTGTAAAT
 AACAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATCCC
 AAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTATAGTGAAG
 CTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAATGTCAAG
 GCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATATTGC
 TGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTG
 AAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAAT
 GGTCTTGTGGTAAAACTCGCATTGTACAAGCGCTCTCTCAAGGAAAAGC
 CTATGCTGACGTACGTGGTGTCTTAGATACGATACACAAGATTTCATTG
 AAACCCCTTACGCTAAAGTAGTTGAGTGTCTCTGGTAAAAAAGCAGGT
 AGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACA
 AGTAACAGAAGCTAAATTTGTTACTGCCGAGGTAAGTGGCATGATTACGC
 GTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCGACCTCATCAGAG
 GCTCAACTAGCAATTTGCTCGAAAAAGCTGGCCAGATATCGATTTTGGCCAT
 GACAAATAATGGTGGCATTCTGTGCTGACTTACTCATCAACCAAGATGGAA
 CAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTA
 CAAGTCGTGCAAAATTTAGTGGTAGAGATCTTTATAAAGCACTCAACGAACA
 ATACGACCAAAACAAATTTCTTCTTCAAAATAGCTGGTCTGCGATACA
 CTTACACAGATAATAAAGAGGGCGGAGAAAGAACCACTTTAAAGTTGTA
 AAAGCTTATAAATCAATGGTGAAGAAATCAATCTGATGCAAAATACAA
 ATTAGTTATCAATGACTTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAGCT
 TCAGAAATGCCAACTTCTAGGAGCCATTAAATCCCGATACAGAGGTATT
 ATGGCTTATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCC
 AAATAATAAACCTTAAATCTATGTCTACTATGAAGATGGTTAATGAACTA
 TTACACAAATGATGGTACACATAGCATTATTAAGAACTTTATTAGAT
 CGACAAGGAAATATTGTAGCAAGAGATTGTATCAGACACTTTAAACCA
 AACAAATCAAAATCTACAAAAATCAACCTGTAACTACAATTCAAAAA
 AACATTACCAATTTACAGCTATTAAACCTATGAGAAATTATGGCAAA
 CCATCAACTCCACTACTGTAAATCAAAACA

SEQ ID NO. 7103

STRAIN A909

GCGTCAATGACTTTTCATGGTGCCTTGACAATACTGGAACAGCAAAATATG
 CCTGACGGAAGTTACTAATGCTGGCACTGCTGCTCAATTAGATGCTTA

Table 71: Comparative Sequences relating to SAG1333

TATGGATGATGCTCAAAAAGATTTCAAACAACTAACCTAATGGTGAAA
GCATTAGAGTTTCAAGCTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCA
GGGCTTCTTCAAGATGAACCAACCGTTAAAAACATTTAATGCAATGAATGT
TGAGTATGGCACATTAGGTAAACCATGAATTTGATGAAGGTTTGGCAGAAT
ACAATCGTATCGTTACTGGAAGGGCCCTGCTCCaGaTTCTAATATAAAT
AATATTACGAAATCATACCCACAGAGCTGCAAAACAAGAAATTTAGT
GGCAAACGTTATTGATAAAGTTAAACAAACAAATCCCTTACAATTGGAAAC
CTTACACTATTAAAAATATTCTGTAAATAACAAAAGTGTGAACGTTGGC
TTTATCGGAATCGTTACCAAGACATCCCAAACTTGTCTTACGTAAAAA
TTATGAACAATATGAATTTTATAGATGAAGCTGAAACAAATCGTTAAATACG
CCAAAGAATTACAAGCTAAAAATGTCAAGGCTATTGTAGTCCTTGCTCAT
GTACCTGCAACAAGCAAGGATGATATTGCTGAAGGTGAAGCAGCAGAAAT
GATGAAAAAAGTCAATCAACTCTTCCCTGAAAAATAGCGTAGATATTGTCT
TTGCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAAACTCGT
ATTGTACAAGCGCTCTCAAGGAAAAGCCTATGCTGATGATCGTGGTGT
CCTAGATACTGATACACAAGATTTCAATTGAAACCCCTTCAGCTAAAGTAA
TTGCAAGTTGCTCTGTTAAAAAAGAGGTAGTGCCGATATTCAAGCCATT
GTTGACCAAGCTAATACTATCGTTAAACCAAGTAACAGAAGCTAAAAATGG
TACTGCCAGGTAAAGTGGCATGATTACGCGTTCTGTTGATCAAGATAATG
TTAGTCCGGTAGGCAGCTCATCACAGAGGCTCAACTAGCAATTGCTCGA
AAAAGCTGGCCAGATATCGATTTTGCCATGACAAATAATGGTGGCATTGG
TGCTGACTTACTCATCAACAGATGGAACAATCACCTGGGGAGCTGCAC
AAGCAGTTCAACCTTTTGGTAATATCTTACAAGTCTGCAAAATTAAGTGT
AGAGATCTTTATAAAGCACTCAACGAACAATACGACCAAAAAACAAATTT
CTTCTTCAAATAGCTGGTCTGCGATACACTTACACAGATAATAAAGAGG
GCGGGGAAGAAACACCATTTAAAGTTGTAAGAGCTTATAAATCAAATGGT
GAGGAAATCAATCCTGATGCAAAATACAAATAGTTATCAATGACTTTTT
ATTGCGTGGTGGTGGTGGCTTTGCAAGCTTCAGAAATGCCAACTCTAG
GAGCCATTAAATCCCGATACAGAGGTATTTATGGCCTATATCACTGATTTA
GAAAAAGCTGGTAAAAAAGTGAAGCTTCCAAATAATAAACCTAAAAATCTA
TGTCACTATGAAGATGGTTAATGAACTATTACACAAATGATGGTACAT
ATAGCATTATTAAGAACTTTATTAGATCGACAAGGAAATATTGTAGCA
CAAGAGATTGTATCAGACACTTTAAACCAACAAATCAAATCTACAAA
AATCAACCTGTAACTACAATTACAAAAAACAAATTACACCAATTTACAG
CTATTAAACCTATGAGAAATATGGCAAAACCATCAAACCTCCACTACTGTA
AAATCAAAACAA

SEQ ID NO. 7104

STRAIN H36B

CCAAGTCCGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCATTG
ACAATAGTGGAAACAGCAAATATGCTGACGGAAAAGTTACTAATGCTGGC
ACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAA
ACAAACTAACCTTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGAATGG
TTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTT
AAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGA
ATTTGATGAAGGTTTGGCAGAATCAATCGTATCGTTACTGGAAAGGCC
CTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACAGAA
GCTGCAAAACAAGAAATTTGATGTCGCAACGTTATTGATAAAGTTAACAA
ACAAATCCCTTACAAATGGAAACCTTACACTATTAAAAATATTCTGTAA
ATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATC
CCAAACCTTGTCTTACGTAAAAATATGAACAATATGAATTTTATAGATGA
AGCTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAATGTCA
AGGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATATT
GCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCC
TGAAAAATAGCGTAGATATTGCTTTGCTGGACACAATCATCAATATACAA
ATGCTCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAA
GCCTATGCTGATGATGACGTGGTGTCTTATGATGATGATACACAAGATTCTAT
TGAAACCCCTTCAGCTAAAGTAATTTGCAAGTTGCTTCTGGTAAAAAAGCAG
GTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAA
CAAGTAACAGAAAGCTAAAAATGGTACTGCCGAGGTAAGTGGCATGATTAC
CGCTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCCTCATCACAG
AGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGGC
ATGACAAATAATGGTGGCATTGCTGCTGACTTACTCATCAACAGATGG
AACATCACTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCT
TACAAGTCTGCGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGAA
CAATACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTGCGATA
CACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCAATTTAAAGTTG
TAAAAGCTTATAAATCAAATGGTGAAGAAATCAATCCTGATGCAAAATAC
AAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAG
CTTCAGAAATGCCAACTTCTAGGAGCCATTAATCCCGATACAGAGGTAT
TTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAAGCTT
CCAAATAATAAACCCTAAAAATCTATGTCATATGAAGATGGTTAATGAAAC
TATTACAAAAATGATGGTACATATAGCATTTATTAAGAACTTTATTTAG
ATCGACAAGGAAATATTGTAGCACAGAGATTGTATCAGACACTTAAAC
CAAAACAAATCAAATCTACAAAAATCAACCTGTAACTACAATTACAA
AAAACAATTACACCAATTTACAGCTATTAAACCTATGAGAAATATGGCA
AACCATCAAACCTCCACTACTGTAATCAAA

SEQ ID NO. 7105

STRAIN 18RS21

GACCAAGTCCGTGTCCAAGTTATAGGCGTCAATGACTTTT
ATGGTGCATTGACAATACTGGAACAGCAAATATGCTGACGGAAAAGTT
AnTAATGCTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCA

Table 71: Comparative Sequences relating to SAG1333

AAAAGATTTCAAACAACTAACCTAATGGTGAAAGCATTAGAGTTCAAG
 CTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCAGGCGCTTCTCAAGAT
 GAACCAACCGTTAAACATTTAATGCAATGAATGTTGAGTATGGCACATT
 AGGTAAACCATGAATTTGATGAAGTTTGGCAGAATACAAATCGTATCGTTA
 CTGGAAAGGCCCTGCTCCAGATTCTAATATAAATAATATACGAAATCA
 TACCCACACGAAGCTGCAAAACAAGAAATTTAGTAGGCAACGTTATTGA
 TAAAGTTAAACAAACAAATCCCTTACAATTTGGAACCTTACACTATTAAAA
 ATATTCTGTAAATAACAAAGTGTGAACGTTGGCTTTATCGGAATCGTT
 ACCAAAGACATCCCAACCTTGTCTTACGTAAAAATTTATGAACATATGA
 ATTTTTAGATGAAGCTGAACAATCGTTAAATACGCCAAAGAATTACAAG
 CTAAAAATGTCAAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGC
 AAGGATGATATGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAA
 TCAACTCTTCCCTGAAAATAGCGTAGATATTGTCTTGTCTGGACACAATC
 ATCAATATACAAATGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTC
 TCTCAAGGAAAGCCCTATGCTGATGTACGTGGTGTCTTAGATACTGATAC
 ACAAGATTTCATTGAAACCCCTTCAGCTAAAGTAAATGCAAGTTGCTCCTG
 GTAAAAAACAGGTAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAAT
 ACTATCGTTAAACAAGTAACAGAAGCTAAAATTTGGTACTGCCGAGGTAAG
 TGGCATGATTACGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCA
 GCCTCATCACAGAGGCTCAACTAGCAATTTGCTGAAAAAGCTGGCCAGAT
 ATCGATTTTGCCATGACAAATAATGGTGGCATTGCTGCTGACTTACTCAT
 CAAACAGATGGAACAATCACTGGGGAGCTGCACAAGCAGTTCAACCTT
 TTGGTAATATCTTACAAGTCGTGCAAAATTAAGTGGTAGAGATCTTTATAAA
 GCACTCAACGAACAATACGACCAAAACAAAAATTTCTTCTTCAATAGC
 TGGTCTGCGATACACTTACACAGATAATAAGAGGGCGGGGAAGAAACAC
 CATTTAAAGTTGTAAGCTTATAAATCAAATGGTGAGGAATCAATCCT
 GATGCAAAATACAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGA
 TGGCTTTGCAAGCTTCAGAAATGCCAAATTTCTAGGAGCCATTATCCCG
 ATACAGAGGTATTTATGGCCATATATCACTGATTAGAAAAAGCTGGTAAA
 AAGGTAGCGTTCCAAATAATAAACCCTAAATCTATGCTCACTATGAAGAT
 GGTTAATGAAACTATTACACAAAATGATGGTACATATAGCATTATTAAGA
 AACTTTATTAGATCGACAAGGAATATTGTAGCACAAGAGATTGTATCA
 GACACTTTAAACCAACAAATCAAATCTACAAAAATCAACCCGTGAAC
 TACAATTCACAAAAACAATTAACCAATTTACAGCTATTAAACCTATGA
 GAAATTATGGCAAACCATCAAACTCCACTACTGTAAATCAAAA

SEQ ID NO. 7106

STRAIN M732

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTT
 GACAATACCTGGAACAGCAAAATATGCTGACGGAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAGATTTC
 AACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG
 GTTGAGCAAGTCCAGCTAACTCAGGCGCTTCTTCAAGATGAACCAACCGT
 TAAAAATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATG
 AATTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCC
 CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
 AGCTGCAAAACAAGAAATTTAGTGGCAACGTTATTGATAAAGTTAACA
 AACAAATCCCTTACAATTGGAACCTTACACTATTAAAAATATTCTGTGA
 AATAACAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACAT
 CCCAAACCTTGTCTTACGTAAAAATTTATGAACAAATATGAATTTTATGATG
 AAGCTGAACAATCGTTAAATACGCAAGAAATTAACAGCTAAAAATGTC
 AAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATAT
 TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCC
 CTGAAAAATAGCGTAGATATTGTCTTGTCTGGACACAATCATCAATATACA
 AATGGTCTTGTGTTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
 AGCCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTC
 TTGAAACCCCTTCAGCTAAAGTAATTGCAAGTTGCTCTCTGGTAAAAAACA
 GGTAGTGCCGATATTCAAGCAATTTGTTGACCAAGCTAATACTATCGTTAA
 ACAAGTAACAGAAGCTAAAAATGGTACTGCCGAGGTAAGTGGCATGATTA
 CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
 GAGGCTCAACTAGCAATTTGCTCGAAAAAGCTGGCCAGATATCGATTTTGC
 CATGACAAATAATGGTGGCATTCTGTCTGACTTACTCATCAAAACAGATG
 GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
 TTACAAGTCGTGCAATTAAGTGGTAGAGATCTTTATAAGCACTCAACGA
 ACAATACGACCAAAAAACAATAATTTCTTCTTCAATAGCTGGTCTGCGAT
 ACCTTACACAGATAATAAGAGGGCGGGGAAGAAACACCAATTTAAAGTT
 GTAAAGCTTATAAATCAATGGTGAGGAAATCAATCTGATGCAAAATA
 CAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGGTGGCTTTGCAA
 GCTTCAGAAATGCCAACTTCTAGGAGCCATTATCCCGATACAGAGGTA
 TTTATGGCCCTATATCACTGATTAGAAAAAGCTGGTAAAAAAGTGAGCAT
 TCCAAATAATAAACCTAAAAATCTATGTCACTATGAAGATGGTTAATGAAA
 CTATTACACAAAATGATGGTACATATAGCATTATTAAGAAACCTTTATTTA
 GATCGACAAGGAATATTGTAGCACAAGAGATTGTATCAGACACTTTAA
 CCAACAAAAATCAAATCTACAAAAATCAACCCGTGAATCAATTTACA
 AAAAAAATTAACCAATTTACAGCTATTAAACCTATGAGAAATTATGGC
 AACCATCAAACTCCACTACTGTAAATCAAAAACA

SEQ ID NO. 7107

STRAIN COH1

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTT
 GACAATACCTGGAACAGCAAAATATGCTGACGGAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAGATTTC
 AACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG

Table 71: Comparative Sequences relating to SAG1333

GTITGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGT
TAAAAACATTTAATGCAATGAATGTTGAGTATGGCACAATTAGGTAACCATG
AATTTGATGAAGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCC
CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
AGCTGCAAAACAAGAAATTTAGTGGCAACGTTATTGATAAAGTTAACA
AACAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCTGTGA
AATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACAT
CCCAACCTTGTCTTACGTAATAATATGAACAATATGAATTTTAGATG
AAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
AAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATAT
TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCC
CTGAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACA
AATGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
AGCCTATGCTGATGTACGTGGTGTCTAGATACGATACACAAGATTCA
TTGAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACA
GGTAGTGCCGATATTCAAGCCATTGTGACCAAGCTAATACTATCGTTAA
ACAAGTAACAGAAGCTAAAAATGGTACTGCCAGGTAAGTGGCATGATTA
CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
GAGGCTCAACTAGCAATTGCTCGAAAAGCTGGCCAGATATCGATTTTGC
CATGACAAATATGGTGGCATTCGTGCTGACTTACTCATCAACCCAGATG
GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
TTACAAGTCGTGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGA
ACAATACGACCAAAAAACAATAATTTCTTCTCAATAGCTGGTCTGCGAT
ACACTTACACAGATAATAAGAGGGCGGGGAAGAAACACCATTAAAGTT
GTAAAGCTTATAAATCAATGGTGAAGAAATCAATCTGATGCAAAATA
CAAATTAGTTATCAATGACTTTTATTCCGGTGGTGGTGGTGGCTTTGCAA
GCTTCAGAAATGCCAACTTCTAGGAGCCATTATCCGATACAGAGGTA
TTTATGGCCTATATCACTGATTAGAAAAAGCTGGTAAAAAGTGGAGCAT
TCCAAATAATAAACCCTAAAAATCTATGTCACTATGAAGATGGTTAATGAAA
CTATTACACAAAATGATGGTACATATAGCATTATTAAGAACTTTATTTA
GATCGACAAGGAAATATGTAGCACAAAGAGATTGTATCAGACACTTTAA
CCAAACAAAATCAAAATCTACAAAATCAACCTGTGAATCAATTCACA
AAAAACAATTACCAAAATTTACAGCTATTAAACCCTATGAGAAATTATGGC
AAACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7108

STRAIN M781

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACCTTGA
CAATACTGGAACAGCAATATGCCTGACGGAAGTTACTAATGCTGGCA
CTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAA
CAAATAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGGATGGT
TGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTA
AAACATTTAATGAATGAATGTTGAGTATGGCACAATTAGGTAACCATGAA
TTTGTATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCCCC
TGCTCCAGATTCTAATAATAAATAATATTACGAATCATACCCACACGAAG
CTGCAAAAACAGAAATGTAGTGGCAACGTTATTGATAAAGTTAACAAA
CAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCCTGTAAA
TAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATCC
CAAACCTTGTCTTACGTAAAAATTAAGAACAATGAATTTTAGATGAA
GCTGAAACAATCGTTAATAACGCAAGAAATTAAGAAGCTAAAAATGTCAA
GGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATATTG
CTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCT
GAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAA
TGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAG
CCTATGCTGATGTACGTGGTGTCTTAGATACGATACACAAGATTTCATT
GAAACCCCTTCAGCTAAAGTAATTCAGTTGCTCCTGGTAAAAAAGCAGG
TAGTGCCGATATTCAAGCCATTGTGACCAAGCTAATACTATCGTTAAAC
AAGTAACAGAAGCTAAATTTGGTACTGCGAGGTAAGTGGCATGATTACG
CGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
GGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
TGACAAATAATGGTGGCATTCTGTCTGACTTACTCATCAACCCAGATGGA
ACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
ACAAGTCGTGCAAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGAAC
AATACGACCAAAAAACAATAATTTCTTCTTCAAATAGCTGGTCTGCGATAC
ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTAAAGTTGT
AAAAGCTTATAAATCAATGGTGAAGAAATCAATCCTGATGCAAAATACA
AATTAGTTATCAATGACTTTTATTCCGGTGGTGGTGGTGGCTTTGCAAGC
TTCAGAAATGCCAACTTCTAGGAGCCATTATCCCGATACAGAGTATT
TATGGCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGGCATTC
CAAATAATAAACCTAAAAATCTATGTCACTATGAAGATGGTTAATGAACT
ATTACAAAAATGATGGTACATATAGCATTATTAAAGAACTTTATTAGTA
TCGACAAGGAAATATGTAGCACAAAGAGATTGTATCAGACACTTTAAACC
AAACAAAATCAAAATCTACAAAATCAACCTGTAACTACAATTCACAAA
AAACAATTACACCAATTTACAGCTATTAAACCCTATGAGAAATTATGGCAA
ACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7109

STRAIN CJB110

GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGC
ACTTGACAATACTGGAACAGCAATATGCCTGACGGAAGAAAGTTACTAATG
CTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGAT
TTCAAAACAACTAACCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGA
TATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAA

Table 71: Comparative Sequences relating to SAG1333

CCGTTAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAAC
 CATGAATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAG
 GGCCCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCAC
 ACGAAGCTGCAAAACAGAAATTTAGTGGCAACCGTTATTGATAAAGTT
 AACAAACAAATCCCTTACAATTGGAACCTTACGCTATTAAAAATATTCC
 TGTAAATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAG
 ACATCCCAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTTTA
 GATGAAGCTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAA
 TGTCAAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATG
 ATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTC
 TTCCTGAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATA
 TACAAATGGTCTTGTGGTAAAACTCGCATTGTACAAGCGCTCTCTCAAG
 GAAAAGCCTATGCTGACGTACGTGGTGTCTAGATACTGATACACAAGAT
 TTCATTGAAACCCCTTACAGTAAAGTAGTTGCAGTTGCTCCTGGTAAAAA
 AACAGGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATATCTATCG
 TTAACAAGATTAACAGAAGCTAAAAATGGTACTGCCGAGGTAAAGTGGCATG
 ATTACGCGTTCTGTGATCAAGATAATGTTAGTCCAGTAGGCAGCCTCAT
 CACAGAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATT
 TTGCCATGACAAATAATGGTGGCATTCTGTGCTGACTTACTCATCAAAACCA
 GATGGAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAA
 TATCTTACAAGTCTGTCGAAATTAAGTGGTAGAGATCTTTATAAGCACTCA
 ACGAACATAACGACCAAAAAAATAATTTCTTCTTCAAATAGCTGGTCTG
 CGATACACTTACACAGATAATAAAGAGGGCGGAGAGAAACACCATTTAA
 AGTTGTAAAAGCTTATAAATCAAAATGGTGAAGAAATCAATCCTGATGCAA
 AATACAAATTAGTTATCAATGACTTTTTATTCTGGTGGTGGTATGGCTTT
 GCAAGCTTCAGAAATGCCAACTTCTAGGAGCCATTAAATCCGATACAGA
 GGTATTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGA
 GCGTTCCAAATAATAAACCTAAAAATCTATGTCACTATGAAGATGGTTAAT
 GAACTATTACACAAATGATGGTACACATAGCATTATTAAGAACTTTA
 TTTAGATCGACAGGAATATTGTAGCACAAGAGATTGTATCAGACACTT
 TAAACCAAAACAAATCAAAATCTACAAATCAACCTGTAACTACAAAT
 CACAAAAACAATTACACCAATTTACAGCTATTAACCTATGAGAAATTA
 TGGCAACCATCAAACTCCACTACTGTAAATCA

SEQ ID NO. 7110

STRAIN 1169NT

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGA
 CAATACTGGAACAGCAAAATATGCCCTGATGGAAGAGTTGCTAATGCTGGTA
 CTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAA
 CAACTAACCCCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGT
 TGGAGCAAGTCCAGCCAACTCTGGCTTCTTCAAGATGAACCAACTGTCA
 AAAATTTTAAATGCAATGAATGTTGAGTATGGCAGATTGGGTAAACATGAA
 TTTGATGAAGGGTTGGCAGAAATATAATCGTATCGTTACTGGTAAAGCCCC
 TGCTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACATGAAG
 CTGCAAAACAAGAAATTTAGTGGCAAAATGTTATTGATAAAGTTAACAAA
 CAAATTCCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCCTGTAAA
 TAACAAAGTGTGAACGTTGGCTTTATCGGGATTGTCAACCAAGACATCC
 CAAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTATGATGAA
 GCTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAATGTCAA
 AGCTATTGTAGTCTCGCACATGTACCTGCAACAAGTAAAAATGATATTG
 CTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCT
 GAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
 TGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAG
 CCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTCATT
 GAGACCCCTTCACTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACAGG
 TAGTGCCGATATTCAAGCCATTGTGACCAAGCTAATACTATCGTTAAAC
 AAGTAACAGAAGCTAAAATGGTACTGCCGAGGTAAGTGTATGATTACG
 CGTTCTGTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
 GGTCAACTAGCAATTTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
 TGACAAATAATGGTGGCATTGCTGCTGACTTACTCATCAAACAGATGGA
 ACAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
 ACAAGTCGTGCAAAATTAAGTAGAGATCTTTATAAGCACTCAACGAAC
 AATACGACCAAAAAAATAATTTCTTCTTCAAATAGCTGGTCTGCGATAC
 ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGT
 AAAAGCTTATAAATCAAAATGGTGAAGGAAATCAATCCTGATGCAAAATACA
 AATTAGTTATCAATGACTTTTATTCTGGTGGTGGTATGGCTTTGCAAGC
 TTCAGAAATGCCAACTTCTAGGAGCCATTAAACCCGATACAGAGGTATT
 TATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGAAGCGTTC
 CAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAACT
 ATTACACAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGA
 TCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACC
 AAACAAATCAAAATCTACAAAAATCAACCTGTAACTACAAATCACAAA
 AAACAATTACACCAATTTACAGCTATTAACCTATGAGAAATTTAGCAA
 ACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7111

STRAIN JM9130013

CGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGACAATA
 CTGGAACAGCAAAATATGCCCTGACGGAAGGTTACTAATGCTGGCACTGCT
 GCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAACAAAC
 TAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTATGATGGTTGGAG
 CAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTAAACCA
 TTTAATGCAATGAATGTTAGTATGGCAGATTAGGTAAACATGAATTTGA

Table 71: Comparative Sequences relating to SAG1333

TGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCTGCTC
 CAGATTcTAATATAAATAATATTACGAAATCATACCCACACGAAGCTGCA
 AAACAAGAAATTTAGTGGCAACGTTATTGATAAAGTTAAACAAACAAAT
 CCCTTACAATTTGGAACCTTACACTATTAAAAATATTCTGTAAATAACA
 AAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCCCAAAC
 CTGTCTTACGTAAAAATTATGAACAATATGAATTTTATAGATGAAGCTGA
 AACAAATCGTTAAATACGCCAAAGAATTACAGCTAAAAATGTCAAGGCTA
 TTGTAGTCTTGTCTCATGTACCTGCAACAGCAAGGATGATATTGCTGAA
 GGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTGAAAA
 TAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAATGGTC
 TTGTTGGTAAAACTCGTATTGTACAGCGCTCTCTCAAGGAAAAGCCTAT
 GCTGATGTACGTGGTGTCTAGATACCTGATACACAAGATTTTATTGAAAC
 CCCTTCAGCTAAAGTAATTGCAAGTTGCTCCTGGTAAAAAACAGGTAGTG
 CCGATATTCAAGCCATTCTTGACCAAGCTAATACTATCGTTAAACAAGTA
 ACAGAAGCTAAAAATGGTACTGCCGAGGTAAAGTGGCATGATTACGCGTTC
 TGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTC
 AACTAGCAATGTCTGAAAAAGCTGGCCAGATATCGATTTTGCCATGACA
 AATAATGGTGGCATTCTGTCTGACTTACTCATCAAACAGATGGAACAAT
 CACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTACAAG
 TCGTCAAAATTAATGTTAGATCTTTATAAAGCACTCAACGAACAATAC
 GACCAAAAAACAAATTTCTTCCTTCAAAATAGCTGGTCTGCGATACACTTA
 CACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAG
 CTTATAAATCAATGGTGGAGAAATCAATCCTGATGCAAAATACAAATTA
 GTTATCAATGACTTTTATTCTGGTGGTGGTGGTGGCTTTGCAAGCTTCAG
 AAATGCCAACTCTTAGGAGCCATTAAATCCCGATACAGAGGTATTATGG
 CCTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGAGCGTTCCAAT
 AATAAACCTAAAAATCTATGCTCACTATGAAGATGGTTAATGAACTATTAC
 ACAAAATGATGGTACATATAGCAATTATTGAGAACTTTATTATAGATCGAC
 AAGGAAATATTGTAGCAACAAGAGATTGTATCAGACACTTTAAACCAAACA
 AAATCAAAATCTACAAAATCAACCTGTAACCTACAATTACAAAAAACA
 ATTACACCAATTTACAGCTATTAAACCTATGAGAAATTTATGGCAAACCAT
 CAACTCCACTACTGTAAATCAAAA

PRETTY of: /biotmp/msa237456.2{*} May 14, 2003 03:20 ..

| | | | | | |
|----------------------------|------------|-------------|------------|------------|------------|
| | 1 | | | | 50 |
| msa237456.2{328_1169NT} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_2603} | atgaaaaaga | aaattattht | gaaaagtagt | gttcttggtt | tagtcgctgg |
| msa237456.2{328_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_H36B} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_M732} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_M781} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_A909} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_090} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_CJB110} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 51 | | | | 100 |
| msa237456.2{328_1169NT} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_2603} | gacttctatt | atgttctcaa | gcgtgttcgc | gGACcaagtc | ggtgtccaag |
| msa237456.2{328_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_H36B} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_M732} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_M781} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_A909} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_090} | ----- | ----- | ----- | ----- | ----- |
| msa237456.2{328_CJB110} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 101 | | | | 150 |
| msa237456.2{328_1169NT} | ttatagGCGT | CAATGACTTT | CATGGTGCAC | TTGACAATAC | TGGAACAGCA |
| msa237456.2{328_2603} | ttatagGCGT | CAATGACTTT | CATGGTGCAC | TTGACAATAC | TGGAACAGCA |
| msa237456.2{328_18RS21} | ttatagGCGT | CAATGACTTT | CATGGTGCAC | TTGACAATAC | TGGAACAGCA |
| msa237456.2{328_H36B} | ttatagGCGT | CAATGACTTT | CATGGTGCAC | TTGACAATAC | TGGAACAGCA |
| msa237456.2{328_COH1} | ttatagGCGT | CAATGACTTT | CATGGTGCAC | TTGACAATAC | TGGAACAGCA |
| msa237456.2{328_M732} | ttatagGCGT | CAATGACTTT | CATGGTGCAC | TTGACAATAC | TGGAACAGCA |
| msa237456.2{328_M781} | ttatagGCGT | CAATGACTTT | CATGGTGCAC | TTGACAATAC | TGGAACAGCA |
| msa237456.2{328_JM9130013} | ttatagGCGT | CAATGACTTT | CATGGTGCAC | TTGACAATAC | TGGAACAGCA |
| msa237456.2{328_A909} | -----GCGT | CAATGACTTT | CATGGTGCAC | TTGACAATAC | TGGAACAGCA |
| msa237456.2{328_090} | ttatagGCGT | CAATGACTTT | CATGGTGCAC | TTGACAATAC | TGGAACAGCA |
| msa237456.2{328_CJB110} | ttatagGCGT | CAATGACTTT | CATGGTGCAC | TTGACAATAC | TGGAACAGCA |
| Consensus | -----**** | ***** | ***** | ***** | ***** |
| | 151 | | | | 200 |
| msa237456.2{328_1169NT} | AATATGCCTG | AtGGAAAAAGT | TgcTAATGCT | GGtACTGCTG | CTCAATTAGA |
| msa237456.2{328_2603} | AATATGCCTG | AtGGAAAAAGT | TgcTAATGCT | GGtACTGCTG | CTCAATTAGA |
| msa237456.2{328_18RS21} | AATATGCCTG | AcGGAAAAAGT | TanTAATGCT | GGcACTGCTG | CTCAATTAGA |
| msa237456.2{328_H36B} | AATATGCCTG | AcGGAAAAAGT | TacTAATGCT | GGcACTGCTG | CTCAATTAGA |
| msa237456.2{328_COH1} | AATATGCCTG | AcGGAAAAAGT | TacTAATGCT | GGcACTGCTG | CTCAATTAGA |

Table 71: Comparative Sequences relating to SAG1333

| | | | | | |
|----------------------------|------------|------------|------------|------------|-------------|
| msa237456.2{328_M732} | AATATGCCTG | AcGGAAAAGT | TacTAATGCT | GGcACTGCTG | CTCAATTAGA |
| msa237456.2{328_M781} | AATATGCCTG | AcGGAAAAGT | TacTAATGCT | GGcACTGCTG | CTCAATTAGA |
| msa237456.2{328_JM9130013} | AATATGCCTG | AcGGAAAAGT | TacTAATGCT | GGcACTGCTG | CTCAATTAGA |
| msa237456.2{328_A909} | AATATGCCTG | AcGGAAAAGT | TacTAATGCT | GGcACTGCTG | CTCAATTAGA |
| msa237456.2{328_CJB110} | AATATGCCTG | AcGGAAAAGT | TacTAATGCT | GGcACTGCTG | CTCAATTAGA |
| Consensus | ***** | *-***** | *-***** | *-***** | ***** |
| msa237456.2{328_1169NT} | TGCTTATATG | GATGAcGCTC | AAAAAGATT | CAAACAACT | AACCCCTAATG |
| msa237456.2{328_2603} | TGCTTATATG | GATGAcGCTC | AAAAAGATT | CAAACAACT | AACCCCTAATG |
| msa237456.2{328_18RS21} | TGCTTATATG | GATGAcGCTC | AAAAAGATT | CAAACAACT | AACCCCTAATG |
| msa237456.2{328_H36B} | TGCTTATATG | GATGAcGCTC | AAAAAGATT | CAAACAACT | AACCCCTAATG |
| msa237456.2{328_COH1} | TGCTTATATG | GATGAcGCTC | AAAAAGATT | CAAACAACT | AACCCCTAATG |
| msa237456.2{328_M732} | TGCTTATATG | GATGAcGCTC | AAAAAGATT | CAAACAACT | AACCCCTAATG |
| msa237456.2{328_M781} | TGCTTATATG | GATGAcGCTC | AAAAAGATT | CAAACAACT | AACCCCTAATG |
| msa237456.2{328_JM9130013} | TGCTTATATG | GATGAcGCTC | AAAAAGATT | CAAACAACT | AACCCCTAATG |
| msa237456.2{328_A909} | TGCTTATATG | GATGAcGCTC | AAAAAGATT | CAAACAACT | AACCCCTAATG |
| msa237456.2{328_090} | TGCTTATATG | GATGAcGCTC | AAAAAGATT | CAAACAACT | AACCCCTAATG |
| msa237456.2{328_CJB110} | TGCTTATATG | GATGAcGCTC | AAAAAGATT | CAAACAACT | AACCCCTAATG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | GTGAAGCAT | TAGgGTTCAA | GcAGGcGATA | TGGTTGGAGC | AAGTCCAGCc |
| msa237456.2{328_2603} | GTGAAGCAT | TAGgGTTCAA | GcAGGcGATA | TGGTTGGAGC | AAGTCCAGCc |
| msa237456.2{328_18RS21} | GTGAAGCAT | TAGgGTTCAA | GcAGGcGATA | TGGTTGGAGC | AAGTCCAGCc |
| msa237456.2{328_H36B} | GTGAAGCAT | TAGgGTTCAA | GcAGGcGATA | TGGTTGGAGC | AAGTCCAGCc |
| msa237456.2{328_COH1} | GTGAAGCAT | TAGgGTTCAA | GcAGGcGATA | TGGTTGGAGC | AAGTCCAGCc |
| msa237456.2{328_M732} | GTGAAGCAT | TAGgGTTCAA | GcAGGcGATA | TGGTTGGAGC | AAGTCCAGCc |
| msa237456.2{328_M781} | GTGAAGCAT | TAGgGTTCAA | GcAGGcGATA | TGGTTGGAGC | AAGTCCAGCc |
| msa237456.2{328_JM9130013} | GTGAAGCAT | TAGgGTTCAA | GcAGGcGATA | TGGTTGGAGC | AAGTCCAGCc |
| msa237456.2{328_A909} | GTGAAGCAT | TAGgGTTCAA | GcAGGcGATA | TGGTTGGAGC | AAGTCCAGCc |
| msa237456.2{328_090} | GTGAAGCAT | TAGgGTTCAA | GcAGGcGATA | TGGTTGGAGC | AAGTCCAGCc |
| msa237456.2{328_CJB110} | GTGAAGCAT | TAGgGTTCAA | GcAGGcGATA | TGGTTGGAGC | AAGTCCAGCc |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | AACCTcGGGC | TTCTTCAAGA | TGAACCAAcT | GtCAAAAaT | TTAATGCAAT |
| msa237456.2{328_2603} | AACCTcGGGC | TTCTTCAAGA | TGAACCAAcT | GtCAAAAaT | TTAATGCAAT |
| msa237456.2{328_18RS21} | AACCTcGGGC | TTCTTCAAGA | TGAACCAAcT | GtCAAAAaT | TTAATGCAAT |
| msa237456.2{328_H36B} | AACCTcGGGC | TTCTTCAAGA | TGAACCAAcT | GtCAAAAaT | TTAATGCAAT |
| msa237456.2{328_COH1} | AACCTcGGGC | TTCTTCAAGA | TGAACCAAcT | GtCAAAAaT | TTAATGCAAT |
| msa237456.2{328_M732} | AACCTcGGGC | TTCTTCAAGA | TGAACCAAcT | GtCAAAAaT | TTAATGCAAT |
| msa237456.2{328_M781} | AACCTcGGGC | TTCTTCAAGA | TGAACCAAcT | GtCAAAAaT | TTAATGCAAT |
| msa237456.2{328_JM9130013} | AACCTcGGGC | TTCTTCAAGA | TGAACCAAcT | GtCAAAAaT | TTAATGCAAT |
| msa237456.2{328_A909} | AACCTcGGGC | TTCTTCAAGA | TGAACCAAcT | GtCAAAAaT | TTAATGCAAT |
| msa237456.2{328_090} | AACCTcGGGC | TTCTTCAAGA | TGAACCAAcT | GtCAAAAaT | TTAATGCAAT |
| msa237456.2{328_CJB110} | AACCTcGGGC | TTCTTCAAGA | TGAACCAAcT | GtCAAAAaT | TTAATGCAAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | GAATGTTGAG | TATGGCACAT | TgGGTAACCA | TGAATTTGAT | GAAGGtTTGG |
| msa237456.2{328_2603} | GAATGTTGAG | TATGGCACAT | TgGGTAACCA | TGAATTTGAT | GAAGGtTTGG |
| msa237456.2{328_18RS21} | GAATGTTGAG | TATGGCACAT | TgGGTAACCA | TGAATTTGAT | GAAGGtTTGG |
| msa237456.2{328_H36B} | GAATGTTGAG | TATGGCACAT | TgGGTAACCA | TGAATTTGAT | GAAGGtTTGG |
| msa237456.2{328_COH1} | GAATGTTGAG | TATGGCACAT | TgGGTAACCA | TGAATTTGAT | GAAGGtTTGG |
| msa237456.2{328_M732} | GAATGTTGAG | TATGGCACAT | TgGGTAACCA | TGAATTTGAT | GAAGGtTTGG |
| msa237456.2{328_M781} | GAATGTTGAG | TATGGCACAT | TgGGTAACCA | TGAATTTGAT | GAAGGtTTGG |
| msa237456.2{328_JM9130013} | GAATGTTGAG | TATGGCACAT | TgGGTAACCA | TGAATTTGAT | GAAGGtTTGG |
| msa237456.2{328_A909} | GAATGTTGAG | TATGGCACAT | TgGGTAACCA | TGAATTTGAT | GAAGGtTTGG |
| msa237456.2{328_090} | GAATGTTGAG | TATGGCACAT | TgGGTAACCA | TGAATTTGAT | GAAGGtTTGG |
| msa237456.2{328_CJB110} | GAATGTTGAG | TATGGCACAT | TgGGTAACCA | TGAATTTGAT | GAAGGtTTGG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | CAGAATAcAA | TCGTATCGTT | ACTGGtAAAg | CCCCTGCTCC | AGATTCTAAT |
| msa237456.2{328_2603} | CAGAATAcAA | TCGTATCGTT | ACTGGtAAAg | CCCCTGCTCC | AGATTCTAAT |
| msa237456.2{328_18RS21} | CAGAATAcAA | TCGTATCGTT | ACTGGaAAgG | CCCCTGCTCC | AGATTCTAAT |
| msa237456.2{328_H36B} | CAGAATAcAA | TCGTATCGTT | ACTGGaAAgG | CCCCTGCTCC | AGATTCTAAT |
| msa237456.2{328_COH1} | CAGAATAcAA | TCGTATCGTT | ACTGGaAAgG | CCCCTGCTCC | AGATTCTAAT |
| msa237456.2{328_M732} | CAGAATAcAA | TCGTATCGTT | ACTGGaAAgG | CCCCTGCTCC | AGATTCTAAT |
| msa237456.2{328_M781} | CAGAATAcAA | TCGTATCGTT | ACTGGaAAgG | CCCCTGCTCC | AGATTCTAAT |
| msa237456.2{328_JM9130013} | CAGAATAcAA | TCGTATCGTT | ACTGGaAAgG | CCCCTGCTCC | AGATTCTAAT |
| msa237456.2{328_A909} | CAGAATAcAA | TCGTATCGTT | ACTGGaAAgG | CCCCTGCTCC | AGATTCTAAT |
| msa237456.2{328_090} | CAGAATAcAA | TCGTATCGTT | ACTGGaAAgG | CCCCTGCTCC | AGATTCTAAT |
| msa237456.2{328_CJB110} | CAGAATAcAA | TCGTATCGTT | ACTGGaAAgG | CCCCTGCTCC | AGATTCTAAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | ATtAATAATA | TTACGAAATC | ATACCCACat | GAAGCTGCAA | AACAAGAAAT |
| msa237456.2{328_2603} | ATtAATAATA | TTACGAAATC | ATACCCACat | GAAGCTGCAA | AACAAGAAAT |
| msa237456.2{328_18RS21} | ATaAATAATA | TTACGAAATC | ATACCCACac | GAAGCTGCAA | AACAAGAAAT |
| msa237456.2{328_H36B} | ATaAATAATA | TTACGAAATC | ATACCCACac | GAAGCTGCAA | AACAAGAAAT |

Table 71: Comparative Sequences relating to SAG1333

| | | | | | | | |
|----------------------------|------------|-------------|-------------|-------------|-------------|------------|-------|
| msa237456.2{328_COH1} | ATAATAATA | TTACGAAATC | ATACCCACac | GAAGCTGCAA | AACAAGAAAT | | |
| msa237456.2{328_M732} | ATAATAATA | TTACGAAATC | ATACCCACac | GAAGCTGCAA | AACAAGAAAT | | |
| msa237456.2{328_M781} | ATAATAATA | TTACGAAATC | ATACCCACac | GAAGCTGCAA | AACAAGAAAT | | |
| msa237456.2{328_JM9130013} | ATAATAATA | TTACGAAATC | ATACCCACac | GAAGCTGCAA | AACAAGAAAT | | |
| msa237456.2{328_A909} | ATAATAATA | TTACGAAATC | ATACCCACac | GAAGCTGCAA | AACAAGAAAT | | |
| msa237456.2{328_090} | ATAATAATA | TTACGAAATC | ATACCCACac | GAAGCTGCAA | AACAAGAAAT | | |
| msa237456.2{328_CJB110} | ATAATAATA | TTACGAAATC | ATACCCACac | GAAGCTGCAA | AACAAGAAAT | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa237456.2{328_1169NT} | 501 | TGTAGTGGCA | AATGTTATTG | ATAAAGTTAA | CAAACAAATc | CCTTACAATT | 550 |
| msa237456.2{328_2603} | TGTAGTGGCA | AATGTTATTG | ATAAAGTTAA | CAAACAAATc | CCTTACAATT | | |
| msa237456.2{328_18RS21} | TGTAGTGGCA | AACGTTATTG | ATAAAGTTAA | CAAACAAATc | CCTTACAATT | | |
| msa237456.2{328_H36B} | TGTAGTGGCA | AACGTTATTG | ATAAAGTTAA | CAAACAAATc | CCTTACAATT | | |
| msa237456.2{328_COH1} | TGTAGTGGCA | AACGTTATTG | ATAAAGTTAA | CAAACAAATc | CCTTACAATT | | |
| msa237456.2{328_M732} | TGTAGTGGCA | AACGTTATTG | ATAAAGTTAA | CAAACAAATc | CCTTACAATT | | |
| msa237456.2{328_M781} | TGTAGTGGCA | AACGTTATTG | ATAAAGTTAA | CAAACAAATc | CCTTACAATT | | |
| msa237456.2{328_JM9130013} | TGTAGTGGCA | AACGTTATTG | ATAAAGTTAA | CAAACAAATc | CCTTACAATT | | |
| msa237456.2{328_A909} | TGTAGTGGCA | AACGTTATTG | ATAAAGTTAA | CAAACAAATc | CCTTACAATT | | |
| msa237456.2{328_090} | TGTAGTGGCA | AACGTTATTG | ATAAAGTTAA | CAAACAAATc | CCTTACAATT | | |
| msa237456.2{328_CJB110} | TGTAGTGGCA | AACGTTATTG | ATAAAGTTAA | CAAACAAATc | CCTTACAATT | | |
| Consensus | ***** | **_***** | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | 551 | GGAAgCCTTA | CgCTATTAAA | AATATTCCCTG | TAAATAACAA | AAGTGTGAAC | 600 |
| msa237456.2{328_2603} | GGAAgCCTTA | CgCTATTAAA | AATATTCCCTG | TAAATAACAA | AAGTGTGAAC | | |
| msa237456.2{328_18RS21} | GGAAaCCTTA | CaCTATTAAA | AATATTCCCTG | TAAATAACAA | AAGTGTGAAC | | |
| msa237456.2{328_H36B} | GGAAaCCTTA | CaCTATTAAA | AATATTCCCTG | TAAATAACAA | AAGTGTGAAC | | |
| msa237456.2{328_COH1} | GGAAaCCTTA | CaCTATTAAA | AATATTCCCTG | TAAATAACAA | AAGTGTGAAC | | |
| msa237456.2{328_M732} | GGAAaCCTTA | CaCTATTAAA | AATATTCCCTG | TAAATAACAA | AAGTGTGAAC | | |
| msa237456.2{328_M781} | GGAAaCCTTA | CaCTATTAAA | AATATTCCCTG | TAAATAACAA | AAGTGTGAAC | | |
| msa237456.2{328_JM9130013} | GGAAaCCTTA | CaCTATTAAA | AATATTCCCTG | TAAATAACAA | AAGTGTGAAC | | |
| msa237456.2{328_A909} | GGAAaCCTTA | CaCTATTAAA | AATATTCCCTG | TAAATAACAA | AAGTGTGAAC | | |
| msa237456.2{328_090} | GGAAaCCTTA | CgCTATTAAA | AATATTCCCTG | TAAATAACAA | AAGTGTGAAC | | |
| msa237456.2{328_CJB110} | GGAAaCCTTA | CgCTATTAAA | AATATTCCCTG | TAAATAACAA | AAGTGTGAAC | | |
| Consensus | ***** | *_***** | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | 601 | GTTGGCTTTA | TCGGgATtGT | cACCAAGAC | ATCCCAACC | TTGTCTTACG | 650 |
| msa237456.2{328_2603} | GTTGGCTTTA | TCGGgATtGT | cACCAAGAC | ATCCCAACC | TTGTCTTACG | | |
| msa237456.2{328_18RS21} | GTTGGCTTTA | TCGGaATcGT | tACCAAGAC | ATCCCAACC | TTGTCTTACG | | |
| msa237456.2{328_H36B} | GTTGGCTTTA | TCGGaATcGT | tACCAAGAC | ATCCCAACC | TTGTCTTACG | | |
| msa237456.2{328_COH1} | GTTGGCTTTA | TCGGaATcGT | tACCAAGAC | ATCCCAACC | TTGTCTTACG | | |
| msa237456.2{328_M732} | GTTGGCTTTA | TCGGaATcGT | tACCAAGAC | ATCCCAACC | TTGTCTTACG | | |
| msa237456.2{328_M781} | GTTGGCTTTA | TCGGaATcGT | tACCAAGAC | ATCCCAACC | TTGTCTTACG | | |
| msa237456.2{328_JM9130013} | GTTGGCTTTA | TCGGaATcGT | tACCAAGAC | ATCCCAACC | TTGTCTTACG | | |
| msa237456.2{328_A909} | GTTGGCTTTA | TCGGaATcGT | tACCAAGAC | ATCCCAACC | TTGTCTTACG | | |
| msa237456.2{328_090} | GTTGGCTTTA | TCGGaATcGT | tACCAAGAC | ATCCCAACC | TTGTCTTACG | | |
| msa237456.2{328_CJB110} | GTTGGCTTTA | TCGGaATcGT | tACCAAGAC | ATCCCAACC | TTGTCTTACG | | |
| Consensus | ***** | *****_**_** | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | 651 | TAAAAATTAT | GAACAATATG | AATTTTTAGA | TGAAGCTGAA | ACAATCGTTA | 700 |
| msa237456.2{328_2603} | TAAAAATTAT | GAACAATATG | AATTTTTAGA | TGAAGCTGAA | ACAATCGTTA | | |
| msa237456.2{328_18RS21} | TAAAAATTAT | GAACAATATG | AATTTTTAGA | TGAAGCTGAA | ACAATCGTTA | | |
| msa237456.2{328_H36B} | TAAAAATTAT | GAACAATATG | AATTTTTAGA | TGAAGCTGAA | ACAATCGTTA | | |
| msa237456.2{328_COH1} | TAAAAATTAT | GAACAATATG | AATTTTTAGA | TGAAGCTGAA | ACAATCGTTA | | |
| msa237456.2{328_M732} | TAAAAATTAT | GAACAATATG | AATTTTTAGA | TGAAGCTGAA | ACAATCGTTA | | |
| msa237456.2{328_M781} | TAAAAATTAT | GAACAATATG | AATTTTTAGA | TGAAGCTGAA | ACAATCGTTA | | |
| msa237456.2{328_JM9130013} | TAAAAATTAT | GAACAATATG | AATTTTTAGA | TGAAGCTGAA | ACAATCGTTA | | |
| msa237456.2{328_A909} | TAAAAATTAT | GAACAATATG | AATTTTTAGA | TGAAGCTGAA | ACAATCGTTA | | |
| msa237456.2{328_090} | TAAAAATTAT | GAACAATATG | AATTTTTAGA | TGAAGCTGAA | ACAATCGTTA | | |
| msa237456.2{328_CJB110} | TAAAAATTAT | GAACAATATG | AATTTTTAGA | TGAAGCTGAA | ACAATCGTTA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | 701 | AATACGCCAA | AGAATTACAA | GCTAAAAATG | TCAAaGCTAT | TGTAGTcCTc | 750 |
| msa237456.2{328_2603} | AATACGCCAA | AGAATTACAA | GCTAAAAATG | TCAAaGCTAT | TGTAGTcCTc | | |
| msa237456.2{328_18RS21} | AATACGCCAA | AGAATTACAA | GCTAAAAATG | TCAAaGCTAT | TGTAGTcCTc | | |
| msa237456.2{328_H36B} | AATACGCCAA | AGAATTACAA | GCTAAAAATG | TCAAaGCTAT | TGTAGTcCTc | | |
| msa237456.2{328_COH1} | AATACGCCAA | AGAATTACAA | GCTAAAAATG | TCAAaGCTAT | TGTAGTcCTc | | |
| msa237456.2{328_M732} | AATACGCCAA | AGAATTACAA | GCTAAAAATG | TCAAaGCTAT | TGTAGTcCTc | | |
| msa237456.2{328_M781} | AATACGCCAA | AGAATTACAA | GCTAAAAATG | TCAAaGCTAT | TGTAGTcCTc | | |
| msa237456.2{328_JM9130013} | AATACGCCAA | AGAATTACAA | GCTAAAAATG | TCAAaGCTAT | TGTAGTcCTc | | |
| msa237456.2{328_A909} | AATACGCCAA | AGAATTACAA | GCTAAAAATG | TCAAaGCTAT | TGTAGTcCTc | | |
| msa237456.2{328_090} | AATACGCCAA | AGAATTACAA | GCTAAAAATG | TCAAaGCTAT | TGTAGTcCTc | | |
| msa237456.2{328_CJB110} | AATACGCCAA | AGAATTACAA | GCTAAAAATG | TCAAaGCTAT | TGTAGTcCTc | | |
| Consensus | ***** | ***** | ***** | ***** | *****_**_** | ***** | ***** |
| msa237456.2{328_1169NT} | 751 | GCaCATGTAC | CTGCAACAAG | tAAaaATGAT | ATTGCTGAAG | GTGAAGCAGC | 800 |
| msa237456.2{328_2603} | GCaCATGTAC | CTGCAACAAG | tAAaaATGAT | ATTGCTGAAG | GTGAAGCAGC | | |
| msa237456.2{328_18RS21} | GcTcATGTAC | CTGCAACAAG | cAagqATGAT | ATTGCTGAAG | GTGAAGCAGC | | |

Table 71: Comparative Sequences relating to SAG1333

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| msa237456.2{328_H36B} | GctCATGTAC | CTGCAACAAG | cAaggATGAT | ATTGCTGAAG | GTGAAGCAGC |
| msa237456.2{328_COH1} | GctCATGTAC | CTGCAACAAG | cAaggATGAT | ATTGCTGAAG | GTGAAGCAGC |
| msa237456.2{328_M732} | GctCATGTAC | CTGCAACAAG | cAaggATGAT | ATTGCTGAAG | GTGAAGCAGC |
| msa237456.2{328_M781} | GctCATGTAC | CTGCAACAAG | cAaggATGAT | ATTGCTGAAG | GTGAAGCAGC |
| msa237456.2{328_JM9130013} | GctCATGTAC | CTGCAACAAG | cAaggATGAT | ATTGCTGAAG | GTGAAGCAGC |
| msa237456.2{328_A909} | GctCATGTAC | CTGCAACAAG | cAaggATGAT | ATTGCTGAAG | GTGAAGCAGC |
| msa237456.2{328_O90} | GctCATGTAC | CTGCAACAAG | cAaggATGAT | ATTGCTGAAG | GTGAAGCAGC |
| msa237456.2{328_CJB110} | GctCATGTAC | CTGCAACAAG | cAaggATGAT | ATTGCTGAAG | GTGAAGCAGC |
| Consensus | ***-***** | *****-*** | *****-*** | *****-*** | *****-*** |
| msa237456.2{328_1169NT} | AGAAATGATG | AAAAAAGTCA | ATCAACTCTT | CCCTGAAAAT | AGCGTAGATA |
| msa237456.2{328_2603} | AGAAATGATG | AAAAAAGTCA | ATCAACTCTT | CCCTGAAAAT | AGCGTAGATA |
| msa237456.2{328_18RS21} | AGAAATGATG | AAAAAAGTCA | ATCAACTCTT | CCCTGAAAAT | AGCGTAGATA |
| msa237456.2{328_H36B} | AGAAATGATG | AAAAAAGTCA | ATCAACTCTT | CCCTGAAAAT | AGCGTAGATA |
| msa237456.2{328_COH1} | AGAAATGATG | AAAAAAGTCA | ATCAACTCTT | CCCTGAAAAT | AGCGTAGATA |
| msa237456.2{328_M732} | AGAAATGATG | AAAAAAGTCA | ATCAACTCTT | CCCTGAAAAT | AGCGTAGATA |
| msa237456.2{328_M781} | AGAAATGATG | AAAAAAGTCA | ATCAACTCTT | CCCTGAAAAT | AGCGTAGATA |
| msa237456.2{328_JM9130013} | AGAAATGATG | AAAAAAGTCA | ATCAACTCTT | CCCTGAAAAT | AGCGTAGATA |
| msa237456.2{328_A909} | AGAAATGATG | AAAAAAGTCA | ATCAACTCTT | CCCTGAAAAT | AGCGTAGATA |
| msa237456.2{328_O90} | AGAAATGATG | AAAAAAGTCA | ATCAACTCTT | CCCTGAAAAT | AGCGTAGATA |
| msa237456.2{328_CJB110} | AGAAATGATG | AAAAAAGTCA | ATCAACTCTT | CCCTGAAAAT | AGCGTAGATA |
| Consensus | *****-*** | *****-*** | *****-*** | *****-*** | *****-*** |
| msa237456.2{328_1169NT} | TTGTCCTTGC | TGGACACAAT | CATCAATATA | CAAATGGTCT | TGTTGGTAAA |
| msa237456.2{328_2603} | TTGTCCTTGC | TGGACACAAT | CATCAATATA | CAAATGGTCT | TGTTGGTAAA |
| msa237456.2{328_18RS21} | TTGTCCTTGC | TGGACACAAT | CATCAATATA | CAAATGGTCT | TGTTGGTAAA |
| msa237456.2{328_H36B} | TTGTCCTTGC | TGGACACAAT | CATCAATATA | CAAATGGTCT | TGTTGGTAAA |
| msa237456.2{328_COH1} | TTGTCCTTGC | TGGACACAAT | CATCAATATA | CAAATGGTCT | TGTTGGTAAA |
| msa237456.2{328_M732} | TTGTCCTTGC | TGGACACAAT | CATCAATATA | CAAATGGTCT | TGTTGGTAAA |
| msa237456.2{328_M781} | TTGTCCTTGC | TGGACACAAT | CATCAATATA | CAAATGGTCT | TGTTGGTAAA |
| msa237456.2{328_JM9130013} | TTGTCCTTGC | TGGACACAAT | CATCAATATA | CAAATGGTCT | TGTTGGTAAA |
| msa237456.2{328_A909} | TTGTCCTTGC | TGGACACAAT | CATCAATATA | CAAATGGTCT | TGTTGGTAAA |
| msa237456.2{328_O90} | TTGTCCTTGC | TGGACACAAT | CATCAATATA | CAAATGGTCT | TGTTGGTAAA |
| msa237456.2{328_CJB110} | TTGTCCTTGC | TGGACACAAT | CATCAATATA | CAAATGGTCT | TGTTGGTAAA |
| Consensus | *****-*** | *****-*** | *****-*** | *****-*** | *****-*** |
| msa237456.2{328_1169NT} | ACTCGcATTG | TACAAGCGCT | CTCTCAAGGA | AAAGCCTATG | CTGatGTACG |
| msa237456.2{328_2603} | ACTCGcATTG | TACAAGCGCT | CTCTCAAGGA | AAAGCCTATG | CTGatGTACG |
| msa237456.2{328_18RS21} | ACTCGcATTG | TACAAGCGCT | CTCTCAAGGA | AAAGCCTATG | CTGatGTACG |
| msa237456.2{328_H36B} | ACTCGcATTG | TACAAGCGCT | CTCTCAAGGA | AAAGCCTATG | CTGatGTACG |
| msa237456.2{328_COH1} | ACTCGcATTG | TACAAGCGCT | CTCTCAAGGA | AAAGCCTATG | CTGatGTACG |
| msa237456.2{328_M732} | ACTCGcATTG | TACAAGCGCT | CTCTCAAGGA | AAAGCCTATG | CTGatGTACG |
| msa237456.2{328_M781} | ACTCGcATTG | TACAAGCGCT | CTCTCAAGGA | AAAGCCTATG | CTGatGTACG |
| msa237456.2{328_JM9130013} | ACTCGcATTG | TACAAGCGCT | CTCTCAAGGA | AAAGCCTATG | CTGatGTACG |
| msa237456.2{328_A909} | ACTCGcATTG | TACAAGCGCT | CTCTCAAGGA | AAAGCCTATG | CTGatGTACG |
| msa237456.2{328_O90} | ACTCGcATTG | TACAAGCGCT | CTCTCAAGGA | AAAGCCTATG | CTGatGTACG |
| msa237456.2{328_CJB110} | ACTCGcATTG | TACAAGCGCT | CTCTCAAGGA | AAAGCCTATG | CTGatGTACG |
| Consensus | *****-*** | *****-*** | *****-*** | *****-*** | *****-*** |
| msa237456.2{328_1169NT} | TGGTGTCTTA | GATACTGATA | CACAAGATTT | CATTGaaACC | CCTTCAGCTA |
| msa237456.2{328_2603} | TGGTGTCTTA | GATACTGATA | CACAAGATTT | CATTGaaACC | CCTTCAGCTA |
| msa237456.2{328_18RS21} | TGGTGTCTTA | GATACTGATA | CACAAGATTT | CATTGaaACC | CCTTCAGCTA |
| msa237456.2{328_H36B} | TGGTGTCTTA | GATACTGATA | CACAAGATTT | CATTGaaACC | CCTTCAGCTA |
| msa237456.2{328_COH1} | TGGTGTCTTA | GATACTGATA | CACAAGATTT | CATTGaaACC | CCTTCAGCTA |
| msa237456.2{328_M732} | TGGTGTCTTA | GATACTGATA | CACAAGATTT | CATTGaaACC | CCTTCAGCTA |
| msa237456.2{328_M781} | TGGTGTCTTA | GATACTGATA | CACAAGATTT | CATTGaaACC | CCTTCAGCTA |
| msa237456.2{328_JM9130013} | TGGTGTCTTA | GATACTGATA | CACAAGATTT | CATTGaaACC | CCTTCAGCTA |
| msa237456.2{328_A909} | TGGTGTCTTA | GATACTGATA | CACAAGATTT | CATTGaaACC | CCTTCAGCTA |
| msa237456.2{328_O90} | TGGTGTCTTA | GATACTGATA | CACAAGATTT | CATTGaaACC | CCTTCAGCTA |
| msa237456.2{328_CJB110} | TGGTGTCTTA | GATACTGATA | CACAAGATTT | CATTGaaACC | CCTTCAGCTA |
| Consensus | *****-*** | *****-*** | *****-*** | *****-*** | *****-*** |
| msa237456.2{328_1169NT} | AAGTAaTTGC | AGTTGCTCCT | GGTAAAAAAA | CAGGTAGTGC | CGATATTCAA |
| msa237456.2{328_2603} | AAGTAaTTGC | AGTTGCTCCT | GGTAAAAAAA | CAGGTAGTGC | CGATATTCAA |
| msa237456.2{328_18RS21} | AAGTAaTTGC | AGTTGCTCCT | GGTAAAAAAA | CAGGTAGTGC | CGATATTCAA |
| msa237456.2{328_H36B} | AAGTAaTTGC | AGTTGCTCCT | GGTAAAAAAA | CAGGTAGTGC | CGATATTCAA |
| msa237456.2{328_COH1} | AAGTAaTTGC | AGTTGCTCCT | GGTAAAAAAA | CAGGTAGTGC | CGATATTCAA |
| msa237456.2{328_M732} | AAGTAaTTGC | AGTTGCTCCT | GGTAAAAAAA | CAGGTAGTGC | CGATATTCAA |
| msa237456.2{328_M781} | AAGTAaTTGC | AGTTGCTCCT | GGTAAAAAAA | CAGGTAGTGC | CGATATTCAA |
| msa237456.2{328_JM9130013} | AAGTAaTTGC | AGTTGCTCCT | GGTAAAAAAA | CAGGTAGTGC | CGATATTCAA |
| msa237456.2{328_A909} | AAGTAaTTGC | AGTTGCTCCT | GGTAAAAAAA | CAGGTAGTGC | CGATATTCAA |
| msa237456.2{328_O90} | AAGTAaTTGC | AGTTGCTCCT | GGTAAAAAAA | CAGGTAGTGC | CGATATTCAA |
| msa237456.2{328_CJB110} | AAGTAaTTGC | AGTTGCTCCT | GGTAAAAAAA | CAGGTAGTGC | CGATATTCAA |
| Consensus | *****-*** | *****-*** | *****-*** | *****-*** | *****-*** |
| msa237456.2{328_1169NT} | GCCATTGTTG | ACCAAGCTAA | TACTATCGTT | AAACAAGTAA | CAGAAGCTAA |
| msa237456.2{328_2603} | GCCATTGTTG | ACCAAGCTAA | TACTATCGTT | AAACAAGTAA | CAGAAGCTAA |

Table 71: Comparative Sequences relating to SAG1333

| | | | | | |
|----------------------------|-------------|------------|------------|------------|------------|
| msa237456.2{328_18RS21} | GCCATTGTTG | ACCAAGCTAA | TACTATCGTT | AAACAAGTAA | CAGAAGCTAA |
| msa237456.2{328_H36B} | GCCATTGTTG | ACCAAGCTAA | TACTATCGTT | AAACAAGTAA | CAGAAGCTAA |
| msa237456.2{328_COH1} | GCCATTGTTG | ACCAAGCTAA | TACTATCGTT | AAACAAGTAA | CAGAAGCTAA |
| msa237456.2{328_M732} | GCCATTGTTG | ACCAAGCTAA | TACTATCGTT | AAACAAGTAA | CAGAAGCTAA |
| msa237456.2{328_M781} | GCCATTGTTG | ACCAAGCTAA | TACTATCGTT | AAACAAGTAA | CAGAAGCTAA |
| msa237456.2{328_JM9130013} | GCCATTGTTG | ACCAAGCTAA | TACTATCGTT | AAACAAGTAA | CAGAAGCTAA |
| msa237456.2{328_A909} | GCCATTGTTG | ACCAAGCTAA | TACTATCGTT | AAACAAGTAA | CAGAAGCTAA |
| msa237456.2{328_090} | GCCATTGTTG | ACCAAGCTAA | TACTATCGTT | AAACAAGTAA | CAGAAGCTAA |
| msa237456.2{328_CJB110} | GCCATTGTTG | ACCAAGCTAA | TACTATCGTT | AAACAAGTAA | CAGAAGCTAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | AATTGGTACT | GCCGAGGTAA | GTGtCATGAT | TACGCGTTCT | GTTGATCAAG |
| msa237456.2{328_2603} | AATTGGTACT | GCCGAGGTAA | GTGtCATGAT | TACGCGTTCT | GTTGATCAAG |
| msa237456.2{328_18RS21} | AATTGGTACT | GCCGAGGTAA | GTGgCATGAT | TACGCGTTCT | GTTGATCAAG |
| msa237456.2{328_H36B} | AATTGGTACT | GCCGAGGTAA | GTGgCATGAT | TACGCGTTCT | GTTGATCAAG |
| msa237456.2{328_COH1} | AATTGGTACT | GCCGAGGTAA | GTGgCATGAT | TACGCGTTCT | GTTGATCAAG |
| msa237456.2{328_M732} | AATTGGTACT | GCCGAGGTAA | GTGgCATGAT | TACGCGTTCT | GTTGATCAAG |
| msa237456.2{328_M781} | AATTGGTACT | GCCGAGGTAA | GTGgCATGAT | TACGCGTTCT | GTTGATCAAG |
| msa237456.2{328_JM9130013} | AATTGGTACT | GCCGAGGTAA | GTGgCATGAT | TACGCGTTCT | GTTGATCAAG |
| msa237456.2{328_A909} | AATTGGTACT | GCCGAGGTAA | GTGgCATGAT | TACGCGTTCT | GTTGATCAAG |
| msa237456.2{328_090} | AATTGGTACT | GCCGAGGTAA | GTGgCATGAT | TACGCGTTCT | GTTGATCAAG |
| msa237456.2{328_CJB110} | AATTGGTACT | GCCGAGGTAA | GTGgCATGAT | TACGCGTTCT | GTTGATCAAG |
| Consensus | ***** | ***** | ***_***** | ***** | ***** |
| msa237456.2{328_1169NT} | ATAATGTTAG | TCCgGTAGGC | AGCCTCATCA | CAGAGGCTCA | ACTAGCAATT |
| msa237456.2{328_2603} | ATAATGTTAG | TCCgGTAGGC | AGCCTCATCA | CAGAGGCTCA | ACTAGCAATT |
| msa237456.2{328_18RS21} | ATAATGTTAG | TCCgGTAGGC | AGCCTCATCA | CAGAGGCTCA | ACTAGCAATT |
| msa237456.2{328_H36B} | ATAATGTTAG | TCCgGTAGGC | AGCCTCATCA | CAGAGGCTCA | ACTAGCAATT |
| msa237456.2{328_COH1} | ATAATGTTAG | TCCgGTAGGC | AGCCTCATCA | CAGAGGCTCA | ACTAGCAATT |
| msa237456.2{328_M732} | ATAATGTTAG | TCCgGTAGGC | AGCCTCATCA | CAGAGGCTCA | ACTAGCAATT |
| msa237456.2{328_M781} | ATAATGTTAG | TCCgGTAGGC | AGCCTCATCA | CAGAGGCTCA | ACTAGCAATT |
| msa237456.2{328_JM9130013} | ATAATGTTAG | TCCgGTAGGC | AGCCTCATCA | CAGAGGCTCA | ACTAGCAATT |
| msa237456.2{328_A909} | ATAATGTTAG | TCCgGTAGGC | AGCCTCATCA | CAGAGGCTCA | ACTAGCAATT |
| msa237456.2{328_090} | ATAATGTTAG | TCCgGTAGGC | AGCCTCATCA | CAGAGGCTCA | ACTAGCAATT |
| msa237456.2{328_CJB110} | ATAATGTTAG | TCCgGTAGGC | AGCCTCATCA | CAGAGGCTCA | ACTAGCAATT |
| Consensus | ***** | ***_***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | GCTCGAAAAA | GCTGGCCAGA | TATCGATTIT | GCCATGACAA | ATAATGGTGG |
| msa237456.2{328_2603} | GCTCGAAAAA | GCTGGCCAGA | TATCGATTIT | GCCATGACAA | ATAATGGTGG |
| msa237456.2{328_18RS21} | GCTCGAAAAA | GCTGGCCAGA | TATCGATTIT | GCCATGACAA | ATAATGGTGG |
| msa237456.2{328_H36B} | GCTCGAAAAA | GCTGGCCAGA | TATCGATTIT | GCCATGACAA | ATAATGGTGG |
| msa237456.2{328_COH1} | GCTCGAAAAA | GCTGGCCAGA | TATCGATTIT | GCCATGACAA | ATAATGGTGG |
| msa237456.2{328_M732} | GCTCGAAAAA | GCTGGCCAGA | TATCGATTIT | GCCATGACAA | ATAATGGTGG |
| msa237456.2{328_M781} | GCTCGAAAAA | GCTGGCCAGA | TATCGATTIT | GCCATGACAA | ATAATGGTGG |
| msa237456.2{328_JM9130013} | GCTCGAAAAA | GCTGGCCAGA | TATCGATTIT | GCCATGACAA | ATAATGGTGG |
| msa237456.2{328_A909} | GCTCGAAAAA | GCTGGCCAGA | TATCGATTIT | GCCATGACAA | ATAATGGTGG |
| msa237456.2{328_090} | GCTCGAAAAA | GCTGGCCAGA | TATCGATTIT | GCCATGACAA | ATAATGGTGG |
| msa237456.2{328_CJB110} | GCTCGAAAAA | GCTGGCCAGA | TATCGATTIT | GCCATGACAA | ATAATGGTGG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | CATTCTGTGCT | GACTTACTCA | TCAAACCAGA | TGGAACAATC | ACCTGGGGAG |
| msa237456.2{328_2603} | CATTCTGTGCT | GACTTACTCA | TCAAACCAGA | TGGAACAATC | ACCTGGGGAG |
| msa237456.2{328_18RS21} | CATTCTGTGCT | GACTTACTCA | TCAAACCAGA | TGGAACAATC | ACCTGGGGAG |
| msa237456.2{328_H36B} | CATTCTGTGCT | GACTTACTCA | TCAAACCAGA | TGGAACAATC | ACCTGGGGAG |
| msa237456.2{328_COH1} | CATTCTGTGCT | GACTTACTCA | TCAAACCAGA | TGGAACAATC | ACCTGGGGAG |
| msa237456.2{328_M732} | CATTCTGTGCT | GACTTACTCA | TCAAACCAGA | TGGAACAATC | ACCTGGGGAG |
| msa237456.2{328_M781} | CATTCTGTGCT | GACTTACTCA | TCAAACCAGA | TGGAACAATC | ACCTGGGGAG |
| msa237456.2{328_JM9130013} | CATTCTGTGCT | GACTTACTCA | TCAAACCAGA | TGGAACAATC | ACCTGGGGAG |
| msa237456.2{328_A909} | CATTCTGTGCT | GACTTACTCA | TCAAACCAGA | TGGAACAATC | ACCTGGGGAG |
| msa237456.2{328_090} | CATTCTGTGCT | GACTTACTCA | TCAAACCAGA | TGGAACAATC | ACCTGGGGAG |
| msa237456.2{328_CJB110} | CATTCTGTGCT | GACTTACTCA | TCAAACCAGA | TGGAACAATC | ACCTGGGGAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | CTGCACAAGC | AGTTCAACCT | TTTGGTAATA | TCTTACAAGT | CGTCGAAATT |
| msa237456.2{328_2603} | CTGCACAAGC | AGTTCAACCT | TTTGGTAATA | TCTTACAAGT | CGTCGAAATT |
| msa237456.2{328_18RS21} | CTGCACAAGC | AGTTCAACCT | TTTGGTAATA | TCTTACAAGT | CGTCGAAATT |
| msa237456.2{328_H36B} | CTGCACAAGC | AGTTCAACCT | TTTGGTAATA | TCTTACAAGT | CGTCGAAATT |
| msa237456.2{328_COH1} | CTGCACAAGC | AGTTCAACCT | TTTGGTAATA | TCTTACAAGT | CGTCGAAATT |
| msa237456.2{328_M732} | CTGCACAAGC | AGTTCAACCT | TTTGGTAATA | TCTTACAAGT | CGTCGAAATT |
| msa237456.2{328_M781} | CTGCACAAGC | AGTTCAACCT | TTTGGTAATA | TCTTACAAGT | CGTCGAAATT |
| msa237456.2{328_JM9130013} | CTGCACAAGC | AGTTCAACCT | TTTGGTAATA | TCTTACAAGT | CGTCGAAATT |
| msa237456.2{328_A909} | CTGCACAAGC | AGTTCAACCT | TTTGGTAATA | TCTTACAAGT | CGTCGAAATT |
| msa237456.2{328_090} | CTGCACAAGC | AGTTCAACCT | TTTGGTAATA | TCTTACAAGT | CGTCGAAATT |
| msa237456.2{328_CJB110} | CTGCACAAGC | AGTTCAACCT | TTTGGTAATA | TCTTACAAGT | CGTCGAAATT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | ACTGGTAGAG | ATCTTTTATA | AGCACTCAAC | GAACAATACG | ACCAAAAACA |

Table 71: Comparative Sequences relating to SAG1333

| | | | | | |
|----------------------------|------------|-------------|-------------|------------|------------|
| msa237456.2{328_1169NT} | GATTTAGAAA | AAGCTGGTAA | AAAAGTGAGC | gTCCAAATA | ATAAACCTAA |
| msa237456.2{328_2603} | GATTTAGAAA | AAGCTGGTAA | AAAAGTGAGC | gTCCAAATA | ATAAACCTAA |
| msa237456.2{328_18RS21} | GATTTAGAAA | AAGCTGGTAA | AAAAGTGAGC | gTCCAAATA | ATAAACCTAA |
| msa237456.2{328_H36B} | GATTTAGAAA | AAGCTGGTAA | AAAAGTGAGC | gTCCAAATA | ATAAACCTAA |
| msa237456.2{328_COH1} | GATTTAGAAA | AAGCTGGTAA | AAAAGTGAGC | aTCCAAATA | ATAAACCTAA |
| msa237456.2{328_M732} | GATTTAGAAA | AAGCTGGTAA | AAAAGTGAGC | aTCCAAATA | ATAAACCTAA |
| msa237456.2{328_M781} | GATTTAGAAA | AAGCTGGTAA | AAAAGTGAGC | aTCCAAATA | ATAAACCTAA |
| msa237456.2{328_JM9130013} | GATTTAGAAA | AAGCTGGTAA | AAAAGTGAGC | gTCCAAATA | ATAAACCTAA |
| msa237456.2{328_A909} | GATTTAGAAA | AAGCTGGTAA | AAAAGTGAGC | gTCCAAATA | ATAAACCTAA |
| msa237456.2{328_090} | GATTTAGAAA | AAGCTGGTAA | AAAAGTGAGC | gTCCAAATA | ATAAACCTAA |
| msa237456.2{328_CJB110} | GATTTAGAAA | AAGCTGGTAA | AAAAGTGAGC | gTCCAAATA | ATAAACCTAA |
| Consensus | ***** | ***** | ***** | -***** | ***** |
| msa237456.2{328_1169NT} | AATCTATGTC | ACTATGAAGA | TGGTTAATGA | AACATTATCA | CAAAATGATG |
| msa237456.2{328_2603} | AATCTATGTC | ACTATGAAGA | TGGTTAATGA | AACATTATCA | CAAAATGATG |
| msa237456.2{328_18RS21} | AATCTATGTC | ACTATGAAGA | TGGTTAATGA | AACATTATCA | CAAAATGATG |
| msa237456.2{328_H36B} | AATCTATGTC | ACTATGAAGA | TGGTTAATGA | AACATTATCA | CAAAATGATG |
| msa237456.2{328_COH1} | AATCTATGTC | ACTATGAAGA | TGGTTAATGA | AACATTATCA | CAAAATGATG |
| msa237456.2{328_M732} | AATCTATGTC | ACTATGAAGA | TGGTTAATGA | AACATTATCA | CAAAATGATG |
| msa237456.2{328_M781} | AATCTATGTC | ACTATGAAGA | TGGTTAATGA | AACATTATCA | CAAAATGATG |
| msa237456.2{328_JM9130013} | AATCTATGTC | ACTATGAAGA | TGGTTAATGA | AACATTATCA | CAAAATGATG |
| msa237456.2{328_A909} | AATCTATGTC | ACTATGAAGA | TGGTTAATGA | AACATTATCA | CAAAATGATG |
| msa237456.2{328_090} | AATCTATGTC | ACTATGAAGA | TGGTTAATGA | AACATTATCA | CAAAATGATG |
| msa237456.2{328_CJB110} | AATCTATGTC | ACTATGAAGA | TGGTTAATGA | AACATTATCA | CAAAATGATG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | GTACACATAG | CATTATTaAG | AAACTTTTATT | TAGATCGACA | AGGAAATATT |
| msa237456.2{328_2603} | GTACACATAG | CATTATTaAG | AAACTTTTATT | TAGATCGACA | AGGAAATATT |
| msa237456.2{328_18RS21} | GTACACATAG | CATTATTaAG | AAACTTTTATT | TAGATCGACA | AGGAAATATT |
| msa237456.2{328_H36B} | GTACACATAG | CATTATTaAG | AAACTTTTATT | TAGATCGACA | AGGAAATATT |
| msa237456.2{328_COH1} | GTACACATAG | CATTATTaAG | AAACTTTTATT | TAGATCGACA | AGGAAATATT |
| msa237456.2{328_M732} | GTACACATAG | CATTATTaAG | AAACTTTTATT | TAGATCGACA | AGGAAATATT |
| msa237456.2{328_M781} | GTACACATAG | CATTATTaAG | AAACTTTTATT | TAGATCGACA | AGGAAATATT |
| msa237456.2{328_JM9130013} | GTACACATAG | CATTATTaAG | AAACTTTTATT | TAGATCGACA | AGGAAATATT |
| msa237456.2{328_A909} | GTACACATAG | CATTATTaAG | AAACTTTTATT | TAGATCGACA | AGGAAATATT |
| msa237456.2{328_090} | GTACACATAG | CATTATTaAG | AAACTTTTATT | TAGATCGACA | AGGAAATATT |
| msa237456.2{328_CJB110} | GTACACATAG | CATTATTaAG | AAACTTTTATT | TAGATCGACA | AGGAAATATT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | GTAGCACAAG | AGATTGTATC | AGACACTTTA | AACCAAACAA | AATCAAATC |
| msa237456.2{328_2603} | GTAGCACAAG | AGATTGTATC | AGACACTTTA | AACCAAACAA | AATCAAATC |
| msa237456.2{328_18RS21} | GTAGCACAAG | AGATTGTATC | AGACACTTTA | AACCAAACAA | AATCAAATC |
| msa237456.2{328_H36B} | GTAGCACAAG | AGATTGTATC | AGACACTTTA | AACCAAACAA | AATCAAATC |
| msa237456.2{328_COH1} | GTAGCACAAG | AGATTGTATC | AGACACTTTA | AACCAAACAA | AATCAAATC |
| msa237456.2{328_M732} | GTAGCACAAG | AGATTGTATC | AGACACTTTA | AACCAAACAA | AATCAAATC |
| msa237456.2{328_M781} | GTAGCACAAG | AGATTGTATC | AGACACTTTA | AACCAAACAA | AATCAAATC |
| msa237456.2{328_JM9130013} | GTAGCACAAG | AGATTGTATC | AGACACTTTA | AACCAAACAA | AATCAAATC |
| msa237456.2{328_A909} | GTAGCACAAG | AGATTGTATC | AGACACTTTA | AACCAAACAA | AATCAAATC |
| msa237456.2{328_090} | GTAGCACAAG | AGATTGTATC | AGACACTTTA | AACCAAACAA | AATCAAATC |
| msa237456.2{328_CJB110} | GTAGCACAAG | AGATTGTATC | AGACACTTTA | AACCAAACAA | AATCAAATC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | TACAAAAATC | AACCCCTGTA | CTACAATTCA | CAAAAAACAA | TTACACCAAT |
| msa237456.2{328_2603} | TACAAAAATC | AACCCCTGTA | CTACAATTCA | CAAAAAACAA | TTACACCAAT |
| msa237456.2{328_18RS21} | TACAAAAATC | AACCCCTGTA | CTACAATTCA | CAAAAAACAA | TTACACCAAT |
| msa237456.2{328_H36B} | TACAAAAATC | AACCCCTGTA | CTACAATTCA | CAAAAAACAA | TTACACCAAT |
| msa237456.2{328_COH1} | TACAAAAATC | AACCCCTGTA | CTACAATTCA | CAAAAAACAA | TTACACCAAT |
| msa237456.2{328_M732} | TACAAAAATC | AACCCCTGTA | CTACAATTCA | CAAAAAACAA | TTACACCAAT |
| msa237456.2{328_M781} | TACAAAAATC | AACCCCTGTA | CTACAATTCA | CAAAAAACAA | TTACACCAAT |
| msa237456.2{328_JM9130013} | TACAAAAATC | AACCCCTGTA | CTACAATTCA | CAAAAAACAA | TTACACCAAT |
| msa237456.2{328_A909} | TACAAAAATC | AACCCCTGTA | CTACAATTCA | CAAAAAACAA | TTACACCAAT |
| msa237456.2{328_090} | TACAAAAATC | AACCCCTGTA | CTACAATTCA | CAAAAAACAA | TTACACCAAT |
| msa237456.2{328_CJB110} | TACAAAAATC | AACCCCTGTA | CTACAATTCA | CAAAAAACAA | TTACACCAAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237456.2{328_1169NT} | TTACAGCTAT | TAACCCCTATG | AGAAATTATG | GCAAACCATC | AAACTCCACT |
| msa237456.2{328_2603} | TTACAGCTAT | TAACCCCTATG | AGAAATTATG | GCAAACCATC | AAACTCCACT |
| msa237456.2{328_18RS21} | TTACAGCTAT | TAACCCCTATG | AGAAATTATG | GCAAACCATC | AAACTCCACT |
| msa237456.2{328_H36B} | TTACAGCTAT | TAACCCCTATG | AGAAATTATG | GCAAACCATC | AAACTCCACT |
| msa237456.2{328_COH1} | TTACAGCTAT | TAACCCCTATG | AGAAATTATG | GCAAACCATC | AAACTCCACT |
| msa237456.2{328_M732} | TTACAGCTAT | TAACCCCTATG | AGAAATTATG | GCAAACCATC | AAACTCCACT |
| msa237456.2{328_M781} | TTACAGCTAT | TAACCCCTATG | AGAAATTATG | GCAAACCATC | AAACTCCACT |
| msa237456.2{328_JM9130013} | TTACAGCTAT | TAACCCCTATG | AGAAATTATG | GCAAACCATC | AAACTCCACT |
| msa237456.2{328_A909} | TTACAGCTAT | TAACCCCTATG | AGAAATTATG | GCAAACCATC | AAACTCCACT |
| msa237456.2{328_090} | TTACAGCTAT | TAACCCCTATG | AGAAATTATG | GCAAACCATC | AAACTCCACT |
| msa237456.2{328_CJB110} | TTACAGCTAT | TAACCCCTATG | AGAAATTATG | GCAAACCATC | AAACTCCACT |
| Consensus | ***** | ***** | ***** | ***** | ***** |

Table 71: Comparative Sequences relating to SAG1333

| | 1951 | | | 2000 |
|----------------------------|----------------------|------------|-------------|-----------------------|
| msa237456.2{328_1169NT} | ACTGTAAAT CAaa----- | ----- | ----- | ----- |
| msa237456.2{328_2603} | ACTGTAAAT CAaaACAAtt | acaaaaaaca | aactctgaat | atggacaatc |
| msa237456.2{328_18RS21} | ACTGTAAAT CAaaA----- | ----- | ----- | ----- |
| msa237456.2{328_H36B} | ACTGTAAAT CAaa----- | ----- | ----- | ----- |
| msa237456.2{328_COH1} | ACTGTAAAT CAaa----- | ----- | ----- | ----- |
| msa237456.2{328_M732} | ACTGTAAAT CAaaACAA-- | ----- | ----- | ----- |
| msa237456.2{328_M781} | ACTGTAAAT CAaa----- | ----- | ----- | ----- |
| msa237456.2{328_JM9130013} | ACTGTAAAT CAaaA----- | ----- | ----- | ----- |
| msa237456.2{328_A909} | ACTGTAAAT CAaaACAA-- | ----- | ----- | ----- |
| msa237456.2{328_090} | ACTGTAAAT CAaaACAA-- | ----- | ----- | ----- |
| msa237456.2{328_CJB110} | ACTGTAAAT CA----- | ----- | ----- | ----- |
| Consensus | ***** **_***** | ***** | ***** | ***** |
| | 2001 | | | 2050 |
| msa237456.2{328_1169NT} | ----- | ----- | ----- | ----- |
| msa237456.2{328_2603} | attccttatg | tctgtctttg | gtgttggaact | tataggaatt gctttaaata |
| msa237456.2{328_18RS21} | ----- | ----- | ----- | ----- |
| msa237456.2{328_H36B} | ----- | ----- | ----- | ----- |
| msa237456.2{328_COH1} | ----- | ----- | ----- | ----- |
| msa237456.2{328_M732} | ----- | ----- | ----- | ----- |
| msa237456.2{328_M781} | ----- | ----- | ----- | ----- |
| msa237456.2{328_JM9130013} | ----- | ----- | ----- | ----- |
| msa237456.2{328_A909} | ----- | ----- | ----- | ----- |
| msa237456.2{328_090} | ----- | ----- | ----- | ----- |
| msa237456.2{328_CJB110} | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ***** | ***** |
| | 2051 | | | 2070 |
| msa237456.2{328_1169NT} | ----- | ----- | ----- | ----- |
| msa237456.2{328_2603} | caaagaaaaa | acatatgaaa | ----- | ----- |
| msa237456.2{328_18RS21} | ----- | ----- | ----- | ----- |
| msa237456.2{328_H36B} | ----- | ----- | ----- | ----- |
| msa237456.2{328_COH1} | ----- | ----- | ----- | ----- |
| msa237456.2{328_M732} | ----- | ----- | ----- | ----- |
| msa237456.2{328_M781} | ----- | ----- | ----- | ----- |
| msa237456.2{328_JM9130013} | ----- | ----- | ----- | ----- |
| msa237456.2{328_A909} | ----- | ----- | ----- | ----- |
| msa237456.2{328_090} | ----- | ----- | ----- | ----- |
| msa237456.2{328_CJB110} | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ----- | ----- |

SEQ ID NO. 7112

STRAIN 2603 frame: 1

MKKKIILKSSVLGLVAGTSIMFSSVFADQVGQVIGVNDVFGALDNTGTANMPDGKVVANA
GTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVGASPANSGLLQDEPTVKNFNAMNVE
YGTGNGHEFDEGLAEYNRIVTGKAPAPDSNINNITKSYPHAAKQEIIVVANVIDKVNKQI
PYNWKPYAIKNI PVNNKSVNVGFIGIVTKDIPNLVLRKNYBQYEFLEDEAETIVKYAKELQ
AKNVKAIIVLAHVPAATSKNDIAEGEAAEMMKVNLFPENSVDIVFAGHNHQTNGLVGK
TRIVQALSQGGKAYADVRGVLDTDTQDFIETPSAKVIAVAPGKKTGSADIQAIQVQANTIV
KQVTEAKIGTAEVSMITRSVDQDNVSPVGSGLITEAQLAIARKSWPIDFAMTNNGGIRAD
LLIKPDGTITWGAAQAVQPFNGILQVVEITGRDLYKALNEQYDQKQNFLLQIAGLRYTY
TDNKEGGEETPFKVVKAYKSNGBEINPDACYKLVINDFLFGGGDGFAFRNAKLLGAINP
DTEVFMAIYITDLEKAGKKVSVPNKPKIYVTMKNVNETITQNDGTHSIIKKLYLDRQGN
VAQEIVSDTLNQTQKSKSTKINPVTTIHKQLHQFTA INPMRNYGKPSNSTTVKSKQLPKT
NSEYQGSFLMSVFGVGLIGIALNTKKKHKM

SEQ ID NO. 7113

STRAIN 090 frame: 3

VGVQVIGVNDVFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRV
QAGDMVGASPANSGLLQDEPTVKTNFAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPDS
NINNITKSYPHAAKQEIIVVANVIDKVNKQIPYNWKPYAIKNI PVNNKSVNVGFIGIVTK
DIPNLVLRKNYBQYEFLEDEAETIVKYAKELQAKNVKAIIVLAHVPAATSKDDIAEGEAAEM
MKVNLFPENSVDIVFAGHNHQTNGLVGKTRIVQALSQGGKAYADVRGVLDTDTQDFIET
TPSAKVAVAPGKKTGSADIQAIQVQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPV
GSLITEAQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFNGILQVVE
ITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGBEINPD
KYKLVINDFLFGGGDGFAFRNAKLLGAINPDTEVFMAIYITDLEKAGKKVSVPNKPKIY
VTMKNVNETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTQKSKSTKINPVTTIHK
QLHQFTA INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7114

STRAIN A909 frame: 3

VNDVFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVG
ASPANSGLLQDEPTVKTNFAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPDSNINNITK
SYPHAAKQEIIVVANVIDKVNKQIPYNWKPYAIKNI PVNNKSVNVGFIGIVTKDIPNLV
RKNYBQYEFLEDEAETIVKYAKELQAKNVKAIIVLAHVPAATSKDDIAEGEAAEMMKVNL
FPENSVDIVFAGHNHQTNGLVGKTRIVQALSQGGKAYADVRGVLDTDTQDFIETPSAKVI
AVAPGKKTGSADIQAIQVQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVGSGLITEA
QLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFNGILQVVEITGRDLY
KALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGBEINPDACYKLVIN
DFLFGGGDGFAFRNAKLLGAINPDTEVFMAIYITDLEKAGKKVSVPNKPKIYVTMKNV
ETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTQKSKSTKINPVTTIHKQLHQFTA

Table 71: Comparative Sequences relating to SAG1333

INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7115

STRAIN H36B frame: 2

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAI VDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQVV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTNDKEGGEETPFKVVKAYKSNGEIINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKVSVPNNKPKI
 YVTMKNVNETITQNDGTYSIIKKLYLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7116

STRAIN 18RS21 frame: 1

DQVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
 RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIV
 TKDI PNLVLRKNYEQYEFLEDAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAA
 EMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDQDFI
 IETPSAKVIAVAPGKKTGSADIQAI VDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVS
 PVGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQVV
 VEITGRDLYKALNEQYDQKQNFLLQIAGLRITYTNDKEGGEETPFKVVKAYKSNGEIINPD
 DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKVSVPNNKPKI
 IYVTMKNVNETITQNDGTYSIIKKLYLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKSK

SEQ ID NO. 7117

STRAIN M732 frame: 3

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAI VDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQVV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTNDKEGGEETPFKVVKAYKSNGEIINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKVSVPNNKPKI
 YVTMKNVNETITQNDGTYSIIKKLYLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7118

STRAIN COH1 frame: 3

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAI VDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQVV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTNDKEGGEETPFKVVKAYKSNGEIINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKVSVPNNKPKI
 YVTMKNVNETITQNDGTYSIIKKLYLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7119

STRAIN M781 frame: 1

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAI VDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQVV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTNDKEGGEETPFKVVKAYKSNGEIINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKVSVPNNKPKI
 YVTMKNVNETITQNDGTYSIIKKLYLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7120

STRAIN CJB110 frame: 1

DQVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
 RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYAI KNI PVNNKSVNVGFIGIV
 TKDI PNLVLRKNYEQYEFLEDAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAA
 EMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDQDFI
 IETPSAKVIAVAPGKKTGSADIQAI VDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVS
 PVGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQVV
 VEITGRDLYKALNEQYDQKQNFLLQIAGLRITYTNDKEGGEETPFKVVKAYKSNGEIINPD

Table 71: Comparative Sequences relating to SAG1333

DAKYKLIVNDLFLGGGDFGAFSRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPK
IYVTMKNVNETITQNDGTHSI IKKLYLDRQGNIVAQEI VSDTLNQTSKSTKINPVTTH
KKQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7121

STRAIN 1169NT frame: 1

QVGQVIGVNDLFGALDNTGTANMPDGKVNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPDNSGLLQDEPTVKFNAMNVEYGTGLGNHEFDEGLAEYNRI VTGKAPAPD
SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYAIKNI PVNNKSVNVGFIGIVT
KDI PNVLVRKNYEQYEFLEAETI VKYAKELQAKNVKAI VVLAHV PATSKND IAEGEAAE
MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQGKAYADVRGVLDTDQDFI
ETPSAKVIAVAPGKKTGSADIQAI VDOQANTIVKQVTEAKIGTAEVSMITRSVDQDNVSP
VGSILTEAQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAQAQVQFPGNQLQV
EITGRDLKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKA YKSNGEIINPD
AKYKLIVNDLFLGGGDFGAFSRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKI
YVTMKNVNETITQNDGTHSI IKKLYLDRQGNIVAQEI VSDTLNQTSKSTKINPVTTHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7122

STRAIN JM9130013 frame: 2

GVQVIGVNDLFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQ
AGDMVGASPDNSGLLQDEPTVKFNAMNVEYGTGLGNHEFDEGLAEYNRI VTGKAPAPDSN
INNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTIKNI PVNNKSVNVGFIGIVTKD
IPNLVLRKNYEQYEFLEAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAEM
KKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQGKAYADVRGVLDTDQDFIET
PSAKVIAVAPGKKTGSADIQAI VDOQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVG
SLITEAQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAQAQVQFPGNQLQVIE
TGRDLKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKA YKSNGEIINPD
YKLIVNDLFLGGGDFGAFSRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKIYV
TMKNVNETITQNDGTHSI IKKLYLDRQGNIVAQEI VSDTLNQTSKSTKINPVTTHKKQ
LHQFTAINPMRNYGKPSNSTTVKS

PRETTY of: /biotmp/msa237615.2{*} May 14, 2003 03:22 ..

| | | | |
|----------------------------|------------|-------------|-----------------------------------|
| | i | | 50 |
| msa237615.2{328_1169NT} | ----- | -----qv | gvqvigVNDF HGALDNTGTA |
| msa237615.2{328_2603} | mkkkilkss | vlglvagtsi | mfssvfadqv gvqvigVNDF HGALDNTGTA |
| msa237615.2{328_A909} | ----- | ----- | -----VNDF HGALDNTGTA |
| msa237615.2{328_M732} | ----- | -----qv | gvqvigVNDF HGALDNTGTA |
| msa237615.2{328_COH1} | ----- | -----qv | gvqvigVNDF HGALDNTGTA |
| msa237615.2{328_M781} | ----- | -----qv | gvqvigVNDF HGALDNTGTA |
| msa237615.2{328_H36B} | ----- | -----qv | gvqvigVNDF HGALDNTGTA |
| msa237615.2{328_JM9130013} | ----- | ----- | gvqvigVNDF HGALDNTGTA |
| msa237615.2{328_18RS21} | ----- | -----Dqv | gvqvigVNDF HGALDNTGTA |
| msa237615.2{328_090} | ----- | -----v | gvqvigVNDF HGALDNTGTA |
| msa237615.2{328_CJB110} | ----- | -----Dqv | gvqvigVNDF HGALDNTGTA |
| Consensus | ***** | ***** | ***** |
| | 51 | | 100 |
| msa237615.2{328_1169NT} | NMPDGKvNA | GTAQAQLDAYM | DDAQKDFKQT NPNGESIRVQ AGDMVGASPA |
| msa237615.2{328_2603} | NMPDGKvNA | GTAQAQLDAYM | DDAQKDFKQT NPNGESIRVQ AGDMVGASPA |
| msa237615.2{328_A909} | NMPDGKvNA | GTAQAQLDAYM | DDAQKDFKQT NPNGESIRVQ AGDMVGASPA |
| msa237615.2{328_M732} | NMPDGKvNA | GTAQAQLDAYM | DDAQKDFKQT NPNGESIRVQ AGDMVGASPA |
| msa237615.2{328_COH1} | NMPDGKvNA | GTAQAQLDAYM | DDAQKDFKQT NPNGESIRVQ AGDMVGASPA |
| msa237615.2{328_M781} | NMPDGKvNA | GTAQAQLDAYM | DDAQKDFKQT NPNGESIRVQ AGDMVGASPA |
| msa237615.2{328_H36B} | NMPDGKvNA | GTAQAQLDAYM | DDAQKDFKQT NPNGESIRVQ AGDMVGASPA |
| msa237615.2{328_JM9130013} | NMPDGKvNA | GTAQAQLDAYM | DDAQKDFKQT NPNGESIRVQ AGDMVGASPA |
| msa237615.2{328_18RS21} | NMPDGKvNA | GTAQAQLDAYM | DDAQKDFKQT NPNGESIRVQ AGDMVGASPA |
| msa237615.2{328_090} | NMPDGKvNA | GTAQAQLDAYM | DDAQKDFKQT NPNGESIRVQ AGDMVGASPA |
| msa237615.2{328_CJB110} | NMPDGKvNA | GTAQAQLDAYM | DDAQKDFKQT NPNGESIRVQ AGDMVGASPA |
| Consensus | ***** | ***** | ***** |
| | 101 | | 150 |
| msa237615.2{328_1169NT} | NSGLLQDEPT | VKnFNAMNVE | YGTGLGNHEFD EGLAEYNRIV TGKAPAPDSN |
| msa237615.2{328_2603} | NSGLLQDEPT | VKnFNAMNVE | YGTGLGNHEFD EGLAEYNRIV TGKAPAPDSN |
| msa237615.2{328_A909} | NSGLLQDEPT | VKtFNAMNVE | YGTGLGNHEFD EGLAEYNRIV TGKAPAPDSN |
| msa237615.2{328_M732} | NSGLLQDEPT | VKtFNAMNVE | YGTGLGNHEFD EGLAEYNRIV TGKAPAPDSN |
| msa237615.2{328_COH1} | NSGLLQDEPT | VKtFNAMNVE | YGTGLGNHEFD EGLAEYNRIV TGKAPAPDSN |
| msa237615.2{328_M781} | NSGLLQDEPT | VKtFNAMNVE | YGTGLGNHEFD EGLAEYNRIV TGKAPAPDSN |
| msa237615.2{328_H36B} | NSGLLQDEPT | VKtFNAMNVE | YGTGLGNHEFD EGLAEYNRIV TGKAPAPDSN |
| msa237615.2{328_JM9130013} | NSGLLQDEPT | VKtFNAMNVE | YGTGLGNHEFD EGLAEYNRIV TGKAPAPDSN |
| msa237615.2{328_18RS21} | NSGLLQDEPT | VKtFNAMNVE | YGTGLGNHEFD EGLAEYNRIV TGKAPAPDSN |
| msa237615.2{328_090} | NSGLLQDEPT | VKtFNAMNVE | YGTGLGNHEFD EGLAEYNRIV TGKAPAPDSN |
| msa237615.2{328_CJB110} | NSGLLQDEPT | VKtFNAMNVE | YGTGLGNHEFD EGLAEYNRIV TGKAPAPDSN |
| Consensus | ***** | ***** | ***** |
| | 151 | | 200 |
| msa237615.2{328_1169NT} | INNITKSYPH | EAAKQEI VVA | NVIDKVNKQI PYNWKPYaIK NIPVNNKSVN |
| msa237615.2{328_2603} | INNITKSYPH | EAAKQEI VVA | NVIDKVNKQI PYNWKPYaIK NIPVNNKSVN |
| msa237615.2{328_A909} | INNITKSYPH | EAAKQEI VVA | NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN |
| msa237615.2{328_M732} | INNITKSYPH | EAAKQEI VVA | NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN |
| msa237615.2{328_COH1} | INNITKSYPH | EAAKQEI VVA | NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN |
| msa237615.2{328_M781} | INNITKSYPH | EAAKQEI VVA | NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN |

Table 71: Comparative Sequences relating to SAG1333

| | | | | | | | |
|----------------------------|------------|-------------|------------|-------------|------------|-------------|-----|
| msa237615.2{328_H36B} | INNITKSYPH | EAAKQEI VVA | NVIDKVNKQI | PYNWKPYtIK | NIPVNNKSVN | | |
| msa237615.2{328_JM9130013} | INNITKSYPH | EAAKQEI VVA | NVIDKVNKQI | PYNWKPYtIK | NIPVNNKSVN | | |
| msa237615.2{328_18RS21} | INNITKSYPH | EAAKQEI VVA | NVIDKVNKQI | PYNWKPYtIK | NIPVNNKSVN | | |
| msa237615.2{328_090} | INNITKSYPH | EAAKQEI VVA | NVIDKVNKQI | PYNWKPYaIK | NIPVNNKSVN | | |
| msa237615.2{328_CJB110} | INNITKSYPH | EAAKQEI VVA | NVIDKVNKQI | PYNWKPYaIK | NIPVNNKSVN | | |
| Consensus | ***** | ***** | ***** | *****_** | ***** | | |
| msa237615.2{328_1169NT} | 201 | VGFIGIVTKD | IPNLVLRKNY | EQYEFLDEAE | TIVKYAKELQ | AKNVKAI VVL | 250 |
| msa237615.2{328_2603} | VGFIGIVTKD | IPNLVLRKNY | EQYEFLDEAE | EQYEFLDEAE | TIVKYAKELQ | AKNVKAI VVL | |
| msa237615.2{328_A909} | VGFIGIVTKD | IPNLVLRKNY | EQYEFLDEAE | EQYEFLDEAE | TIVKYAKELQ | AKNVKAI VVL | |
| msa237615.2{328_M732} | VGFIGIVTKD | IPNLVLRKNY | EQYEFLDEAE | EQYEFLDEAE | TIVKYAKELQ | AKNVKAI VVL | |
| msa237615.2{328_COH1} | VGFIGIVTKD | IPNLVLRKNY | EQYEFLDEAE | EQYEFLDEAE | TIVKYAKELQ | AKNVKAI VVL | |
| msa237615.2{328_M781} | VGFIGIVTKD | IPNLVLRKNY | EQYEFLDEAE | EQYEFLDEAE | TIVKYAKELQ | AKNVKAI VVL | |
| msa237615.2{328_H36B} | VGFIGIVTKD | IPNLVLRKNY | EQYEFLDEAE | EQYEFLDEAE | TIVKYAKELQ | AKNVKAI VVL | |
| msa237615.2{328_JM9130013} | VGFIGIVTKD | IPNLVLRKNY | EQYEFLDEAE | EQYEFLDEAE | TIVKYAKELQ | AKNVKAI VVL | |
| msa237615.2{328_18RS21} | VGFIGIVTKD | IPNLVLRKNY | EQYEFLDEAE | EQYEFLDEAE | TIVKYAKELQ | AKNVKAI VVL | |
| msa237615.2{328_090} | VGFIGIVTKD | IPNLVLRKNY | EQYEFLDEAE | EQYEFLDEAE | TIVKYAKELQ | AKNVKAI VVL | |
| msa237615.2{328_CJB110} | VGFIGIVTKD | IPNLVLRKNY | EQYEFLDEAE | EQYEFLDEAE | TIVKYAKELQ | AKNVKAI VVL | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | |
| msa237615.2{328_1169NT} | 251 | AHVPATSKnD | IAEGEAAEMM | KKVNQLFPEN | SVDIVFAGHN | HQYTNGLVGK | 300 |
| msa237615.2{328_2603} | AHVPATSKnD | IAEGEAAEMM | KKVNQLFPEN | KKVNQLFPEN | SVDIVFAGHN | HQYTNGLVGK | |
| msa237615.2{328_A909} | AHVPATSKnD | IAEGEAAEMM | KKVNQLFPEN | KKVNQLFPEN | SVDIVFAGHN | HQYTNGLVGK | |
| msa237615.2{328_M732} | AHVPATSKnD | IAEGEAAEMM | KKVNQLFPEN | KKVNQLFPEN | SVDIVFAGHN | HQYTNGLVGK | |
| msa237615.2{328_COH1} | AHVPATSKnD | IAEGEAAEMM | KKVNQLFPEN | KKVNQLFPEN | SVDIVFAGHN | HQYTNGLVGK | |
| msa237615.2{328_M781} | AHVPATSKnD | IAEGEAAEMM | KKVNQLFPEN | KKVNQLFPEN | SVDIVFAGHN | HQYTNGLVGK | |
| msa237615.2{328_H36B} | AHVPATSKnD | IAEGEAAEMM | KKVNQLFPEN | KKVNQLFPEN | SVDIVFAGHN | HQYTNGLVGK | |
| msa237615.2{328_JM9130013} | AHVPATSKnD | IAEGEAAEMM | KKVNQLFPEN | KKVNQLFPEN | SVDIVFAGHN | HQYTNGLVGK | |
| msa237615.2{328_18RS21} | AHVPATSKnD | IAEGEAAEMM | KKVNQLFPEN | KKVNQLFPEN | SVDIVFAGHN | HQYTNGLVGK | |
| msa237615.2{328_090} | AHVPATSKnD | IAEGEAAEMM | KKVNQLFPEN | KKVNQLFPEN | SVDIVFAGHN | HQYTNGLVGK | |
| msa237615.2{328_CJB110} | AHVPATSKnD | IAEGEAAEMM | KKVNQLFPEN | KKVNQLFPEN | SVDIVFAGHN | HQYTNGLVGK | |
| Consensus | *****_* | ***** | ***** | ***** | ***** | ***** | |
| msa237615.2{328_1169NT} | 301 | TRIVQALSQ | KAYADVRGVL | DTDTQDFIET | PSAKViAVAP | GKKTGSADIQ | 350 |
| msa237615.2{328_2603} | TRIVQALSQ | KAYADVRGVL | DTDTQDFIET | DTDTQDFIET | PSAKViAVAP | GKKTGSADIQ | |
| msa237615.2{328_A909} | TRIVQALSQ | KAYADVRGVL | DTDTQDFIET | DTDTQDFIET | PSAKViAVAP | GKKTGSADIQ | |
| msa237615.2{328_M732} | TRIVQALSQ | KAYADVRGVL | DTDTQDFIET | DTDTQDFIET | PSAKViAVAP | GKKTGSADIQ | |
| msa237615.2{328_COH1} | TRIVQALSQ | KAYADVRGVL | DTDTQDFIET | DTDTQDFIET | PSAKViAVAP | GKKTGSADIQ | |
| msa237615.2{328_M781} | TRIVQALSQ | KAYADVRGVL | DTDTQDFIET | DTDTQDFIET | PSAKViAVAP | GKKTGSADIQ | |
| msa237615.2{328_H36B} | TRIVQALSQ | KAYADVRGVL | DTDTQDFIET | DTDTQDFIET | PSAKViAVAP | GKKTGSADIQ | |
| msa237615.2{328_JM9130013} | TRIVQALSQ | KAYADVRGVL | DTDTQDFIET | DTDTQDFIET | PSAKViAVAP | GKKTGSADIQ | |
| msa237615.2{328_18RS21} | TRIVQALSQ | KAYADVRGVL | DTDTQDFIET | DTDTQDFIET | PSAKViAVAP | GKKTGSADIQ | |
| msa237615.2{328_090} | TRIVQALSQ | KAYADVRGVL | DTDTQDFIET | DTDTQDFIET | PSAKViAVAP | GKKTGSADIQ | |
| msa237615.2{328_CJB110} | TRIVQALSQ | KAYADVRGVL | DTDTQDFIET | DTDTQDFIET | PSAKViAVAP | GKKTGSADIQ | |
| Consensus | ***** | ***** | ***** | ***** | *****_**** | ***** | |
| msa237615.2{328_1169NT} | 351 | AIVDQANTIV | KQVTEAKIGT | AEVSvMITRS | VDQDNVSPVG | SLITEAQLAI | 400 |
| msa237615.2{328_2603} | AIVDQANTIV | KQVTEAKIGT | AEVSvMITRS | VDQDNVSPVG | VDQDNVSPVG | SLITEAQLAI | |
| msa237615.2{328_A909} | AIVDQANTIV | KQVTEAKIGT | AEVSgMITRS | VDQDNVSPVG | VDQDNVSPVG | SLITEAQLAI | |
| msa237615.2{328_M732} | AIVDQANTIV | KQVTEAKIGT | AEVSgMITRS | VDQDNVSPVG | VDQDNVSPVG | SLITEAQLAI | |
| msa237615.2{328_COH1} | AIVDQANTIV | KQVTEAKIGT | AEVSgMITRS | VDQDNVSPVG | VDQDNVSPVG | SLITEAQLAI | |
| msa237615.2{328_M781} | AIVDQANTIV | KQVTEAKIGT | AEVSgMITRS | VDQDNVSPVG | VDQDNVSPVG | SLITEAQLAI | |
| msa237615.2{328_H36B} | AIVDQANTIV | KQVTEAKIGT | AEVSgMITRS | VDQDNVSPVG | VDQDNVSPVG | SLITEAQLAI | |
| msa237615.2{328_JM9130013} | AIVDQANTIV | KQVTEAKIGT | AEVSgMITRS | VDQDNVSPVG | VDQDNVSPVG | SLITEAQLAI | |
| msa237615.2{328_18RS21} | AIVDQANTIV | KQVTEAKIGT | AEVSgMITRS | VDQDNVSPVG | VDQDNVSPVG | SLITEAQLAI | |
| msa237615.2{328_090} | AIVDQANTIV | KQVTEAKIGT | AEVSgMITRS | VDQDNVSPVG | VDQDNVSPVG | SLITEAQLAI | |
| msa237615.2{328_CJB110} | AIVDQANTIV | KQVTEAKIGT | AEVSgMITRS | VDQDNVSPVG | VDQDNVSPVG | SLITEAQLAI | |
| Consensus | ***** | ***** | ***** | *****_***** | ***** | ***** | |
| msa237615.2{328_1169NT} | 401 | ARKSWPDIDF | AMTNNGGIRA | DLLIKPDGTI | TWGAAQAVQP | FGNILQVVEI | 450 |
| msa237615.2{328_2603} | ARKSWPDIDF | AMTNNGGIRA | DLLIKPDGTI | DLLIKPDGTI | TWGAAQAVQP | FGNILQVVEI | |
| msa237615.2{328_A909} | ARKSWPDIDF | AMTNNGGIRA | DLLIKPDGTI | DLLIKPDGTI | TWGAAQAVQP | FGNILQVVEI | |
| msa237615.2{328_M732} | ARKSWPDIDF | AMTNNGGIRA | DLLIKPDGTI | DLLIKPDGTI | TWGAAQAVQP | FGNILQVVEI | |
| msa237615.2{328_COH1} | ARKSWPDIDF | AMTNNGGIRA | DLLIKPDGTI | DLLIKPDGTI | TWGAAQAVQP | FGNILQVVEI | |
| msa237615.2{328_M781} | ARKSWPDIDF | AMTNNGGIRA | DLLIKPDGTI | DLLIKPDGTI | TWGAAQAVQP | FGNILQVVEI | |
| msa237615.2{328_H36B} | ARKSWPDIDF | AMTNNGGIRA | DLLIKPDGTI | DLLIKPDGTI | TWGAAQAVQP | FGNILQVVEI | |
| msa237615.2{328_JM9130013} | ARKSWPDIDF | AMTNNGGIRA | DLLIKPDGTI | DLLIKPDGTI | TWGAAQAVQP | FGNILQVVEI | |
| msa237615.2{328_18RS21} | ARKSWPDIDF | AMTNNGGIRA | DLLIKPDGTI | DLLIKPDGTI | TWGAAQAVQP | FGNILQVVEI | |
| msa237615.2{328_090} | ARKSWPDIDF | AMTNNGGIRA | DLLIKPDGTI | DLLIKPDGTI | TWGAAQAVQP | FGNILQVVEI | |
| msa237615.2{328_CJB110} | ARKSWPDIDF | AMTNNGGIRA | DLLIKPDGTI | DLLIKPDGTI | TWGAAQAVQP | FGNILQVVEI | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | |
| msa237615.2{328_1169NT} | 451 | TGRDLYKALN | EQYDQKQNF | LQIAGLRITY | TDNKEGGEET | PFKVV KAYKS | 500 |
| msa237615.2{328_2603} | TGRDLYKALN | EQYDQKQNF | LQIAGLRITY | LQIAGLRITY | TDNKEGGEET | PFKVV KAYKS | |
| msa237615.2{328_A909} | TGRDLYKALN | EQYDQKQNF | LQIAGLRITY | LQIAGLRITY | TDNKEGGEET | PFKVV KAYKS | |
| msa237615.2{328_M732} | TGRDLYKALN | EQYDQKQNF | LQIAGLRITY | LQIAGLRITY | TDNKEGGEET | PFKVV KAYKS | |
| msa237615.2{328_COH1} | TGRDLYKALN | EQYDQKQNF | LQIAGLRITY | LQIAGLRITY | TDNKEGGEET | PFKVV KAYKS | |

Table 71: Comparative Sequences relating to SAG1333

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| msa237615.2{328_M781} | TGRDLYKALN | EQYDQKQNF | LQIAGLRYTY | TDNKEGGEET | PFKVVKAYKS |
| msa237615.2{328_H36B} | TGRDLYKALN | EQYDQKQNF | LQIAGLRYTY | TDNKEGGEET | PFKVVKAYKS |
| msa237615.2{328_JM9130013} | TGRDLYKALN | EQYDQKQNF | LQIAGLRYTY | TDNKEGGEET | PFKVVKAYKS |
| msa237615.2{328_18RS21} | TGRDLYKALN | EQYDQKQNF | LQIAGLRYTY | TDNKEGGEET | PFKVVKAYKS |
| msa237615.2{328_090} | TGRDLYKALN | EQYDQKQNF | LQIAGLRYTY | TDNKEGGEET | PFKVVKAYKS |
| msa237615.2{328_CJB110} | TGRDLYKALN | EQYDQKQNF | LQIAGLRYTY | TDNKEGGEET | PFKVVKAYKS |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237615.2{328_1169NT} | NGEEINPDAK | YKLVINDFLF | GGGDGFASFR | NAKLLGAINP | DTEVFMAYIT |
| msa237615.2{328_2603} | NGEEINPDAK | YKLVINDFLF | GGGDGFASFR | NAKLLGAINP | DTEVFMAYIT |
| msa237615.2{328_A909} | NGEEINPDAK | YKLVINDFLF | GGGDGFASFR | NAKLLGAINP | DTEVFMAYIT |
| msa237615.2{328_M732} | NGEEINPDAK | YKLVINDFLF | GGGDGFASFR | NAKLLGAINP | DTEVFMAYIT |
| msa237615.2{328_COH1} | NGEEINPDAK | YKLVINDFLF | GGGDGFASFR | NAKLLGAINP | DTEVFMAYIT |
| msa237615.2{328_M781} | NGEEINPDAK | YKLVINDFLF | GGGDGFASFR | NAKLLGAINP | DTEVFMAYIT |
| msa237615.2{328_H36B} | NGEEINPDAK | YKLVINDFLF | GGGDGFASFR | NAKLLGAINP | DTEVFMAYIT |
| msa237615.2{328_JM9130013} | NGEEINPDAK | YKLVINDFLF | GGGDGFASFR | NAKLLGAINP | DTEVFMAYIT |
| msa237615.2{328_18RS21} | NGEEINPDAK | YKLVINDFLF | GGGDGFASFR | NAKLLGAINP | DTEVFMAYIT |
| msa237615.2{328_090} | NGEEINPDAK | YKLVINDFLF | GGGDGFASFR | NAKLLGAINP | DTEVFMAYIT |
| msa237615.2{328_CJB110} | NGEEINPDAK | YKLVINDFLF | GGGDGFASFR | NAKLLGAINP | DTEVFMAYIT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237615.2{328_1169NT} | DLEKAGKKVS | VPNNKPKIYV | TMKMVNETIT | QNDGThSIik | KLYLDRQGNi |
| msa237615.2{328_2603} | DLEKAGKKVS | VPNNKPKIYV | TMKMVNETIT | QNDGThSIik | KLYLDRQGNi |
| msa237615.2{328_A909} | DLEKAGKKVS | VPNNKPKIYV | TMKMVNETIT | QNDGThSIik | KLYLDRQGNi |
| msa237615.2{328_M732} | DLEKAGKKVS | VPNNKPKIYV | TMKMVNETIT | QNDGThSIik | KLYLDRQGNi |
| msa237615.2{328_COH1} | DLEKAGKKVS | VPNNKPKIYV | TMKMVNETIT | QNDGThSIik | KLYLDRQGNi |
| msa237615.2{328_M781} | DLEKAGKKVS | VPNNKPKIYV | TMKMVNETIT | QNDGThSIik | KLYLDRQGNi |
| msa237615.2{328_H36B} | DLEKAGKKVS | VPNNKPKIYV | TMKMVNETIT | QNDGThSIik | KLYLDRQGNi |
| msa237615.2{328_JM9130013} | DLEKAGKKVS | VPNNKPKIYV | TMKMVNETIT | QNDGThSIik | KLYLDRQGNi |
| msa237615.2{328_18RS21} | DLEKAGKKVS | VPNNKPKIYV | TMKMVNETIT | QNDGThSIik | KLYLDRQGNi |
| msa237615.2{328_090} | DLEKAGKKVS | VPNNKPKIYV | TMKMVNETIT | QNDGThSIik | KLYLDRQGNi |
| msa237615.2{328_CJB110} | DLEKAGKKVS | VPNNKPKIYV | TMKMVNETIT | QNDGThSIik | KLYLDRQGNi |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237615.2{328_1169NT} | VAQEIVSDTL | NQTKSKSTKI | NPVTTIHKKQ | LHQFTAINPM | RNYGKPSNST |
| msa237615.2{328_2603} | VAQEIVSDTL | NQTKSKSTKI | NPVTTIHKKQ | LHQFTAINPM | RNYGKPSNST |
| msa237615.2{328_A909} | VAQEIVSDTL | NQTKSKSTKI | NPVTTIHKKQ | LHQFTAINPM | RNYGKPSNST |
| msa237615.2{328_M732} | VAQEIVSDTL | NQTKSKSTKI | NPVTTIHKKQ | LHQFTAINPM | RNYGKPSNST |
| msa237615.2{328_COH1} | VAQEIVSDTL | NQTKSKSTKI | NPVTTIHKKQ | LHQFTAINPM | RNYGKPSNST |
| msa237615.2{328_M781} | VAQEIVSDTL | NQTKSKSTKI | NPVTTIHKKQ | LHQFTAINPM | RNYGKPSNST |
| msa237615.2{328_H36B} | VAQEIVSDTL | NQTKSKSTKI | NPVTTIHKKQ | LHQFTAINPM | RNYGKPSNST |
| msa237615.2{328_JM9130013} | VAQEIVSDTL | NQTKSKSTKI | NPVTTIHKKQ | LHQFTAINPM | RNYGKPSNST |
| msa237615.2{328_18RS21} | VAQEIVSDTL | NQTKSKSTKI | NPVTTIHKKQ | LHQFTAINPM | RNYGKPSNST |
| msa237615.2{328_090} | VAQEIVSDTL | NQTKSKSTKI | NPVTTIHKKQ | LHQFTAINPM | RNYGKPSNST |
| msa237615.2{328_CJB110} | VAQEIVSDTL | NQTKSKSTKI | NPVTTIHKKQ | LHQFTAINPM | RNYGKPSNST |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa237615.2{328_1169NT} | TVKS----- | ----- | ----- | ----- | 690 |
| msa237615.2{328_2603} | TVKSKQlpkt | nseyggsflm | svfgvgligi | alntkckhmk | |
| msa237615.2{328_A909} | TVKSKQ---- | ----- | ----- | ----- | |
| msa237615.2{328_M732} | TVKSKQ---- | ----- | ----- | ----- | |
| msa237615.2{328_COH1} | TVKS----- | ----- | ----- | ----- | |
| msa237615.2{328_M781} | TVKS----- | ----- | ----- | ----- | |
| msa237615.2{328_H36B} | TVKS----- | ----- | ----- | ----- | |
| msa237615.2{328_JM9130013} | TVKSK----- | ----- | ----- | ----- | |
| msa237615.2{328_18RS21} | TVKSK----- | ----- | ----- | ----- | |
| msa237615.2{328_090} | TVKSKQ---- | ----- | ----- | ----- | |
| msa237615.2{328_CJB110} | TVKS----- | ----- | ----- | ----- | |
| Consensus | ***** | ***** | ***** | ***** | |

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7201

STRAIN 2603

ATGAATAAACGCGTAAAAATCGTTGCAACACTTGGTCCTGCGGTTGAATTCGGTGGTG
 GTAAGAAGTTTGGTGAGTCTGGATACCTGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAG
 AAAAAATTGCTCAATTGATTAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCACATG
 GAGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAGAGATTGCAG
 GACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAATTCGTACAGAAGCTTTTG
 AAGATGGTGACAGATTTCCATTCAATATACAACAGGTACAAAAATTACGTGTTGCTACTAAGC
 AAGGTATCAAATCACTCCAGAAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCT
 TTGATGACGTTGAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAGTAACTAGGTCTTACTG
 TGTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCCCTTA
 TTGGTAAACAAAAAGGTGTAACATCCCTTATATAAAATTCCTTTCCAGCACTTGCGAG
 AACGCGATAATGCTGATATCCGTTTGGACTTGAGCAAGGACTTAACCTTATTGCTATCT
 CATTTGTACGTACTGCTAAAAGATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGsm
 ATGGACACGTTAAGTTGTTTCTAAAATTTGAAATCAACAAGGTATCGATAATATTGATG
 AGATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCGAAGTTC
 CATTTGAAATGTTTCCAGTTTACCAAAAAATGATCATTAATAAGTTAATGCAGCTGGTA
 AAGCAGTTATTACAGCAACAAATATGCTTGAACAATGACTGATAAACCCAGTGCAGCTC
 GTTCAGAAGTATCTGATGCTTCAATGCTGTTTATTGATGGTACTGATGCTACAATGCTTT
 CAGGTGAGTCAGCTAATGGTAAATACCCAGTTGAGTCAGTTGTAACAATGGCTACTATTG
 ATAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTGCATTTCCAC
 GTAATAACAAAACTGATGTTATTGCTATCTGCGGTTAAAGATGCAACACACTCAATGGATA
 TCAAACTTGTGTTAACAATTAAGTAAACAGGTAAATACAGCTCGTGCCATTCTAAATTC
 GTCCAGATGCAACACTTTTGGCTGTTACATTTGATGAAAAAGTACAACGTTTCAATGATGA
 TTAAGTGGGTTGTTATCCCTGCTTGCAGACAAACAGCATCTACAGATGATATGTTTG
 AGGTTGCAGAAGCTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATAATATCGTTA
 TCGTTGACGGTGTTCGTAGGTACAGGTGGAACAAACAATGCGTGTTCGTACTGTTA
 AA

SEQ ID NO. 7202

STRAIN 090

AATAAACGCGTAAAAATCGTTGCAACACT
 TGGTCCTGCGGTAGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTGGAT
 ACTGGGGTGAAGCCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCTCAA
 TTGATTAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCACATGGAGA
 TCAATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAGAGA
 TTGCAGGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAAT
 CGTACAGAACTTTTGAAGATGGTTGAGATTCCATTTCATATACAACAGG
 TACAGAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAGAAG
 TGATTGCAATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAA
 GTTGGTAAAGCAATCCTTGTGATGATGGTAAACTAGGTCTTACTGTGTT
 TGCAAAAGATAAAGCACTCGTGAATTTGAAGTAGTTGTTGAGAATGATG
 GCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAATTCCT
 TTCCCAgCACTTGCAAGCAGGATAATGCTGATCCGTTTGGACTTGA
 GCAAGGACTTAACCTTTATTGCTATCTCATTGTGACGTACTGCTAAGATG
 TTAATGAAGTTCGTGCTATTGTTGAAGAACTGGCAATGGACATGTTAAG
 TTGTTTGTCTAAATTTGAAATCAACAAGGTATCGATAATATTGATGAGAT
 TATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCG
 AAGTTCCTATTGAAATGGTTCCAGTTTACCAAAAAATGATCACTATAAA
 GTTAATGCACTGGTAAAGCAGTTATTACAGCAACAATATGCTTGAAC
 AATGACTGATAAACCAGCTGCGACTCGTTCAGAAGTATCTGATGCTTCA
 ATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCAGCT
 AATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGATAA
 AATGCTCAAACTTACTCAATGAGTATGGTCGCTTAGACTCATCTGCAT
 TCCCACTAATAACAAAACTGATGTTATTGCTATCTGCGGTTAAAGATGCA
 ACACACTCAATGGATATCAAACCTTGTGTCATAATTACTGAAACAGGTAA
 TACAGCTCGTGCCATTCTAAATTCGTCAGATGACAGATTTTGGCTG
 TTACATTTGATGAAAAAGTACAACGTTTCAATGATGATTAACTGGGGTGT
 ATCCCTGTCTTGCAGACAAACAGCATCTACAGATGATATGTTTGAGGT
 TGCAGAAGCTGTAGCACTTGAAGCAGGACTTGTGAATCAGGCGATAATA
 TCGTTATCGTTGACGGTGTTCGTAGGTACAGGTGGAACAAACAATG
 CGTGTTCGTACTGTTAAA

SEQ ID NO. 7203

STRAIN A909

AATAAACGCGTAAAAATCGTTGCAACACTTGGTC
 CTGCGGTTGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTGGATCTGG
 GGTGAAGCCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCTCAATTGAT
 TAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCACATGGAGATCATG
 CTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAGAGATTGCA
 GGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAATTCGTAC
 AGAAGCTTTTGAAGATGGTGAGATTTCATTTCATATACAACAGGTACAA
 AATTACGTTGTTGCTACTAAGCAAGGTATCAAATCACTCCAGAAGTGATT
 GCAATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAAGTTGG
 TAAGCAAACTCCTTGTGATGATGGTAAACTAGGTCTTACTGTGTTTGCAA
 AAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCTTT
 ATTGGTAAACAAAAAGGTGTAACATCCCTTATATAAAATTCCTTTCC
 AGCACTTGCAAGACGCGATAATGCTGATATCCGTTTGGACTTGAGCAAG
 GACTTAACCTTTATTGCTATCTCATTGTACGTACTGCTAAAGATGTTAAT
 GAAGTTCTGCTATTTTGAAGAACTGGCAATGGACAGCTTAAGTTGTT
 TGCTAAAAATTTGAAATCAACAAGGTATCGATAATATTGATGAGATTATCG
 AAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCGAAGTT
 CCATTGAAATGTTTCCAGTTTACCAAAAAATGATCATTAATAAGTTAA

Table 72: Comparative Sequences relating to SAG0941

TGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGAAACAATGA
CTGATAAACCCAGTCGCGACTCGTTTCAGAGATCTGATGTCTTCAATGCT
GTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCAGCTAATGG
TAAATACCCAGTTGAGTCAGTTTCGTACATGGCTACTATTGATAAAAATG
CTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTGCATTCCCA
CGTAATAACAAAACTGATGTTATTGCACTCGCGTTAAAGATGCAACACA
CTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGGTAATACAG
CTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGGCTGTTACA
TTTGATGAAAAAGTACAACGTTTCATTGATGATTAACITGGGGTGTATCCC
TGCTCTGCAGACAAACCAGCATCTACAGATGATATGTTTGGAGTTGCAG
AACGTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATAATATCGTT
ATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACCAATGCGGTG
TCGTACTGTTAAA

SEQ ID NO. 7204

STRAIN H36B

AATAAACCGGTAAAAATCGTTGCAAC

ACTTGGTCTCGCGTTGAAATTCGGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCTGTAAGCAGAAG
AGATTGCAAGGACAAAAAGTTGGCTTCTCTTGATACTAAAGGACCTGAA
ATTTCGTACAGAACTTTTGAAGATGGTGAGATTTCATTATATACAAC
AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
GTTTGC AAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
CCTTTCAGCACTTGCAAGACGCGATAATGCTGATATCCGTTTGGACT
TGAGCAAGGACTTAACCTTATTGCTATCTCATTGTGACTGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
AAGTTGTTTGTCTAAAAATGAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCAITACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACCAATGACTGATAAACACCGTGCAGCTCGTTGAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CAITCCCACGTAATAACAAACTGATGTTATTGCACTCGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTTCATTGATGATTAACITGGGGT
GTTATCCCTGTCTTCGAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7205

STRAIN 18RS21

AATAAACCGGTAAAAATCGTTGCAAC

ACTTGGTCTCGCGTTGAAATTCGGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCTGTAAGCAGAAG
AGATTGCAAGGACAAAAAGTTGGCTTCTCTTGATACTAAAGGACCTGAA
ATTTCGTACAGAACTTTTGAAGATGGTGAGATTTCATTATATACAAC
AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
GTTTGC AAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
CCTTTCAGCACTTGCAAGACGCGATAATGCTGATATCCGTTTGGACT
TGAGCAAGGACTTAACCTTATTGCTATCTCATTGCTAGCTAGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
AAGTTGTTTGTCTAAAAATGAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCAITACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACCAATGACTGATAAACACCGTGCAGCTCGTTGAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CAITCCCACGTAATAACAAACTGATGTTATTGCACTCGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTTCATTGATGATTAACITGGGGT
GTTATCCCTGTCTTCGAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7206

Table 72: Comparative Sequences relating to SAG0941

STRAIN M732

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATATAAAGGACCTGAA
 ATTGCTACAGAACTTTTGAAGATGGTGAGATTCCATTATATACAAC
 AGGTACAAAATTACGTTGTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAGTAAGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCGAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATGCTATCTCATTGTGACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGCTAAAAATTGAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCAACGTGCGACTCGTTGAGAAGTATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCTGTAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAATTTGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGCTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTCAATGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACAGCATCTACAGATGATATGTTGA
 GGTTCAGAACGTTGACACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAA

SEQ ID NO. 7207

STRAIN COH1

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATATAAAGGACCTGAA
 ATTGCTACAGAACTTTTGAAGATGGTGAGATTCCATTATATACAAC
 AGGTACAAAATTACGTTGTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGTTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCGAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATGCTATCTCATTGTGACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGCTAAAAATTGAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGCTGATAAACCAACGTGCGACTCGTTGAGAAGTATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCTGTAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAATTTGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGCTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTCAATGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACAGCATCTACAGATGATATGTTGA
 GGTTCAGAACGTTGACACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAA

SEQ ID NO. 7208

STRAIN M781

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATATAAAGGACCTGAA
 ATTGCTACAGAACTTTTGAAGATGGTGAGATTCCATTATATACAAC
 AGGTACAAAATTACGTTGTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGTTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCGAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATGCTATCTCATTGTGACGTACTGCTAAAG

Table 72: Comparative Sequences relating to SAG0941

ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGTCTAAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTA
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACACCGTGCGACTCGTTGAGAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAGTTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGACACTTGAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTTATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7209

STRAIN CJB110

AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTTGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCGGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGCAGCTCGTATGGCTACTGTTTCTGTAAGCAGAAG
 AGATTGACAGGACAAAAAGTTGGCTTCTCTTGTATCTAAAGGACCTGAA
 ATTGCTACAGAACTTTTGAAGATGGTGAGATTTCCATTCTATATACAAC
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAATCAACTCCAG
 AAGTGATTGCAATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAACAAGGACTTAACCTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCTGCTATTTGTGAAGAACTGGCAATGGACAGTT
 AAGTTGTTTGTCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTA
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACACCGTGCGACTCGTTGAGAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGACACTTGAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTATATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7210

STRAIN 1169NT

AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTGAAGTTCCGGTGGTGAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCGGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGCAGCTCGTATGGCTACTGTTTCTGTAAGCAGAAG
 AGATTGACAGGACAAAAAGTTGGCTTCTCTTGTATCTAAAGGACCTGAA
 ATTGCTACAGAACTTTTGAAGATGGTGAGATTTCCATTCTATATACAAC
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAATCAACTCCAG
 AAGTGATTGCAATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAGCAAGGACTTAACCTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCTGCTATTTGTGAAGAACTGGCAATGGACAGTT
 AAGTTGTTTGTCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTA
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACACCGTGCGACTCGTTGAGAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGACACTTGAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTATATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAAA

Table 72: Comparative Sequences relating to SAG0941

ATATCGTTATCGTTGCAGGTGTTCTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAA

SEQ ID NO. 7211

STRAIN JM9130013

AATAAACCGGTAAAAATCGTTGCAAC

ACTTGGTCCCTGCGGTAGAAATCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACCTGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTCCGTTCACACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCTGTAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCTCTCTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTGAAGATGGTTCAGATTTCCATTTCATATACAAC
AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAAATCCTTGTGTGATGATGGTAACTAGGTCTTACTGT
GTTTGCAGAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
CCTTTCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTGGGACT
TGAGCAAGGACTTAACCTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTTCTGCTATTGTGTAAGAACTGGCAATGGACATGTT
AAGTTGTTTGTCTAAAATTGAATAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAAGCTGGTAAAGCAGTTATACAGCAACAATATGCTTGA
AACAAATGACTGATAAACCCAGTGCAGCTCGTTTCAAGATATCTGATGCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCACTTCTGTAATGGCTACTATTGA
TAAAAATGCTCAACATTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
CATTCCACGTAATAACAAAACTGATGTTATGCACTGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTGTTGTGACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATCCGTCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACTGGGT
GTTATCCCTGTCCTTGCAGACAAACAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAGcACTTGAAGCAGGACTTGTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAA

PRETTY of: /biotmp/msa277466.2{*} February 24, 2003 01:44 ..

| | | | |
|----------------------------|------------|------------|------------|
| | 1 | | 50 |
| msa277466.2{330_090} | ---AATAAAC | GCGTAAAAAT | CGTTGCAACA |
| msa277466.2{330_JM9130013} | ---AATAAAC | GCGTAAAAAT | CGTTGCAACA |
| msa277466.2{330_18RS21} | ---AATAAAC | GCGTAAAAAT | CGTTGCAACA |
| msa277466.2{330_2603} | atgAATAAAC | GCGTAAAAAT | CGTTGCAACA |
| msa277466.2{330_A909} | ---AATAAAC | GCGTAAAAAT | CGTTGCAACA |
| msa277466.2{330_H36B} | ---AATAAAC | GCGTAAAAAT | CGTTGCAACA |
| msa277466.2{330_CJB110} | ---AATAAAC | GCGTAAAAAT | CGTTGCAACA |
| msa277466.2{330_COH1} | ---AATAAAC | GCGTAAAAAT | CGTTGCAACA |
| msa277466.2{330_M732} | ---AATAAAC | GCGTAAAAAT | CGTTGCAACA |
| msa277466.2{330_1169NT} | ---AATAAAC | GCGTAAAAAT | CGTTGCAACA |
| msa277466.2{330_M781} | ---AATAAAC | GCGTAAAAAT | CGTTGCAACA |
| Consensus | ***** | ***** | ***** |
| | 51 | | 100 |
| msa277466.2{330_090} | CCGTGGTGGT | AAGAAGTTTG | GTGAGTCTGG |
| msa277466.2{330_JM9130013} | CCGTGGTGGT | AAGAAGTTTG | GTGAGTCTGG |
| msa277466.2{330_18RS21} | CCGTGGTGGT | AAGAAGTTTG | GTGAGTCTGG |
| msa277466.2{330_2603} | CCGTGGTGGT | AAGAAGTTTG | GTGAGTCTGG |
| msa277466.2{330_A909} | CCGTGGTGGT | AAGAAGTTTG | GTGAGTCTGG |
| msa277466.2{330_H36B} | CCGTGGTGGT | AAGAAGTTTG | GTGAGTCTGG |
| msa277466.2{330_CJB110} | CCGTGGTGGT | AAGAAGTTTG | GTGAGTCTGG |
| msa277466.2{330_COH1} | CCGTGGTGGT | AAGAAGTTTG | GTGAGTCTGG |
| msa277466.2{330_M732} | CCGTGGTGGT | AAGAAGTTTG | GTGAGTCTGG |
| msa277466.2{330_1169NT} | CCGTGGTGGT | AAGAAGTTTG | GTGAGTCTGG |
| msa277466.2{330_M781} | CCGTGGTGGT | AAGAAGTTTG | GTGAGTCTGG |
| Consensus | ***** | ***** | ***** |
| | 101 | | 150 |
| msa277466.2{330_090} | ACGTAGAAGC | TTCAGCAGAA | AAAATTGCTC |
| msa277466.2{330_JM9130013} | ACGTAGAAGC | TTCAGCAGAA | AAAATTGCTC |
| msa277466.2{330_18RS21} | ACGTAGAAGC | TTCAGCAGAA | AAAATTGCTC |
| msa277466.2{330_2603} | ACGTAGAAGC | TTCAGCAGAA | AAAATTGCTC |
| msa277466.2{330_A909} | ACGTAGAAGC | TTCAGCAGAA | AAAATTGCTC |
| msa277466.2{330_H36B} | ACGTAGAAGC | TTCAGCAGAA | AAAATTGCTC |
| msa277466.2{330_CJB110} | ACGTAGAAGC | TTCAGCAGAA | AAAATTGCTC |
| msa277466.2{330_COH1} | ACGTAGAAGC | TTCAGCAGAA | AAAATTGCTC |
| msa277466.2{330_M732} | ACGTAGAAGC | TTCAGCAGAA | AAAATTGCTC |
| msa277466.2{330_1169NT} | ACGTAGAAGC | TTCAGCAGAA | AAAATTGCTC |
| msa277466.2{330_M781} | ACGTAGAAGC | TTCAGCAGAA | AAAATTGCTC |
| Consensus | ***** | ***** | ***** |
| | 151 | | 200 |
| msa277466.2{330_090} | AACGTTTTTC | GTTTCAACTT | CTCACATGGA |

Table 72: Comparative Sequences relating to SAG0941

| | | | | | |
|----------------------------|------------|-------------|------------|------------|------------|
| msa277466.2{330_JM9130013} | AACGTTTTCC | GTTTCAACTT | CTCACATGGA | GATCATGCTG | AGCAAGGAGC |
| msa277466.2{330_18RS21} | AACGTTTTCC | GTTTCAACTT | CTCACATGGA | GATCATGCTG | AGCAAGGAGC |
| msa277466.2{330_2603} | AACGTTTTCC | GTTTCAACTT | CTCACATGGA | GATCATGCTG | AGCAAGGAGC |
| msa277466.2{330_A909} | AACGTTTTCC | GTTTCAACTT | CTCACATGGA | GATCATGCTG | AGCAAGGAGC |
| msa277466.2{330_H36B} | AACGTTTTCC | GTTTCAACTT | CTCACATGGA | GATCATGCTG | AGCAAGGAGC |
| msa277466.2{330_CJB110} | AACGTTTTCC | GTTTCAACTT | CTCACATGGA | GATCATGCTG | AGCAAGGAGC |
| msa277466.2{330_COH1} | AACGTTTTCC | GTTTCAACTT | CTCACATGGA | GATCATGCTG | AGCAAGGAGC |
| msa277466.2{330_M732} | AACGTTTTCC | GTTTCAACTT | CTCACATGGA | GATCATGCTG | AGCAAGGAGC |
| msa277466.2{330_1169NT} | AACGTTTTCC | GTTTCAACTT | CTCACATGGA | GATCATGCTG | AGCAAGGAGC |
| msa277466.2{330_M781} | AACGTTTTCC | GTTTCAACTT | CTCACATGGA | GATCATGCTG | AGCAAGGAGC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa277466.2{330_090} | TCGTATGGCT | ACTGTTTCGTA | AAGCAGAAGA | GATTGCAGGA | CAAAAAGTTG |
| msa277466.2{330_JM9130013} | TCGTATGGCT | ACTGTTTCGTA | AAGCAGAAGA | GATTGCAGGA | CAAAAAGTTG |
| msa277466.2{330_18RS21} | TCGTATGGCT | ACTGTTTCGTA | AAGCAGAAGA | GATTGCAGGA | CAAAAAGTTG |
| msa277466.2{330_2603} | TCGTATGGCT | ACTGTTTCGTA | AAGCAGAAGA | GATTGCAGGA | CAAAAAGTTG |
| msa277466.2{330_A909} | TCGTATGGCT | ACTGTTTCGTA | AAGCAGAAGA | GATTGCAGGA | CAAAAAGTTG |
| msa277466.2{330_H36B} | TCGTATGGCT | ACTGTTTCGTA | AAGCAGAAGA | GATTGCAGGA | CAAAAAGTTG |
| msa277466.2{330_CJB110} | TCGTATGGCT | ACTGTTTCGTA | AAGCAGAAGA | GATTGCAGGA | CAAAAAGTTG |
| msa277466.2{330_COH1} | TCGTATGGCT | ACTGTTTCGTA | AAGCAGAAGA | GATTGCAGGA | CAAAAAGTTG |
| msa277466.2{330_M732} | TCGTATGGCT | ACTGTTTCGTA | AAGCAGAAGA | GATTGCAGGA | CAAAAAGTTG |
| msa277466.2{330_1169NT} | TCGTATGGCT | ACTGTTTCGTA | AAGCAGAAGA | GATTGCAGGA | CAAAAAGTTG |
| msa277466.2{330_M781} | TCGTATGGCT | ACTGTTTCGTA | AAGCAGAAGA | GATTGCAGGA | CAAAAAGTTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa277466.2{330_090} | GCTTCCTCCT | TGATACTAAA | GGACCTGAAA | TTCGTACAGA | ACTTTTGTAA |
| msa277466.2{330_JM9130013} | GCTTCCTCCT | TGATACTAAA | GGACCTGAAA | TTCGTACAGA | ACTTTTGTAA |
| msa277466.2{330_18RS21} | GCTTCCTCCT | TGATACTAAA | GGACCTGAAA | TTCGTACAGA | ACTTTTGTAA |
| msa277466.2{330_2603} | GCTTCCTCCT | TGATACTAAA | GGACCTGAAA | TTCGTACAGA | ACTTTTGTAA |
| msa277466.2{330_A909} | GCTTCCTCCT | TGATACTAAA | GGACCTGAAA | TTCGTACAGA | ACTTTTGTAA |
| msa277466.2{330_H36B} | GCTTCCTCCT | TGATACTAAA | GGACCTGAAA | TTCGTACAGA | ACTTTTGTAA |
| msa277466.2{330_CJB110} | GCTTCCTCCT | TGATACTAAA | GGACCTGAAA | TTCGTACAGA | ACTTTTGTAA |
| msa277466.2{330_COH1} | GCTTCCTCCT | TGATACTAAA | GGACCTGAAA | TTCGTACAGA | ACTTTTGTAA |
| msa277466.2{330_M732} | GCTTCCTCCT | TGATACTAAA | GGACCTGAAA | TTCGTACAGA | ACTTTTGTAA |
| msa277466.2{330_1169NT} | GCTTCCTCCT | TGATACTAAA | GGACCTGAAA | TTCGTACAGA | ACTTTTGTAA |
| msa277466.2{330_M781} | GCTTCCTCCT | TGATACTAAA | GGACCTGAAA | TTCGTACAGA | ACTTTTGTAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa277466.2{330_090} | GATGGTtCAG | ATTTCcATTC | ATATACAACA | GGTACaAAT | TACGTGTTGC |
| msa277466.2{330_JM9130013} | GATGGTtCAG | ATTTCcATTC | ATATACAACA | GGTACaAAT | TACGTGTTGC |
| msa277466.2{330_18RS21} | GATGGTgCAG | ATTTCcATTC | ATATACAACA | GGTACaAAT | TACGTGTTGC |
| msa277466.2{330_2603} | GATGGTgCAG | ATTTCcATTC | ATATACAACA | GGTACaAAT | TACGTGTTGC |
| msa277466.2{330_A909} | GATGGTgCAG | ATTTCcATTC | ATATACAACA | GGTACaAAT | TACGTGTTGC |
| msa277466.2{330_H36B} | GATGGTgCAG | ATTTCcATTC | ATATACAACA | GGTACaAAT | TACGTGTTGC |
| msa277466.2{330_CJB110} | GATGGTgCAG | ATTTCcATTC | ATATACAACA | GGTACaAAT | TACGTGTTGC |
| msa277466.2{330_COH1} | GATGGTgCAG | ATTTCcATTC | ATATACAACA | GGTACaAAT | TACGTGTTGC |
| msa277466.2{330_M732} | GATGGTgCAG | ATTTCcATTC | ATATACAACA | GGTACaAAT | TACGTGTTGC |
| msa277466.2{330_1169NT} | GATGGTgCAG | ATTTCcATTC | ATATACAACA | GGTACaAAT | TACGTGTTGC |
| msa277466.2{330_M781} | GATGGTgCAG | ATTTCcATTC | ATATACAACA | GGTACaAAT | TACGTGTTGC |
| Consensus | *****_*** | ***** | ***** | *****_*** | ***** |
| msa277466.2{330_090} | TACTAAGCAA | GGTATCAAAT | CAACTCCAGA | AGTGATTGCA | TTGAATGTTG |
| msa277466.2{330_JM9130013} | TACTAAGCAA | GGTATCAAAT | CAACTCCAGA | AGTGATTGCA | TTGAATGTTG |
| msa277466.2{330_18RS21} | TACTAAGCAA | GGTATCAAAT | CAACTCCAGA | AGTGATTGCA | TTGAATGTTG |
| msa277466.2{330_2603} | TACTAAGCAA | GGTATCAAAT | CAACTCCAGA | AGTGATTGCA | TTGAATGTTG |
| msa277466.2{330_A909} | TACTAAGCAA | GGTATCAAAT | CAACTCCAGA | AGTGATTGCA | TTGAATGTTG |
| msa277466.2{330_H36B} | TACTAAGCAA | GGTATCAAAT | CAACTCCAGA | AGTGATTGCA | TTGAATGTTG |
| msa277466.2{330_CJB110} | TACTAAGCAA | GGTATCAAAT | CAACTCCAGA | AGTGATTGCA | TTGAATGTTG |
| msa277466.2{330_COH1} | TACTAAGCAA | GGTATCAAAT | CAACTCCAGA | AGTGATTGCA | TTGAATGTTG |
| msa277466.2{330_M732} | TACTAAGCAA | GGTATCAAAT | CAACTCCAGA | AGTGATTGCA | TTGAATGTTG |
| msa277466.2{330_1169NT} | TACTAAGCAA | GGTATCAAAT | CAACTCCAGA | AGTGATTGCA | TTGAATGTTG |
| msa277466.2{330_M781} | TACTAAGCAA | GGTATCAAAT | CAACTCCAGA | AGTGATTGCA | TTGAATGTTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa277466.2{330_090} | CTGGTGGACT | TGACATCITT | GATGACGTTG | AAGTTGGTAA | GCAAATCCTT |
| msa277466.2{330_JM9130013} | CTGGTGGACT | TGACATCITT | GATGACGTTG | AAGTTGGTAA | GCAAATCCTT |
| msa277466.2{330_18RS21} | CTGGTGGACT | TGACATCITT | GATGACGTTG | AAGTTGGTAA | GCAAATCCTT |
| msa277466.2{330_2603} | CTGGTGGACT | TGACATCITT | GATGACGTTG | AAGTTGGTAA | GCAAATCCTT |
| msa277466.2{330_A909} | CTGGTGGACT | TGACATCITT | GATGACGTTG | AAGTTGGTAA | GCAAATCCTT |
| msa277466.2{330_H36B} | CTGGTGGACT | TGACATCITT | GATGACGTTG | AAGTTGGTAA | GCAAATCCTT |
| msa277466.2{330_CJB110} | CTGGTGGACT | TGACATCITT | GATGACGTTG | AAGTTGGTAA | GCAAATCCTT |
| msa277466.2{330_COH1} | CTGGTGGACT | TGACATCITT | GATGACGTTG | AAGTTGGTAA | GCAAATCCTT |
| msa277466.2{330_M732} | CTGGTGGACT | TGACATCITT | GATGACGTTG | AAGTTGGTAA | GCAAATCCTT |
| msa277466.2{330_1169NT} | CTGGTGGACT | TGACATCITT | GATGACGTTG | AAGTTGGTAA | GCAAATCCTT |
| msa277466.2{330_M781} | CTGGTGGACT | TGACATCITT | GATGACGTTG | AAGTTGGTAA | GCAAATCCTT |
| Consensus | ***** | ***** | ***** | ***** | ***** |

451

500

Table 72: Comparative Sequences relating to SAG0941

| | | | | | |
|----------------------------|------------|------------|------------|------------|-------------|
| msa277466.2{330_090} | GTTGATGATG | GTAAGCTAGG | TCCTACTGTG | TTTGCAAAAG | ATAAAGACAC |
| msa277466.2{330_JM9130013} | GTTGATGATG | GTAAGCTAGG | TCCTACTGTG | TTTGCAAAAG | ATAAAGACAC |
| msa277466.2{330_18RS21} | GTTGATGATG | GTAAGCTAGG | TCCTACTGTG | TTTGCAAAAG | ATAAAGACAC |
| msa277466.2{330_2603} | GTTGATGATG | GTAAGCTAGG | TCCTACTGTG | TTTGCAAAAG | ATAAAGACAC |
| msa277466.2{330_A909} | GTTGATGATG | GTAAGCTAGG | TCCTACTGTG | TTTGCAAAAG | ATAAAGACAC |
| msa277466.2{330_H36B} | GTTGATGATG | GTAAGCTAGG | TCCTACTGTG | TTTGCAAAAG | ATAAAGACAC |
| msa277466.2{330_CJB110} | GTTGATGATG | GTAAGCTAGG | TCCTACTGTG | TTTGCAAAAG | ATAAAGACAC |
| msa277466.2{330_COH1} | GTTGATGATG | GTAAGCTAGG | TCCTACTGTG | TTTGCAAAAG | ATAAAGACAC |
| msa277466.2{330_M732} | GTTGATGATG | GTAAGCTAGG | TCCTACTGTG | TTTGCAAAAG | ATAAAGACAC |
| msa277466.2{330_1169NT} | GTTGATGATG | GTAAGCTAGG | TCCTACTGTG | TTTGCAAAAG | ATAAAGACAC |
| msa277466.2{330_M781} | GTTGATGATG | GTAAGCTAGG | TCCTACTGTG | TTTGCAAAAG | ATAAAGACAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa277466.2{330_090} | TCGTGAATTT | GAAGTAGTTG | TTGAGAATGA | TGGCCTTATT | GGTAAACAAA |
| msa277466.2{330_JM9130013} | TCGTGAATTT | GAAGTAGTTG | TTGAGAATGA | TGGCCTTATT | GGTAAACAAA |
| msa277466.2{330_18RS21} | TCGTGAATTT | GAAGTAGTTG | TTGAGAATGA | TGGCCTTATT | GGTAAACAAA |
| msa277466.2{330_2603} | TCGTGAATTT | GAAGTAGTTG | TTGAGAATGA | TGGCCTTATT | GGTAAACAAA |
| msa277466.2{330_A909} | TCGTGAATTT | GAAGTAGTTG | TTGAGAATGA | TGGCCTTATT | GGTAAACAAA |
| msa277466.2{330_H36B} | TCGTGAATTT | GAAGTAGTTG | TTGAGAATGA | TGGCCTTATT | GGTAAACAAA |
| msa277466.2{330_CJB110} | TCGTGAATTT | GAAGTAGTTG | TTGAGAATGA | TGGCCTTATT | GGTAAACAAA |
| msa277466.2{330_COH1} | TCGTGAATTT | GAAGTAGTTG | TTGAGAATGA | TGGCCTTATT | GGTAAACAAA |
| msa277466.2{330_M732} | TCGTGAATTT | GAAGTAGTTG | TTGAGAATGA | TGGCCTTATT | GGTAAACAAA |
| msa277466.2{330_1169NT} | TCGTGAATTT | GAAGTAGTTG | TTGAGAATGA | TGGCCTTATT | GGTAAACAAA |
| msa277466.2{330_M781} | TCGTGAATTT | GAAGTAGTTG | TTGAGAATGA | TGGCCTTATT | GGTAAACAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa277466.2{330_090} | AAGGTGTAAA | CATCCCTTAT | ACTAAATTC | CITTCACGAG | ACTTGCAGAA |
| msa277466.2{330_JM9130013} | AAGGTGTAAA | CATCCCTTAT | ACTAAATTC | CITTCACGAG | ACTTGCAGAA |
| msa277466.2{330_18RS21} | AAGGTGTAAA | CATCCCTTAT | ACTAAATTC | CITTCACGAG | ACTTGCAGAA |
| msa277466.2{330_2603} | AAGGTGTAAA | CATCCCTTAT | ACTAAATTC | CITTCACGAG | ACTTGCAGAA |
| msa277466.2{330_A909} | AAGGTGTAAA | CATCCCTTAT | ACTAAATTC | CITTCACGAG | ACTTGCAGAA |
| msa277466.2{330_H36B} | AAGGTGTAAA | CATCCCTTAT | ACTAAATTC | CITTCACGAG | ACTTGCAGAA |
| msa277466.2{330_CJB110} | AAGGTGTAAA | CATCCCTTAT | ACTAAATTC | CITTCACGAG | ACTTGCAGAA |
| msa277466.2{330_COH1} | AAGGTGTAAA | CATCCCTTAT | ACTAAATTC | CITTCACGAG | ACTTGCAGAA |
| msa277466.2{330_M732} | AAGGTGTAAA | CATCCCTTAT | ACTAAATTC | CITTCACGAG | ACTTGCAGAA |
| msa277466.2{330_1169NT} | AAGGTGTAAA | CATCCCTTAT | ACTAAATTC | CITTCACGAG | ACTTGCAGAA |
| msa277466.2{330_M781} | AAGGTGTAAA | CATCCCTTAT | ACTAAATTC | CITTCACGAG | ACTTGCAGAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa277466.2{330_090} | CGCGATAATG | CTGATATCCG | TTTTGGACTT | GAGCAAGGAC | TTAACTTTAT |
| msa277466.2{330_JM9130013} | CGCGATAATG | CTGATATCCG | TTTTGGACTT | GAGCAAGGAC | TTAACTTTAT |
| msa277466.2{330_18RS21} | CGCGATAATG | CTGATATCCG | TTTTGGACTT | GAGCAAGGAC | TTAACTTTAT |
| msa277466.2{330_2603} | CGCGATAATG | CTGATATCCG | TTTTGGACTT | GAGCAAGGAC | TTAACTTTAT |
| msa277466.2{330_A909} | CGCGATAATG | CTGATATCCG | TTTTGGACTT | GAGCAAGGAC | TTAACTTTAT |
| msa277466.2{330_H36B} | CGCGATAATG | CTGATATCCG | TTTTGGACTT | GAGCAAGGAC | TTAACTTTAT |
| msa277466.2{330_CJB110} | CGCGATAATG | CTGATATCCG | TTTTGGACTT | GAGCAAGGAC | TTAACTTTAT |
| msa277466.2{330_COH1} | CGCGATAATG | CTGATATCCG | TTTTGGACTT | GAGCAAGGAC | TTAACTTTAT |
| msa277466.2{330_M732} | CGCGATAATG | CTGATATCCG | TTTTGGACTT | GAGCAAGGAC | TTAACTTTAT |
| msa277466.2{330_1169NT} | CGCGATAATG | CTGATATCCG | TTTTGGACTT | GAGCAAGGAC | TTAACTTTAT |
| msa277466.2{330_M781} | CGCGATAATG | CTGATATCCG | TTTTGGACTT | GAGCAAGGAC | TTAACTTTAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa277466.2{330_090} | TGCTATCTCA | TTTGTACGTA | CTGCTAAAGA | TGTTAATGAA | GTTTCGTGCTA |
| msa277466.2{330_JM9130013} | TGCTATCTCA | TTTGTACGTA | CTGCTAAAGA | TGTTAATGAA | GTTTCGTGCTA |
| msa277466.2{330_18RS21} | TGCTATCTCA | TTTGTACGTA | CTGCTAAAGA | TGTTAATGAA | GTTTCGTGCTA |
| msa277466.2{330_2603} | TGCTATCTCA | TTTGTACGTA | CTGCTAAAGA | TGTTAATGAA | GTTTCGTGCTA |
| msa277466.2{330_A909} | TGCTATCTCA | TTTGTACGTA | CTGCTAAAGA | TGTTAATGAA | GTTTCGTGCTA |
| msa277466.2{330_H36B} | TGCTATCTCA | TTTGTACGTA | CTGCTAAAGA | TGTTAATGAA | GTTTCGTGCTA |
| msa277466.2{330_CJB110} | TGCTATCTCA | TTTGTACGTA | CTGCTAAAGA | TGTTAATGAA | GTTTCGTGCTA |
| msa277466.2{330_COH1} | TGCTATCTCA | TTTGTACGTA | CTGCTAAAGA | TGTTAATGAA | GTTTCGTGCTA |
| msa277466.2{330_M732} | TGCTATCTCA | TTTGTACGTA | CTGCTAAAGA | TGTTAATGAA | GTTTCGTGCTA |
| msa277466.2{330_1169NT} | TGCTATCTCA | TTTGTACGTA | CTGCTAAAGA | TGTTAATGAA | GTTTCGTGCTA |
| msa277466.2{330_M781} | TGCTATCTCA | TTTGTACGTA | CTGCTAAAGA | TGTTAATGAA | GTTTCGTGCTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa277466.2{330_090} | TTTGTGAAGA | AACGGGcaAT | GGACAcGTTA | AGTTGTTTGC | TAAAATTGAA |
| msa277466.2{330_JM9130013} | TTTGTGAAGA | AACGGGcaAT | GGACAcGTTA | AGTTGTTTGC | TAAAATTGAA |
| msa277466.2{330_18RS21} | TTTGTGAAGA | AACGGGcaAT | GGACAcGTTA | AGTTGTTTGC | TAAAATTGAA |
| msa277466.2{330_2603} | TTTGTGAAGA | AACGGGsmAT | GGACAcGTTA | AGTTGTTTGC | TAAAATTGAA |
| msa277466.2{330_A909} | TTTGTGAAGA | AACGGGcaAT | GGACAcGTTA | AGTTGTTTGC | TAAAATTGAA |
| msa277466.2{330_H36B} | TTTGTGAAGA | AACGGGcaAT | GGACAcGTTA | AGTTGTTTGC | TAAAATTGAA |
| msa277466.2{330_CJB110} | TTTGTGAAGA | AACGGGcaAT | GGACAcGTTA | AGTTGTTTGC | TAAAATTGAA |
| msa277466.2{330_COH1} | TTTGTGAAGA | AACGGGcaAT | GGACAcGTTA | AGTTGTTTGC | TAAAATTGAA |
| msa277466.2{330_M732} | TTTGTGAAGA | AACGGGcaAT | GGACAcGTTA | AGTTGTTTGC | TAAAATTGAA |
| msa277466.2{330_1169NT} | TTTGTGAAGA | AACGGGcaAT | GGACAcGTTA | AGTTGTTTGC | TAAAATTGAA |
| msa277466.2{330_M781} | TTTGTGAAGA | AACGGGcaAT | GGACAcGTTA | AGTTGTTTGC | TAAAATTGAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |

Table 72: Comparative Sequences relating to SAG0941

| | | | | | | | |
|----------------------------|------------|------------|------------|------------|------------|--|------|
| | | 751 | | | | | 800 |
| msa277466.2{330_090} | AATCAACAAG | GTATCGATAA | TATTGATGAG | ATTATCGAAG | CAGCAGATGG | | |
| msa277466.2{330_JM9130013} | AATCAACAAG | GTATCGATAA | TATTGATGAG | ATTATCGAAG | CAGCAGATGG | | |
| msa277466.2{330_18RS21} | AATCAACAAG | GTATCGATAA | TATTGATGAG | ATTATCGAAG | CAGCAGATGG | | |
| msa277466.2{330_2603} | AATCAACAAG | GTATCGATAA | TATTGATGAG | ATTATCGAAG | CAGCAGATGG | | |
| msa277466.2{330_A909} | AATCAACAAG | GTATCGATAA | TATTGATGAG | ATTATCGAAG | CAGCAGATGG | | |
| msa277466.2{330_H36B} | AATCAACAAG | GTATCGATAA | TATTGATGAG | ATTATCGAAG | CAGCAGATGG | | |
| msa277466.2{330_CJB110} | AATCAACAAG | GTATCGATAA | TATTGATGAG | ATTATCGAAG | CAGCAGATGG | | |
| msa277466.2{330_COH1} | AATCAACAAG | GTATCGATAA | TATTGATGAG | ATTATCGAAG | CAGCAGATGG | | |
| msa277466.2{330_M732} | AATCAACAAG | GTATCGATAA | TATTGATGAG | ATTATCGAAG | CAGCAGATGG | | |
| msa277466.2{330_1169NT} | AATCAACAAG | GTATCGATAA | TATTGATGAG | ATTATCGAAG | CAGCAGATGG | | |
| msa277466.2{330_M781} | AATCAACAAG | GTATCGATAA | TATTGATGAG | ATTATCGAAG | CAGCAGATGG | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | 801 | | | | | 850 |
| msa277466.2{330_090} | TATTATGATT | GCTCGTGGTG | ATATGGGTAT | CGAAGTTCCA | TTTGAAATGG | | |
| msa277466.2{330_JM9130013} | TATTATGATT | GCTCGTGGTG | ATATGGGTAT | CGAAGTTCCA | TTTGAAATGG | | |
| msa277466.2{330_18RS21} | TATTATGATT | GCTCGTGGTG | ATATGGGTAT | CGAAGTTCCA | TTTGAAATGG | | |
| msa277466.2{330_2603} | TATTATGATT | GCTCGTGGTG | ATATGGGTAT | CGAAGTTCCA | TTTGAAATGG | | |
| msa277466.2{330_A909} | TATTATGATT | GCTCGTGGTG | ATATGGGTAT | CGAAGTTCCA | TTTGAAATGG | | |
| msa277466.2{330_H36B} | TATTATGATT | GCTCGTGGTG | ATATGGGTAT | CGAAGTTCCA | TTTGAAATGG | | |
| msa277466.2{330_CJB110} | TATTATGATT | GCTCGTGGTG | ATATGGGTAT | CGAAGTTCCA | TTTGAAATGG | | |
| msa277466.2{330_COH1} | TATTATGATT | GCTCGTGGTG | ATATGGGTAT | CGAAGTTCCA | TTTGAAATGG | | |
| msa277466.2{330_M732} | TATTATGATT | GCTCGTGGTG | ATATGGGTAT | CGAAGTTCCA | TTTGAAATGG | | |
| msa277466.2{330_1169NT} | TATTATGATT | GCTCGTGGTG | ATATGGGTAT | CGAAGTTCCA | TTTGAAATGG | | |
| msa277466.2{330_M781} | TATTATGATT | GCTCGTGGTG | ATATGGGTAT | CGAAGTTCCA | TTTGAAATGG | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | 851 | | | | | 900 |
| msa277466.2{330_090} | TTCCAGTTTA | CCAAAAAATG | ATCATTACTA | AAGTTAATGC | AGCTGGTAAA | | |
| msa277466.2{330_JM9130013} | TTCCAGTTTA | CCAAAAAATG | ATCATTACTA | AAGTTAATGC | AGCTGGTAAA | | |
| msa277466.2{330_18RS21} | TTCCAGTTTA | CCAAAAAATG | ATCATTACTA | AAGTTAATGC | AGCTGGTAAA | | |
| msa277466.2{330_2603} | TTCCAGTTTA | CCAAAAAATG | ATCATTACTA | AAGTTAATGC | AGCTGGTAAA | | |
| msa277466.2{330_A909} | TTCCAGTTTA | CCAAAAAATG | ATCATTACTA | AAGTTAATGC | AGCTGGTAAA | | |
| msa277466.2{330_H36B} | TTCCAGTTTA | CCAAAAAATG | ATCATTACTA | AAGTTAATGC | AGCTGGTAAA | | |
| msa277466.2{330_CJB110} | TTCCAGTTTA | CCAAAAAATG | ATCATTACTA | AAGTTAATGC | AGCTGGTAAA | | |
| msa277466.2{330_COH1} | TTCCAGTTTA | CCAAAAAATG | ATCATTACTA | AAGTTAATGC | AGCTGGTAAA | | |
| msa277466.2{330_M732} | TTCCAGTTTA | CCAAAAAATG | ATCATTACTA | AAGTTAATGC | AGCTGGTAAA | | |
| msa277466.2{330_1169NT} | TTCCAGTTTA | CCAAAAAATG | ATCATTACTA | AAGTTAATGC | AGCTGGTAAA | | |
| msa277466.2{330_M781} | TTCCAGTTTA | CCAAAAAATG | ATCATTACTA | AAGTTAATGC | AGCTGGTAAA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | 901 | | | | | 950 |
| msa277466.2{330_090} | GCAGTTATTA | CAGCAACAAA | TATGCTTGAA | ACAATGACTG | ATAAACCCAG | | |
| msa277466.2{330_JM9130013} | GCAGTTATTA | CAGCAACAAA | TATGCTTGAA | ACAATGACTG | ATAAACCCAG | | |
| msa277466.2{330_18RS21} | GCAGTTATTA | CAGCAACAAA | TATGCTTGAA | ACAATGACTG | ATAAACCCAG | | |
| msa277466.2{330_2603} | GCAGTTATTA | CAGCAACAAA | TATGCTTGAA | ACAATGACTG | ATAAACCCAG | | |
| msa277466.2{330_A909} | GCAGTTATTA | CAGCAACAAA | TATGCTTGAA | ACAATGACTG | ATAAACCCAG | | |
| msa277466.2{330_H36B} | GCAGTTATTA | CAGCAACAAA | TATGCTTGAA | ACAATGACTG | ATAAACCCAG | | |
| msa277466.2{330_CJB110} | GCAGTTATTA | CAGCAACAAA | TATGCTTGAA | ACAATGACTG | ATAAACCCAG | | |
| msa277466.2{330_COH1} | GCAGTTATTA | CAGCAACAAA | TATGCTTGAA | ACAATGACTG | ATAAACCCAG | | |
| msa277466.2{330_M732} | GCAGTTATTA | CAGCAACAAA | TATGCTTGAA | ACAATGACTG | ATAAACCCAG | | |
| msa277466.2{330_1169NT} | GCAGTTATTA | CAGCAACAAA | TATGCTTGAA | ACAATGACTG | ATAAACCCAG | | |
| msa277466.2{330_M781} | GCAGTTATTA | CAGCAACAAA | TATGCTTGAA | ACAATGACTG | ATAAACCCAG | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | 951 | | | | | 1000 |
| msa277466.2{330_090} | TGCGACTCGT | TCAGAAGTAT | CTGATGCTCT | CAATGCTGTT | ATTGATGGTA | | |
| msa277466.2{330_JM9130013} | TGCGACTCGT | TCAGAAGTAT | CTGATGCTCT | CAATGCTGTT | ATTGATGGTA | | |
| msa277466.2{330_18RS21} | TGCGACTCGT | TCAGAAGTAT | CTGATGCTCT | CAATGCTGTT | ATTGATGGTA | | |
| msa277466.2{330_2603} | TGCGACTCGT | TCAGAAGTAT | CTGATGCTCT | CAATGCTGTT | ATTGATGGTA | | |
| msa277466.2{330_A909} | TGCGACTCGT | TCAGAAGTAT | CTGATGCTCT | CAATGCTGTT | ATTGATGGTA | | |
| msa277466.2{330_H36B} | TGCGACTCGT | TCAGAAGTAT | CTGATGCTCT | CAATGCTGTT | ATTGATGGTA | | |
| msa277466.2{330_CJB110} | TGCGACTCGT | TCAGAAGTAT | CTGATGCTCT | CAATGCTGTT | ATTGATGGTA | | |
| msa277466.2{330_COH1} | TGCGACTCGT | TCAGAAGTAT | CTGATGCTCT | CAATGCTGTT | ATTGATGGTA | | |
| msa277466.2{330_M732} | TGCGACTCGT | TCAGAAGTAT | CTGATGCTCT | CAATGCTGTT | ATTGATGGTA | | |
| msa277466.2{330_1169NT} | TGCGACTCGT | TCAGAAGTAT | CTGATGCTCT | CAATGCTGTT | ATTGATGGTA | | |
| msa277466.2{330_M781} | TGCGACTCGT | TCAGAAGTAT | CTGATGCTCT | CAATGCTGTT | ATTGATGGTA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | 1001 | | | | | 1050 |
| msa277466.2{330_090} | CTGATGCTAC | AATGCTTTCA | GGTGAGTCAG | CTAATGGTAA | ATACCCAGTT | | |
| msa277466.2{330_JM9130013} | CTGATGCTAC | AATGCTTTCA | GGTGAGTCAG | CTAATGGTAA | ATACCCAGTT | | |
| msa277466.2{330_18RS21} | CTGATGCTAC | AATGCTTTCA | GGTGAGTCAG | CTAATGGTAA | ATACCCAGTT | | |
| msa277466.2{330_2603} | CTGATGCTAC | AATGCTTTCA | GGTGAGTCAG | CTAATGGTAA | ATACCCAGTT | | |
| msa277466.2{330_A909} | CTGATGCTAC | AATGCTTTCA | GGTGAGTCAG | CTAATGGTAA | ATACCCAGTT | | |
| msa277466.2{330_H36B} | CTGATGCTAC | AATGCTTTCA | GGTGAGTCAG | CTAATGGTAA | ATACCCAGTT | | |
| msa277466.2{330_CJB110} | CTGATGCTAC | AATGCTTTCA | GGTGAGTCAG | CTAATGGTAA | ATACCCAGTT | | |
| msa277466.2{330_COH1} | CTGATGCTAC | AATGCTTTCA | GGTGAGTCAG | CTAATGGTAA | ATACCCAGTT | | |
| msa277466.2{330_M732} | CTGATGCTAC | AATGCTTTCA | GGTGAGTCAG | CTAATGGTAA | ATACCCAGTT | | |
| msa277466.2{330_1169NT} | CTGATGCTAC | AATGCTTTCA | GGTGAGTCAG | CTAATGGTAA | ATACCCAGTT | | |
| msa277466.2{330_M781} | CTGATGCTAC | AATGCTTTCA | GGTGAGTCAG | CTAATGGTAA | ATACCCAGTT | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |

Table 72: Comparative Sequences relating to SAG0941

| | | | | | |
|----------------------------|--|------------|------------|-------------|------------|
| | | 1051 | | | 1100 |
| msa277466.2{330_090} | | GAGTCAGTTC | GTACAATGGC | TACTATTGAT | AAAAATGCTC |
| msa277466.2{330_JM9130013} | | GAGTCAGTTC | GTACAATGGC | TACTATTGAT | AAAAATGCTC |
| msa277466.2{330_18RS21} | | GAGTCAGTTC | GTACAATGGC | TACTATTGAT | AAAAATGCTC |
| msa277466.2{330_2603} | | GAGTCAGTTC | GTACAATGGC | TACTATTGAT | AAAAATGCTC |
| msa277466.2{330_A909} | | GAGTCAGTTC | GTACAATGGC | TACTATTGAT | AAAAATGCTC |
| msa277466.2{330_H36B} | | GAGTCAGTTC | GTACAATGGC | TACTATTGAT | AAAAATGCTC |
| msa277466.2{330_CJB110} | | GAGTCAGTTC | GTACAATGGC | TACTATTGAT | AAAAATGCTC |
| msa277466.2{330_COH1} | | GAGTCAGTTC | GTACAATGGC | TACTATTGAT | AAAAATGCTC |
| msa277466.2{330_M732} | | GAGTCAGTTC | GTACAATGGC | TACTATTGAT | AAAAATGCTC |
| msa277466.2{330_1169NT} | | GAGTCAGTTC | GTACAATGGC | TACTATTGAT | AAAAATGCTC |
| msa277466.2{330_M781} | | GAGTCAGTTC | GTACAATGGC | TACTATTGAT | AAAAATGCTC |
| Consensus | | ***** | ***** | ***** | ***** |
| | | 1101 | | | 1150 |
| msa277466.2{330_090} | | CAATGAGTAT | GGTCGcTTAG | ACTCATCTGC | ATTCCCACGT |
| msa277466.2{330_JM9130013} | | CAATGAGTAT | GGTCGcTTAG | ACTCATCTGC | ATTCCCACGT |
| msa277466.2{330_18RS21} | | CAATGAGTAT | GGTCGcTTAG | ACTCATCTGC | ATTCCCACGT |
| msa277466.2{330_2603} | | CAATGAGTAT | GGTCGcTTAG | ACTCATCTGC | ATTCCCACGT |
| msa277466.2{330_A909} | | CAATGAGTAT | GGTCGcTTAG | ACTCATCTGC | ATTCCCACGT |
| msa277466.2{330_H36B} | | CAATGAGTAT | GGTCGcTTAG | ACTCATCTGC | ATTCCCACGT |
| msa277466.2{330_CJB110} | | CAATGAGTAT | GGTCGcTTAG | ACTCATCTGC | ATTCCCACGT |
| msa277466.2{330_COH1} | | CAATGAGTAT | GGTCGcTTAG | ACTCATCTGC | ATTCCCACGT |
| msa277466.2{330_M732} | | CAATGAGTAT | GGTCGcTTAG | ACTCATCTGC | ATTCCCACGT |
| msa277466.2{330_1169NT} | | CAATGAGTAT | GGTCGcTTAG | ACTCATCTGC | ATTCCCACGT |
| msa277466.2{330_M781} | | CAATGAGTAT | GGTCGcTTAG | ACTCATCTGC | ATTCCCACGT |
| Consensus | | ***** | ***** | ***** | ***** |
| | | 1151 | | | 1200 |
| msa277466.2{330_090} | | CTGATGTTAT | TGCATCTGCG | GTTAAAGATG | CAACACACTC |
| msa277466.2{330_JM9130013} | | CTGATGTTAT | TGCATCTGCG | GTTAAAGATG | CAACACACTC |
| msa277466.2{330_18RS21} | | CTGATGTTAT | TGCATCTGCG | GTTAAAGATG | CAACACACTC |
| msa277466.2{330_2603} | | CTGATGTTAT | TGCATCTGCG | GTTAAAGATG | CAACACACTC |
| msa277466.2{330_A909} | | CTGATGTTAT | TGCATCTGCG | GTTAAAGATG | CAACACACTC |
| msa277466.2{330_H36B} | | CTGATGTTAT | TGCATCTGCG | GTTAAAGATG | CAACACACTC |
| msa277466.2{330_CJB110} | | CTGATGTTAT | TGCATCTGCG | GTTAAAGATG | CAACACACTC |
| msa277466.2{330_COH1} | | CTGATGTTAT | TGCATCTGCG | GTTAAAGATG | CAACACACTC |
| msa277466.2{330_M732} | | CTGATGTTAT | TGCATCTGCG | GTTAAAGATG | CAACACACTC |
| msa277466.2{330_1169NT} | | CTGATGTTAT | TGCATCTGCG | GTTAAAGATG | CAACACACTC |
| msa277466.2{330_M781} | | CTGATGTTAT | TGCATCTGCG | GTTAAAGATG | CAACACACTC |
| Consensus | | ***** | ***** | ***** | ***** |
| | | 1201 | | | 1250 |
| msa277466.2{330_090} | | AAACTTGTG | TgACAATTAC | TGAAACAGGT | AATACAGCTC |
| msa277466.2{330_JM9130013} | | AAACTTGTG | TgACAATTAC | TGAAACAGGT | AATACAGCTC |
| msa277466.2{330_18RS21} | | AAACTTGTG | TaACAATTAC | TGAAACAGGT | AATACAGCTC |
| msa277466.2{330_2603} | | AAACTTGTG | TaACAATTAC | TGAAACAGGT | AATACAGCTC |
| msa277466.2{330_A909} | | AAACTTGTG | TaACAATTAC | TGAAACAGGT | AATACAGCTC |
| msa277466.2{330_H36B} | | AAACTTGTG | TaACAATTAC | TGAAACAGGT | AATACAGCTC |
| msa277466.2{330_CJB110} | | AAACTTGTG | TaACAATTAC | TGAAACAGGT | AATACAGCTC |
| msa277466.2{330_COH1} | | AAACTTGTG | TaACAATTAC | TGAAACAGGT | AATACAGCTC |
| msa277466.2{330_M732} | | AAACTTGTG | TaACAATTAC | TGAAACAGGT | AATACAGCTC |
| msa277466.2{330_1169NT} | | AAACTTGTG | TaACAATTAC | TGAAACAGGT | AATACAGCTC |
| msa277466.2{330_M781} | | AAACTTGTG | TaACAATTAC | TGAAACAGGT | AATACAGCTC |
| Consensus | | ***** | ***** | ***** | ***** |
| | | 1251 | | | 1300 |
| msa277466.2{330_090} | | TAAaTTCCGT | CCAGATGCAG | ACATTTTGGC | TGTTACATTT |
| msa277466.2{330_JM9130013} | | TAAaTTCCGT | CCAGATGCAG | ACATTTTGGC | TGTTACATTT |
| msa277466.2{330_18RS21} | | TAAaTTCCGT | CCAGATGCAG | ACATTTTGGC | TGTTACATTT |
| msa277466.2{330_2603} | | TAAaTTCCGT | CCAGATGCAG | ACATTTTGGC | TGTTACATTT |
| msa277466.2{330_A909} | | TAAaTTCCGT | CCAGATGCAG | ACATTTTGGC | TGTTACATTT |
| msa277466.2{330_H36B} | | TAAaTTCCGT | CCAGATGCAG | ACATTTTGGC | TGTTACATTT |
| msa277466.2{330_CJB110} | | TAAaTTCCGT | CCAGATGCAG | ACATTTTGGC | TGTTACATTT |
| msa277466.2{330_COH1} | | TAAaTTCCGT | CCAGATGCAG | ACATTTTGGC | TGTTACATTT |
| msa277466.2{330_M732} | | TAAaTTCCGT | CCAGATGCAG | ACATTTTGGC | TGTTACATTT |
| msa277466.2{330_1169NT} | | TAAaTTCCGT | CCAGATGCAG | ACATTTTGGC | TGTTACATTT |
| msa277466.2{330_M781} | | TAAgTTCCGT | CCAGATGCAG | ACATTTTGGC | TGTTACATTT |
| Consensus | | ***-***** | ***** | ***** | ***** |
| | | 1301 | | | 1350 |
| msa277466.2{330_090} | | TACAACGTTT | ATTGATGATT | AAC TGGGGTG | TTATCCCTGT |
| msa277466.2{330_JM9130013} | | TACAACGTTT | ATTGATGATT | AAC TGGGGTG | TTATCCCTGT |
| msa277466.2{330_18RS21} | | TACAACGTTT | ATTGATGATT | AAC TGGGGTG | TTATCCCTGT |
| msa277466.2{330_2603} | | TACAACGTTT | ATTGATGATT | AAC TGGGGTG | TTATCCCTGT |
| msa277466.2{330_A909} | | TACAACGTTT | ATTGATGATT | AAC TGGGGTG | TTATCCCTGT |
| msa277466.2{330_H36B} | | TACAACGTTT | ATTGATGATT | AAC TGGGGTG | TTATCCCTGT |
| msa277466.2{330_CJB110} | | TACAACGTTT | ATTGATGATT | AAC TGGGGTG | TTATCCCTGT |
| msa277466.2{330_COH1} | | TACAACGTTT | ATTGATGATT | AAC TGGGGTG | TTATCCCTGT |
| msa277466.2{330_M732} | | TACAACGTTT | ATTGATGATT | AAC TGGGGTG | TTATCCCTGT |
| msa277466.2{330_1169NT} | | TACAACGTTT | ATTGATGATT | AAC TGGGGTG | TTATCCCTGT |
| msa277466.2{330_M781} | | TACAACGTTT | ATTGATGATT | AAC TGGGGTG | TTATCCCTGT |

Table 72: Comparative Sequences relating to SAG0941

| Consensus | ***** | ***** | ***** | ***** | ***** |
|----------------------------|-------------|------------|------------|------------|------------|
| | 1351 | | | | 1400 |
| msa277466.2{330_090} | AAACCAGCAT | CTACAGATGA | TATGTTTGAG | GTTGCAGAAC | GTGTAGCACT |
| msa277466.2{330_JM9130013} | AAACCAGCAT | CTACAGATGA | TATGTTTGAG | GTTGCAGAAC | GTGTAGCACT |
| msa277466.2{330_18RS21} | AAACCAGCAT | CTACAGATGA | TATGTTTGAG | GTTGCAGAAC | GTGTAGCACT |
| msa277466.2{330_2603} | AAACCAGCAT | CTACAGATGA | TATGTTTGAG | GTTGCAGAAC | GTGTAGCACT |
| msa277466.2{330_A909} | AAACCAGCAT | CTACAGATGA | TATGTTTGAG | GTTGCAGAAC | GTGTAGCACT |
| msa277466.2{330_H36B} | AAACCAGCAT | CTACAGATGA | TATGTTTGAG | GTTGCAGAAC | GTGTAGCACT |
| msa277466.2{330_CJB110} | AAACCAGCAT | CTACAGATGA | TATGTTTGAG | GTTGCAGAAC | GTGTAGCACT |
| msa277466.2{330_COH1} | AAACCAGCAT | CTACAGATGA | TATGTTTGAG | GTTGCAGAAC | GTGTAGCACT |
| msa277466.2{330_M732} | AAACCAGCAT | CTACAGATGA | TATGTTTGAG | GTTGCAGAAC | GTGTAGCACT |
| msa277466.2{330_1169NT} | AAACCAGCAT | CTACAGATGA | TATGTTTGAG | GTTGCAGAAC | GTGTAGCACT |
| msa277466.2{330_M781} | AAACCAGCAT | CTACAGATGA | TATGTTTGAG | GTTGCAGAAC | GTGTAGCACT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 1401 | | | | 1450 |
| msa277466.2{330_090} | TGAAGCAGGA | CTTGTGTAAT | CAGGCGATAA | TATCGTTATC | GTTGCAGGTG |
| msa277466.2{330_JM9130013} | TGAAGCAGGA | CTTGTGTAAT | CAGGCGATAA | TATCGTTATC | GTTGCAGGTG |
| msa277466.2{330_18RS21} | TGAAGCAGGA | CTTGTGTAAT | CAGGCGATAA | TATCGTTATC | GTTGCAGGTG |
| msa277466.2{330_2603} | TGAAGCAGGA | CTTGTGTAAT | CAGGCGATAA | TATCGTTATC | GTTGCAGGTG |
| msa277466.2{330_A909} | TGAAGCAGGA | CTTGTGTAAT | CAGGCGATAA | TATCGTTATC | GTTGCAGGTG |
| msa277466.2{330_H36B} | TGAAGCAGGA | CTTGTGTAAT | CAGGCGATAA | TATCGTTATC | GTTGCAGGTG |
| msa277466.2{330_CJB110} | TGAAGCAGGA | CTTGTGTAAT | CAGGCGATAA | TATCGTTATC | GTTGCAGGTG |
| msa277466.2{330_COH1} | TGAAGCAGGA | CTTGTGTAAT | CAGGCGATAA | TATCGTTATC | GTTGCAGGTG |
| msa277466.2{330_M732} | TGAAGCAGGA | CTTGTGTAAT | CAGGCGATAA | TATCGTTATC | GTTGCAGGTG |
| msa277466.2{330_1169NT} | TGAAGCAGGA | CTTGTGTAAT | CAGGCGATAA | TATCGTTATC | GTTGCAGGTG |
| msa277466.2{330_M781} | TGAAGCAGGA | CTTGTGTAAT | CAGGCGATAA | TATCGTTATC | GTTGCAGGTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 1451 | | | | 1500 |
| msa277466.2{330_090} | TTCCCTGTAGG | TACAGGTGGA | ACTAACACAA | TGCGTGTTCG | TACTGTTAAA |
| msa277466.2{330_JM9130013} | TTCCCTGTAGG | TACAGGTGGA | ACTAACACAA | TGCGTGTTCG | TACTGTTAAA |
| msa277466.2{330_18RS21} | TTCCCTGTAGG | TACAGGTGGA | ACTAACACAA | TGCGTGTTCG | TACTGTTAAA |
| msa277466.2{330_2603} | TTCCCTGTAGG | TACAGGTGGA | ACTAACACAA | TGCGTGTTCG | TACTGTTAAA |
| msa277466.2{330_A909} | TTCCCTGTAGG | TACAGGTGGA | ACTAACACAA | TGCGTGTTCG | TACTGTTAAA |
| msa277466.2{330_H36B} | TTCCCTGTAGG | TACAGGTGGA | ACTAACACAA | TGCGTGTTCG | TACTGTTAAA |
| msa277466.2{330_CJB110} | TTCCCTGTAGG | TACAGGTGGA | ACTAACACAA | TGCGTGTTCG | TACTGTTAAA |
| msa277466.2{330_COH1} | TTCCCTGTAGG | TACAGGTGGA | ACTAACACAA | TGCGTGTTCG | TACTGTTAAA |
| msa277466.2{330_M732} | TTCCCTGTAGG | TACAGGTGGA | ACTAACACAA | TGCGTGTTCG | TACTGTTAAA |
| msa277466.2{330_1169NT} | TTCCCTGTAGG | TACAGGTGGA | ACTAACACAA | TGCGTGTTCG | TACTGTTAAA |
| msa277466.2{330_M781} | TTCCCTGTAGG | TACAGGTGGA | ACTAACACAA | TGCGTGTTCG | TACTGTTAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |

SEQ ID NO. 7212

STRAIN 2603 frame: 1

MNKRKIVATLGPVAFVFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHG
 DHAEQGMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGTCLRVATKQ
 GIKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGITVFAKDKDTREFEVVENDGLI
 GKQGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGX
 GHVKLFAKIEHQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGK
 AVITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATID
 KNAQTLLNEYGRLDSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTTITETGNTARAI SKFRP
 PDADILAVTFDEKVRQSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNI VIV
 VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7213

STRAIN 090 frame: 1

NKRKIVATLGPVAFVFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGTCLRVATKQ
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGITVFAKDKDTREFEVVENDGLI
 GKQGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGX
 HVKLFKIEHQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTTITETGNTARAI SKFRP
 DADILAVTFDEKVRQSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNI VIV
 VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7214

STRAIN A909 frame: 1

NKRKIVATLGPVAFVFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGTCLRVATKQ
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGITVFAKDKDTREFEVVENDGLI
 GKQGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGX
 HVKLFKIEHQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTTITETGNTARAI SKFRP
 DADILAVTFDEKVRQSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNI VIV
 VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7215

STRAIN H36B frame: 1

Table 72: Comparative Sequences relating to SAG0941

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICBETGNG
HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDSSAFPRNNKTDV IASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7216

STRAIN 18RS21 frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICBETGNG
HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDSSAFPRNNKTDV IASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7217

STRAIN M732 frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICBETGNG
HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDSSAFPRNNKTDV IASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7218

STRAIN COH1 frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICBETGNG
HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDSSAFPRNNKTDV IASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7219

STRAIN M781 frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICBETGNG
HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDSSAFPRNNKTDV IASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7220

STRAIN CJB110 frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICBETGNG
HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDSSAFPRNNKTDV IASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7221

STRAIN 1169NT frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICBETGNG
HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDSSAFPRNNKTDV IASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

Table 72: Comparative Sequences relating to SAG0941.

SEQ ID NO. 7222

STRAIN JM9130013 frame: 1

NKRVKIVATLGPVAFRGGKFGESGYWGESLDVEASAEKIAQLIKEGANVFRNFHSHG
 HAEQGMATVRKAEIAGQKVGFLDITKGPETELFEDGSDHFSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGITVFAKDKDTREFEVVENDGLIG
 KQKGVNIPYTKIPFPALAEADNADIRFGLGGLNFIAISFVRTAKDVNSVRAICEETGNG
 HVKLFKAIENQOQIDNIDEIIEAADGIMIAARGDMGIEVFPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVDFNAVIDGTDATLMSGESANGKYPVESVTRMATIDK
 NAQTLLNEYGRLLDSSAFPRNKTDVIAASAVKDATHSMDIKLVVTTITETGTARAIKFRP
 DADILAVTFDEKVRSLMINKGVIPLADKPASTDDMFEVAERVALEAGLVESGDNIIVIV
 AGVPVGTGGTNTMVRVTVK

PRETTY of: /biotmp/msa277662.2{*} February 24, 2003 01:49 ..

| | | | |
|----------------------------|------------|-----------|------------|
| | 1 | | 50 |
| msa277662.2{330_18RS21} | ~NKRVKIVAT | LGPVAFRGG | KKFGESGYWG |
| msa277662.2{330_A909} | ~NKRVKIVAT | LGPVAFRGG | KKFGESGYWG |
| msa277662.2{330_CJB110} | ~NKRVKIVAT | LGPVAFRGG | KKFGESGYWG |
| msa277662.2{330_H36B} | ~NKRVKIVAT | LGPVAFRGG | KKFGESGYWG |
| msa277662.2{330_1169NT} | ~NKRVKIVAT | LGPVAFRGG | KKFGESGYWG |
| msa277662.2{330_COH1} | ~NKRVKIVAT | LGPVAFRGG | KKFGESGYWG |
| msa277662.2{330_M732} | ~NKRVKIVAT | LGPVAFRGG | KKFGESGYWG |
| msa277662.2{330_M781} | ~NKRVKIVAT | LGPVAFRGG | KKFGESGYWG |
| msa277662.2{330_JM9130013} | ~NKRVKIVAT | LGPVAFRGG | KKFGESGYWG |
| msa277662.2{330_090} | ~NKRVKIVAT | LGPVAFRGG | KKFGESGYWG |
| msa277662.2{330_2603} | ~NKRVKIVAT | LGPVAFRGG | KKFGESGYWG |
| Consensus | ***** | ***** | ***** |

| | | | |
|----------------------------|------------|------------|------------|
| | 51 | | 100 |
| msa277662.2{330_18RS21} | NVFRNFHSHG | DHAEQGARMA | TVRKAEEIAG |
| msa277662.2{330_A909} | NVFRNFHSHG | DHAEQGARMA | TVRKAEEIAG |
| msa277662.2{330_CJB110} | NVFRNFHSHG | DHAEQGARMA | TVRKAEEIAG |
| msa277662.2{330_H36B} | NVFRNFHSHG | DHAEQGARMA | TVRKAEEIAG |
| msa277662.2{330_1169NT} | NVFRNFHSHG | DHAEQGARMA | TVRKAEEIAG |
| msa277662.2{330_COH1} | NVFRNFHSHG | DHAEQGARMA | TVRKAEEIAG |
| msa277662.2{330_M732} | NVFRNFHSHG | DHAEQGARMA | TVRKAEEIAG |
| msa277662.2{330_M781} | NVFRNFHSHG | DHAEQGARMA | TVRKAEEIAG |
| msa277662.2{330_JM9130013} | NVFRNFHSHG | DHAEQGARMA | TVRKAEEIAG |
| msa277662.2{330_090} | NVFRNFHSHG | DHAEQGARMA | TVRKAEEIAG |
| msa277662.2{330_2603} | NVFRNFHSHG | DHAEQGARMA | TVRKAEEIAG |
| Consensus | ***** | ***** | ***** |

| | | | |
|----------------------------|------------|------------|------------|
| | 101 | | 150 |
| msa277662.2{330_18RS21} | DGADFHSYTT | GTKLRVATKQ | GIKSTPEVIA |
| msa277662.2{330_A909} | DGADFHSYTT | GTKLRVATKQ | GIKSTPEVIA |
| msa277662.2{330_CJB110} | DGADFHSYTT | GTKLRVATKQ | GIKSTPEVIA |
| msa277662.2{330_H36B} | DGADFHSYTT | GTKLRVATKQ | GIKSTPEVIA |
| msa277662.2{330_1169NT} | DGADFHSYTT | GTKLRVATKQ | GIKSTPEVIA |
| msa277662.2{330_COH1} | DGADFHSYTT | GTKLRVATKQ | GIKSTPEVIA |
| msa277662.2{330_M732} | DGADFHSYTT | GTKLRVATKQ | GIKSTPEVIA |
| msa277662.2{330_M781} | DGADFHSYTT | GTKLRVATKQ | GIKSTPEVIA |
| msa277662.2{330_JM9130013} | DGADFHSYTT | GTKLRVATKQ | GIKSTPEVIA |
| msa277662.2{330_090} | DGADFHSYTT | GTKLRVATKQ | GIKSTPEVIA |
| msa277662.2{330_2603} | DGADFHSYTT | GTKLRVATKQ | GIKSTPEVIA |
| Consensus | ***** | ***** | ***** |

| | | | |
|----------------------------|------------|------------|------------|
| | 151 | | 200 |
| msa277662.2{330_18RS21} | VDDGKLGITV | FAKDKDTREF | EVVVENDGLI |
| msa277662.2{330_A909} | VDDGKLGITV | FAKDKDTREF | EVVVENDGLI |
| msa277662.2{330_CJB110} | VDDGKLGITV | FAKDKDTREF | EVVVENDGLI |
| msa277662.2{330_H36B} | VDDGKLGITV | FAKDKDTREF | EVVVENDGLI |
| msa277662.2{330_1169NT} | VDDGKLGITV | FAKDKDTREF | EVVVENDGLI |
| msa277662.2{330_COH1} | VDDGKLGITV | FAKDKDTREF | EVVVENDGLI |
| msa277662.2{330_M732} | VDDGKLGITV | FAKDKDTREF | EVVVENDGLI |
| msa277662.2{330_M781} | VDDGKLGITV | FAKDKDTREF | EVVVENDGLI |
| msa277662.2{330_JM9130013} | VDDGKLGITV | FAKDKDTREF | EVVVENDGLI |
| msa277662.2{330_090} | VDDGKLGITV | FAKDKDTREF | EVVVENDGLI |
| msa277662.2{330_2603} | VDDGKLGITV | FAKDKDTREF | EVVVENDGLI |
| Consensus | ***** | ***** | ***** |

| | | | |
|----------------------------|------------|------------|------------|
| | 201 | | 250 |
| msa277662.2{330_18RS21} | RDNADIRFGL | EQGLNFIAIS | FVRTAKDVNE |
| msa277662.2{330_A909} | RDNADIRFGL | EQGLNFIAIS | FVRTAKDVNE |
| msa277662.2{330_CJB110} | RDNADIRFGL | EQGLNFIAIS | FVRTAKDVNE |
| msa277662.2{330_H36B} | RDNADIRFGL | EQGLNFIAIS | FVRTAKDVNE |
| msa277662.2{330_1169NT} | RDNADIRFGL | EQGLNFIAIS | FVRTAKDVNE |
| msa277662.2{330_COH1} | RDNADIRFGL | EQGLNFIAIS | FVRTAKDVNE |
| msa277662.2{330_M732} | RDNADIRFGL | EQGLNFIAIS | FVRTAKDVNE |
| msa277662.2{330_M781} | RDNADIRFGL | EQGLNFIAIS | FVRTAKDVNE |
| msa277662.2{330_JM9130013} | RDNADIRFGL | EQGLNFIAIS | FVRTAKDVNE |
| msa277662.2{330_090} | RDNADIRFGL | EQGLNFIAIS | FVRTAKDVNE |
| msa277662.2{330_2603} | RDNADIRFGL | EQGLNFIAIS | FVRTAKDVNE |
| Consensus | ***** | ***** | ***** |

Table 72: Comparative Sequences relating to SAG0941

| | | | | | |
|----------------------------|------------|-------------|------------|------------|------------|
| | 251 | | | | 300 |
| msa277662.2{330_18RS21} | NQQGIDNIDE | IIEAADGIMI | ARGDMGIEVP | FEMVPVYQKM | IITKVNAAGK |
| msa277662.2{330_A909} | NQQGIDNIDE | IIEAADGIMI | ARGDMGIEVP | FEMVPVYQKM | IITKVNAAGK |
| msa277662.2{330_CJB110} | NQQGIDNIDE | IIEAADGIMI | ARGDMGIEVP | FEMVPVYQKM | IITKVNAAGK |
| msa277662.2{330_H36B} | NQQGIDNIDE | IIEAADGIMI | ARGDMGIEVP | FEMVPVYQKM | IITKVNAAGK |
| msa277662.2{330_1169NT} | NQQGIDNIDE | IIEAADGIMI | ARGDMGIEVP | FEMVPVYQKM | IITKVNAAGK |
| msa277662.2{330_COH1} | NQQGIDNIDE | IIEAADGIMI | ARGDMGIEVP | FEMVPVYQKM | IITKVNAAGK |
| msa277662.2{330_M732} | NQQGIDNIDE | IIEAADGIMI | ARGDMGIEVP | FEMVPVYQKM | IITKVNAAGK |
| msa277662.2{330_M781} | NQQGIDNIDE | IIEAADGIMI | ARGDMGIEVP | FEMVPVYQKM | IITKVNAAGK |
| msa277662.2{330_JM9130013} | NQQGIDNIDE | IIEAADGIMI | ARGDMGIEVP | FEMVPVYQKM | IITKVNAAGK |
| msa277662.2{330_090} | NQQGIDNIDE | IIEAADGIMI | ARGDMGIEVP | FEMVPVYQKM | IITKVNAAGK |
| msa277662.2{330_2603} | NQQGIDNIDE | IIEAADGIMI | ARGDMGIEVP | FEMVPVYQKM | IITKVNAAGK |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 301 | | | | 350 |
| msa277662.2{330_18RS21} | AVITATNMLE | TMTDKPRATR | SEVSDVFNAV | IDGTDATMLS | GESANGKYPV |
| msa277662.2{330_A909} | AVITATNMLE | TMTDKPRATR | SEVSDVFNAV | IDGTDATMLS | GESANGKYPV |
| msa277662.2{330_CJB110} | AVITATNMLE | TMTDKPRATR | SEVSDVFNAV | IDGTDATMLS | GESANGKYPV |
| msa277662.2{330_H36B} | AVITATNMLE | TMTDKPRATR | SEVSDVFNAV | IDGTDATMLS | GESANGKYPV |
| msa277662.2{330_1169NT} | AVITATNMLE | TMTDKPRATR | SEVSDVFNAV | IDGTDATMLS | GESANGKYPV |
| msa277662.2{330_COH1} | AVITATNMLE | TMTDKPRATR | SEVSDVFNAV | IDGTDATMLS | GESANGKYPV |
| msa277662.2{330_M732} | AVITATNMLE | TMTDKPRATR | SEVSDVFNAV | IDGTDATMLS | GESANGKYPV |
| msa277662.2{330_M781} | AVITATNMLE | TMTDKPRATR | SEVSDVFNAV | IDGTDATMLS | GESANGKYPV |
| msa277662.2{330_JM9130013} | AVITATNMLE | TMTDKPRATR | SEVSDVFNAV | IDGTDATMLS | GESANGKYPV |
| msa277662.2{330_090} | AVITATNMLE | TMTDKPRATR | SEVSDVFNAV | IDGTDATMLS | GESANGKYPV |
| msa277662.2{330_2603} | AVITATNMLE | TMTDKPRATR | SEVSDVFNAV | IDGTDATMLS | GESANGKYPV |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 351 | | | | 400 |
| msa277662.2{330_18RS21} | ESVRTMATID | KNAQTLLENEY | GRLDSSAFPR | NNKTDVIAA | VKDATHSMDI |
| msa277662.2{330_A909} | ESVRTMATID | KNAQTLLENEY | GRLDSSAFPR | NNKTDVIAA | VKDATHSMDI |
| msa277662.2{330_CJB110} | ESVRTMATID | KNAQTLLENEY | GRLDSSAFPR | NNKTDVIAA | VKDATHSMDI |
| msa277662.2{330_H36B} | ESVRTMATID | KNAQTLLENEY | GRLDSSAFPR | NNKTDVIAA | VKDATHSMDI |
| msa277662.2{330_1169NT} | ESVRTMATID | KNAQTLLENEY | GRLDSSAFPR | NNKTDVIAA | VKDATHSMDI |
| msa277662.2{330_COH1} | ESVRTMATID | KNAQTLLENEY | GRLDSSAFPR | NNKTDVIAA | VKDATHSMDI |
| msa277662.2{330_M732} | ESVRTMATID | KNAQTLLENEY | GRLDSSAFPR | NNKTDVIAA | VKDATHSMDI |
| msa277662.2{330_M781} | ESVRTMATID | KNAQTLLENEY | GRLDSSAFPR | NNKTDVIAA | VKDATHSMDI |
| msa277662.2{330_JM9130013} | ESVRTMATID | KNAQTLLENEY | GRLDSSAFPR | NNKTDVIAA | VKDATHSMDI |
| msa277662.2{330_090} | ESVRTMATID | KNAQTLLENEY | GRLDSSAFPR | NNKTDVIAA | VKDATHSMDI |
| msa277662.2{330_2603} | ESVRTMATID | KNAQTLLENEY | GRLDSSAFPR | NNKTDVIAA | VKDATHSMDI |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 401 | | | | 450 |
| msa277662.2{330_18RS21} | KLVTITETG | NTARAIKFR | PDADILAVTF | DEKVQSLMI | NWGVIPVLAD |
| msa277662.2{330_A909} | KLVTITETG | NTARAIKFR | PDADILAVTF | DEKVQSLMI | NWGVIPVLAD |
| msa277662.2{330_CJB110} | KLVTITETG | NTARAIKFR | PDADILAVTF | DEKVQSLMI | NWGVIPVLAD |
| msa277662.2{330_H36B} | KLVTITETG | NTARAIKFR | PDADILAVTF | DEKVQSLMI | NWGVIPVLAD |
| msa277662.2{330_1169NT} | KLVTITETG | NTARAIKFR | PDADILAVTF | DEKVQSLMI | NWGVIPVLAD |
| msa277662.2{330_COH1} | KLVTITETG | NTARAIKFR | PDADILAVTF | DEKVQSLMI | NWGVIPVLAD |
| msa277662.2{330_M732} | KLVTITETG | NTARAIKFR | PDADILAVTF | DEKVQSLMI | NWGVIPVLAD |
| msa277662.2{330_M781} | KLVTITETG | NTARAIKFR | PDADILAVTF | DEKVQSLMI | NWGVIPVLAD |
| msa277662.2{330_JM9130013} | KLVTITETG | NTARAIKFR | PDADILAVTF | DEKVQSLMI | NWGVIPVLAD |
| msa277662.2{330_090} | KLVTITETG | NTARAIKFR | PDADILAVTF | DEKVQSLMI | NWGVIPVLAD |
| msa277662.2{330_2603} | KLVTITETG | NTARAIKFR | PDADILAVTF | DEKVQSLMI | NWGVIPVLAD |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 451 | | | | 500 |
| msa277662.2{330_18RS21} | KPASTDDMFE | VAERVALEAG | FVESGDNIVI | VAGVPVGTGG | TNTMRVRTVK |
| msa277662.2{330_A909} | KPASTDDMFE | VAERVALEAG | FVESGDNIVI | VAGVPVGTGG | TNTMRVRTVK |
| msa277662.2{330_CJB110} | KPASTDDMFE | VAERVALEAG | FVESGDNIVI | VAGVPVGTGG | TNTMRVRTVK |
| msa277662.2{330_H36B} | KPASTDDMFE | VAERVALEAG | FVESGDNIVI | VAGVPVGTGG | TNTMRVRTVK |
| msa277662.2{330_1169NT} | KPASTDDMFE | VAERVALEAG | FVESGDNIVI | VAGVPVGTGG | TNTMRVRTVK |
| msa277662.2{330_COH1} | KPASTDDMFE | VAERVALEAG | FVESGDNIVI | VAGVPVGTGG | TNTMRVRTVK |
| msa277662.2{330_M732} | KPASTDDMFE | VAERVALEAG | FVESGDNIVI | VAGVPVGTGG | TNTMRVRTVK |
| msa277662.2{330_M781} | KPASTDDMFE | VAERVALEAG | FVESGDNIVI | VAGVPVGTGG | TNTMRVRTVK |
| msa277662.2{330_JM9130013} | KPASTDDMFE | VAERVALEAG | FVESGDNIVI | VAGVPVGTGG | TNTMRVRTVK |
| msa277662.2{330_090} | KPASTDDMFE | VAERVALEAG | FVESGDNIVI | VAGVPVGTGG | TNTMRVRTVK |
| msa277662.2{330_2603} | KPASTDDMFE | VAERVALEAG | FVESGDNIVI | VAGVPVGTGG | TNTMRVRTVK |
| Consensus | ***** | ***** | ***** | ***** | ***** |

Table 73: Comparative Sequences relating to SAG0981

SEQ ID NO. 7301

STRAIN 2603

TTGCTCTATAATAGACAAAAAGGTGGTGATATTTATGTATTTAGCATTAAATCGGTGAT
 ATCATTAAATCAAACAGATACCTGAAACGTGAAACCTTCCAAACAGTCTTTTCAGCAACTA
 ATGACCGAACTATCTGATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCT
 GGTGATGAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCAT
 ATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTACAGGAAACATTATA
 ACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCTGCCTACTGGCATGCTCGC
 TCAGCTATTAAATCATATACATGATAAAATGATTATGGAACAGTTCAAGTAGCTATTGTC
 CTTGATGATGAAGACCAAAACCTTGAATTAACACTAAATAGTCTCATTTTCAGCTGGTGAT
 TTTATCAAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAA
 GATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGGAAAATATTGAACCT
 AGTGCGCTGACTAAACGCCCTTAAAGCAAGCGGTCTGAAGATTTACTTAAGAACGAGAACA
 CAGGCAGCCGATCTATTAGTTAAAGTTGCACCTCAAACTAAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7302

STRAIN 090

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTT
 AGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTGAAACGTGAAA
 CTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAACTATCTGATGTATAT
 GGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTTCA
 AGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCATATTTC
 AACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTACAGGAAAC
 ATTATAACATCCATCAATTTAAATGAAAGTATCGGTGCTGATGGTCTGCTG
 CTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAAAATGATT
 ATGGAACAGTTTCAAGTAGCTATTGCTTGGATGATGAAGACCAAAACCTT
 GAATTAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTATCAAGTCAAA
 ATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGATA
 ATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGGAAAATATT
 GAACCTAGTGCGCTGACTAAACGCCCTTAAAGCAAGCGGTCTGAAGATTTA
 CTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCACCTC
 AAATAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7303

STRAIN A909

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTAT
 TTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTGAAACGTGA
 AACTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAACTATCTGATGTAT
 ATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTT
 CAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCATAT
 TCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTACAGGAA
 ACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGATGGTCTCT
 GCCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAAAATGA
 TTATGGAACAGTTCAAGTAGCTATTGCTTGGATGATGAAGACCAAAACC
 TTGAATTAAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTATCAAGTCA
 AAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGA
 TAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGGAAAATA
 TTGAACCTAGTGCGCTGACTAAACGCCCTTAAAGCAAGCGGTCTGAAGATT
 TACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCAC
 TCAAACTAAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7304

STRAIN H36B

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTTGA
 ACGTGAACCTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGA
 CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTA
 CAGGAACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTGCTTGGATGATGAAGACC
 AAAACCTTGAATTAAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTATC
 AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCGCTGACTAAACGCCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACTAAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7305

STRAIN 18RS21

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTTGA
 ACGTGAACCTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGA
 CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTA
 CAGGAACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTGCTTGGATGATGAAGACC
 AAAACCTTGAATTAAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTATC
 AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCGCTGACTAAACGCCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACTAAAGGGGAAGCTATGATTTTC

Table 73: Comparative Sequences relating to SAG0981

TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACATAAGGGGAAGCTATGATTTC

SEQ ID NO. 7306

STRAIN M732

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTG
 AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
 GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 TGAATTTCAAGCTTTATTTGAAACaATCAAAAAAGGTATTTCAAATTTATTG
 ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGT
 ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
 TGGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
 CAAAACCTTGAATTAACTAAATAGTCTCATTTCAGCTGGTGATTTTAT
 CAAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATAC
 TTCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTG
 GAAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCT
 GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAA
 GTTGCACTCAAACATAAGGGGAAGCTATGATTTC

SEQ ID NO. 7307

STRAIN COH1

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTG
 AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
 GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 TGAATTTCAAGCTTTATTTGAAACaATCAAAAAAGGTATTTCAAATTTATTG
 ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGT
 ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
 TGGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
 CAAAACCTTGAATTAACTAAATAGTCTCATTTCAGCTGGTGATTTTAT
 CAAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATAC
 TTCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTG
 GAAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCT
 GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAA
 GTTGCACTCAAACATAAGGGGAAGCTATGATTTC

SEQ ID NO. 7308

STRAIN M781

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTTGAAACaATCAAAAAAGGTATTTCAAATTTATTGA
 CCAATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGTGA
 CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AATGATTATGGAACAGTTCAAGTAGCTATTTGCCITGATGATGAAGACC
 AAAACCTTGAATTAACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
 AAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACATAAGGGGAAGCTATGATTTC

SEQ ID NO. 7309

STRAIN CJB110

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TTTATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACT
 TGAACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTAT
 CTGATGTATATGGTGAAGAGCTGATTTCTCTATTCACTATTACAGCTGGT
 GATGAATTTCAAGCTTTATTTGAAACCATCAAAAAAGGTATTTCAAATTTAT
 TGACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCG
 GTACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCT
 GATGGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 TAAAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCITGATGATGAAG
 ACCAAAACCTTGAATTAACTAAATAGTCTCATTTCAGCTGGTGATTTT
 ATCAAGTCAAAATGGACTACTAACCATTTCAAATGCTTGAGCACTTAAT
 ACTTCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACT
 TGGAAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGT
 CTGAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAA
 AAGTTGCACTCAAACATAAGGGGAAGCTATGATTTC

SEQ ID NO. 7310

STRAIN JM9130013

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG

Table 73: Comparative Sequences relating to SAG0981

| | | | | | |
|---|------------|------------|------------|------------|------------|
| ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT GAATTTCAAGCTTTATGAAACCATCAAAAAAGGTATTTCAAATTATTGA CCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTTCCGGCTCGGTA CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT GGTCTGCTACTGCGCATGCTCGCTCAGCTATTATCATATACATGATAA AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC AAAACCTTGAATTAACTAACTAAATAGTCTCATTTCAGCTGGTGATTTATC AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCACTGG AAAATATTGAACCTAGTGCCTGACTAAACGCCTTAAGCAAGCGGTCTG AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG TTGCACTCAAATAAAGGGGAAGCTATGATTTTC | | | | | |
| PRETTY of: /biotmp/msa31912.2{*} February 18, 2003 08:19 .. | | | | | |
| msa31912.2{338_18RS21} | 1 | 50 | | | |
| msa31912.2{338_2603} | ---TCTGCTA | TAATAGACAA | AAAGGTGGTG | aTATTTATGT | ATTAGCATT |
| msa31912.2{338_A909} | ttgTCTGCTA | TAATAGACAA | AAAGGTGGTG | aTATTTATGT | ATTAGCATT |
| msa31912.2{338_H36B} | ---TCTGCTA | TAATAGACAA | AAAGGTGGTG | aTATTTATGT | ATTAGCATT |
| msa31912.2{338_JM9130013} | ---TCTGCTA | TAATAGACAA | AAAGGTGGTG | aTATTTATGT | ATTAGCATT |
| msa31912.2{338_COH1} | ---TCTGCTA | TAATAGACAA | AAAGGTGGTG | aTATTTATGT | ATTAGCATT |
| msa31912.2{338_M732} | ---TCTGCTA | TAATAGACAA | AAAGGTGGTG | aTATTTATGT | ATTAGCATT |
| msa31912.2{338_M781} | ---TCTGCTA | TAATAGACAA | AAAGGTGGTG | aTATTTATGT | ATTAGCATT |
| msa31912.2{338_090} | ---TCTGCTA | TAATAGACAA | AAAGGTGGTG | aTATTTATGT | ATTAGCATT |
| msa31912.2{338_CJB110} | ---TCTGCTA | TAATAGACAA | AAAGGTGGTG | gTATTTATGT | ATTAGCATT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31912.2{338_18RS21} | 51 | 100 | | | |
| msa31912.2{338_2603} | AATCGGTGAT | ATCATTAAAT | CAAAACAGAT | ACTTGAACGT | GAAACTTTCC |
| msa31912.2{338_A909} | AATCGGTGAT | ATCATTAAAT | CAAAACAGAT | ACTTGAACGT | GAAACTTTCC |
| msa31912.2{338_H36B} | AATCGGTGAT | ATCATTAAAT | CAAAACAGAT | ACTTGAACGT | GAAACTTTCC |
| msa31912.2{338_JM9130013} | AATCGGTGAT | ATCATTAAAT | CAAAACAGAT | ACTTGAACGT | GAAACTTTCC |
| msa31912.2{338_COH1} | AATCGGTGAT | ATCATTAAAT | CAAAACAGAT | ACTTGAACGT | GAAACTTTCC |
| msa31912.2{338_M732} | AATCGGTGAT | ATCATTAAAT | CAAAACAGAT | ACTTGAACGT | GAAACTTTCC |
| msa31912.2{338_M781} | AATCGGTGAT | ATCATTAAAT | CAAAACAGAT | ACTTGAACGT | GAAACTTTCC |
| msa31912.2{338_090} | AATCGGTGAT | ATCATTAAAT | CAAAACAGAT | ACTTGAACGT | GAAACTTTCC |
| msa31912.2{338_CJB110} | AATCGGTGAT | ATCATTAAAT | CAAAACAGAT | ACTTGAACGT | GAAACTTTCC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31912.2{338_18RS21} | 101 | 150 | | | |
| msa31912.2{338_2603} | AACAGTCTTT | TCAGCAACTA | ATGACCGAAC | TATCTGATGT | ATATGGTGAA |
| msa31912.2{338_A909} | AACAGTCTTT | TCAGCAACTA | ATGACCGAAC | TATCTGATGT | ATATGGTGAA |
| msa31912.2{338_H36B} | AACAGTCTTT | TCAGCAACTA | ATGACCGAAC | TATCTGATGT | ATATGGTGAA |
| msa31912.2{338_JM9130013} | AACAGTCTTT | TCAGCAACTA | ATGACCGAAC | TATCTGATGT | ATATGGTGAA |
| msa31912.2{338_COH1} | AACAGTCTTT | TCAGCAACTA | ATGACCGAAC | TATCTGATGT | ATATGGTGAA |
| msa31912.2{338_M732} | AACAGTCTTT | TCAGCAACTA | ATGACCGAAC | TATCTGATGT | ATATGGTGAA |
| msa31912.2{338_M781} | AACAGTCTTT | TCAGCAACTA | ATGACCGAAC | TATCTGATGT | ATATGGTGAA |
| msa31912.2{338_090} | AACAGTCTTT | TCAGCAACTA | ATGACCGAAC | TATCTGATGT | ATATGGTGAA |
| msa31912.2{338_CJB110} | AACAGTCTTT | TCAGCAACTA | ATGACCGAAC | TATCTGATGT | ATATGGTGAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31912.2{338_18RS21} | 151 | 200 | | | |
| msa31912.2{338_2603} | GAGCTGATTT | CTCATTAC | TATTACAGCT | GGTGATGAAT | TTCAAGCTTT |
| msa31912.2{338_A909} | GAGCTGATTT | CTCATTAC | TATTACAGCT | GGTGATGAAT | TTCAAGCTTT |
| msa31912.2{338_H36B} | GAGCTGATTT | CTCATTAC | TATTACAGCT | GGTGATGAAT | TTCAAGCTTT |
| msa31912.2{338_JM9130013} | GAGCTGATTT | CTCATTAC | TATTACAGCT | GGTGATGAAT | TTCAAGCTTT |
| msa31912.2{338_COH1} | GAGCTGATTT | CTCATTAC | TATTACAGCT | GGTGATGAAT | TTCAAGCTTT |
| msa31912.2{338_M732} | GAGCTGATTT | CTCATTAC | TATTACAGCT | GGTGATGAAT | TTCAAGCTTT |
| msa31912.2{338_M781} | GAGCTGATTT | CTCATTAC | TATTACAGCT | GGTGATGAAT | TTCAAGCTTT |
| msa31912.2{338_090} | GAGCTGATTT | CTCATTAC | TATTACAGCT | GGTGATGAAT | TTCAAGCTTT |
| msa31912.2{338_CJB110} | GAGCTGATTT | CTCATTAC | TATTACAGCT | GGTGATGAAT | TTCAAGCTTT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31912.2{338_18RS21} | 201 | 250 | | | |
| msa31912.2{338_2603} | ATTGAAACCa | TCAAAAAAGG | TATTTCAAAT | TATTGACCAT | ATTCAACTAG |
| msa31912.2{338_A909} | ATTGAAACCa | TCAAAAAAGG | TATTTCAAAT | TATTGACCAT | ATTCAACTAG |
| msa31912.2{338_H36B} | ATTGAAACCa | TCAAAAAAGG | TATTTCAAAT | TATTGACCAT | ATTCAACTAG |
| msa31912.2{338_JM9130013} | ATTGAAACCa | TCAAAAAAGG | TATTTCAAAT | TATTGACCAT | ATTCAACTAG |
| msa31912.2{338_COH1} | ATTGAAACCa | TCAAAAAAGG | TATTTCAAAT | TATTGACCAT | ATTCAACTAG |
| msa31912.2{338_M732} | ATTGAAACCa | TCAAAAAAGG | TATTTCAAAT | TATTGACCAT | ATTCAACTAG |
| msa31912.2{338_M781} | ATTGAAACCa | TCAAAAAAGG | TATTTCAAAT | TATTGACCAT | ATTCAACTAG |
| msa31912.2{338_090} | ATTGAAACCa | TCAAAAAAGG | TATTTCAAAT | TATTGACCAT | ATTCAACTAG |
| msa31912.2{338_CJB110} | ATTGAAACCa | TCAAAAAAGG | TATTTCAAAT | TATTGACCAT | ATTCAACTAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31912.2{338_18RS21} | 251 | 300 | | | |
| msa31912.2{338_2603} | CTCTAAACC | TGTTAATGTA | AGGTTCCGCC | TCGGTACAGG | AAACATTATA |
| | CTCTAAACC | TGTTAATGTA | AGGTTCCGCC | TCGGTACAGG | AAACATTATA |

Table 73: Comparative Sequences relating to SAG0981

| | | | | | | | |
|---------------------------|------------|------------|-------------|------------|-------------|-----|-------------|
| msa31912.2{338_A909} | CTCTAAAACC | TGTTAATGTA | AGGTTTCGGCC | TCGGTACAGG | AAACATTATA | | |
| msa31912.2{338_H36B} | CTCTAAAACC | TGTTAATGTA | AGGTTTCGGCC | TCGGTACAGG | AAACATTATA | | |
| msa31912.2{338_JM9130013} | CTCTAAAACC | TGTTAATGTA | AGGTTTCGGCC | TCGGTACAGG | AAACATTATA | | |
| msa31912.2{338_COH1} | CTCTAAAACC | TGTTAATGTA | AGGTTTCGGCC | TCGGTACAGG | AAACATTATA | | |
| msa31912.2{338_M732} | CTCTAAAACC | TGTTAATGTA | AGGTTTCGGCC | TCGGTACAGG | AAACATTATA | | |
| msa31912.2{338_M781} | CTCTAAAACC | TGTTAATGTA | AGGTTTCGGCC | TCGGTACAGG | AAACATTATA | | |
| msa31912.2{338_090} | CTCTAAAACC | TGTTAATGTA | AGGTTTCGGCC | TCGGTACAGG | AAACATTATA | | |
| msa31912.2{338_CJB110} | CTCTAAAACC | TGTTAATGTA | AGGTTTCGGCC | TCGGTACAGG | AAACATTATA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa31912.2{338_18RS21} | 301 | ACATCCATCA | ATTCAAATGA | AAGTATCGGT | GCTGATGGTC | 350 | CTGCCTACTG |
| msa31912.2{338_2603} | ACATCCATCA | ATTCAAATGA | AAGTATCGGT | GCTGATGGTC | CTGCCTACTG | | |
| msa31912.2{338_A909} | ACATCCATCA | ATTCAAATGA | AAGTATCGGT | GCTGATGGTC | CTGCCTACTG | | |
| msa31912.2{338_H36B} | ACATCCATCA | ATTCAAATGA | AAGTATCGGT | GCTGATGGTC | CTGCCTACTG | | |
| msa31912.2{338_JM9130013} | ACATCCATCA | ATTCAAATGA | AAGTATCGGT | GCTGATGGTC | CTGCCTACTG | | |
| msa31912.2{338_COH1} | ACATCCATCA | ATTCAAATGA | AAGTATCGGT | GCTGATGGTC | CTGCCTACTG | | |
| msa31912.2{338_M732} | ACATCCATCA | ATTCAAATGA | AAGTATCGGT | GCTGATGGTC | CTGCCTACTG | | |
| msa31912.2{338_M781} | ACATCCATCA | ATTCAAATGA | AAGTATCGGT | GCTGATGGTC | CTGCCTACTG | | |
| msa31912.2{338_090} | ACATCCATCA | ATTCAAATGA | AAGTATCGGT | GCTGATGGTC | CTGCCTACTG | | |
| msa31912.2{338_CJB110} | ACATCCATCA | ATTCAAATGA | AAGTATCGGT | GCTGATGGTC | CTGCCTACTG | | |
| Consensus | ***** | ***_***** | ***** | ***** | ***** | | |
| msa31912.2{338_18RS21} | 351 | GCATGCTCGC | TCAGCTATTA | ATCATATACA | TGATAAAAAT | 400 | GATTATGGAA |
| msa31912.2{338_2603} | GCATGCTCGC | TCAGCTATTA | ATCATATACA | TGATAAAAAT | GATTATGGAA | | |
| msa31912.2{338_A909} | GCATGCTCGC | TCAGCTATTA | ATCATATACA | TGATAAAAAT | GATTATGGAA | | |
| msa31912.2{338_H36B} | GCATGCTCGC | TCAGCTATTA | ATCATATACA | TGATAAAAAT | GATTATGGAA | | |
| msa31912.2{338_JM9130013} | GCATGCTCGC | TCAGCTATTA | ATCATATACA | TGATAAAAAT | GATTATGGAA | | |
| msa31912.2{338_COH1} | GCATGCTCGC | TCAGCTATTA | ATCATATACA | TGATAAAAAT | GATTATGGAA | | |
| msa31912.2{338_M732} | GCATGCTCGC | TCAGCTATTA | ATCATATACA | TGATAAAAAT | GATTATGGAA | | |
| msa31912.2{338_M781} | GCATGCTCGC | TCAGCTATTA | ATCATATACA | TGATAAAAAT | GATTATGGAA | | |
| msa31912.2{338_090} | GCATGCTCGC | TCAGCTATTA | ATCATATACA | TGATAAAAAT | GATTATGGAA | | |
| msa31912.2{338_CJB110} | GCATGCTCGC | TCAGCTATTA | ATCATATACA | TGATAAAAAT | GATTATGGAA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa31912.2{338_18RS21} | 401 | CAGTTCAAGT | AGCTATTGTC | CTTGATGATG | AAGACCAAAA | 450 | CCTTGAATTA |
| msa31912.2{338_2603} | CAGTTCAAGT | AGCTATTGTC | CTTGATGATG | AAGACCAAAA | CCTTGAATTA | | |
| msa31912.2{338_A909} | CAGTTCAAGT | AGCTATTGTC | CTTGATGATG | AAGACCAAAA | CCTTGAATTA | | |
| msa31912.2{338_H36B} | CAGTTCAAGT | AGCTATTGTC | CTTGATGATG | AAGACCAAAA | CCTTGAATTA | | |
| msa31912.2{338_JM9130013} | CAGTTCAAGT | AGCTATTGTC | CTTGATGATG | AAGACCAAAA | CCTTGAATTA | | |
| msa31912.2{338_COH1} | CAGTTCAAGT | AGCTATTGTC | CTTGATGATG | AAGACCAAAA | CCTTGAATTA | | |
| msa31912.2{338_M732} | CAGTTCAAGT | AGCTATTGTC | CTTGATGATG | AAGACCAAAA | CCTTGAATTA | | |
| msa31912.2{338_M781} | CAGTTCAAGT | AGCTATTGTC | CTTGATGATG | AAGACCAAAA | CCTTGAATTA | | |
| msa31912.2{338_090} | CAGTTCAAGT | AGCTATTGTC | CTTGATGATG | AAGACCAAAA | CCTTGAATTA | | |
| msa31912.2{338_CJB110} | CAGTTCAAGT | AGCTATTGTC | CTTGATGATG | AAGACCAAAA | CCTTGAATTA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa31912.2{338_18RS21} | 451 | ACACTAAATA | GTCTCATTTT | AGCTGGTGAT | TTTATCAAGT | 500 | CAAAATGGAC |
| msa31912.2{338_2603} | ACACTAAATA | GTCTCATTTT | AGCTGGTGAT | TTTATCAAGT | CAAAATGGAC | | |
| msa31912.2{338_A909} | ACACTAAATA | GTCTCATTTT | AGCTGGTGAT | TTTATCAAGT | CAAAATGGAC | | |
| msa31912.2{338_H36B} | ACACTAAATA | GTCTCATTTT | AGCTGGTGAT | TTTATCAAGT | CAAAATGGAC | | |
| msa31912.2{338_JM9130013} | ACACTAAATA | GTCTCATTTT | AGCTGGTGAT | TTTATCAAGT | CAAAATGGAC | | |
| msa31912.2{338_COH1} | ACACTAAATA | GTCTCATTTT | AGCTGGTGAT | TTTATCAAGT | CAAAATGGAC | | |
| msa31912.2{338_M732} | ACACTAAATA | GTCTCATTTT | AGCTGGTGAT | TTTATCAAGT | CAAAATGGAC | | |
| msa31912.2{338_M781} | ACACTAAATA | GTCTCATTTT | AGCTGGTGAT | TTTATCAAGT | CAAAATGGAC | | |
| msa31912.2{338_090} | ACACTAAATA | GTCTCATTTT | AGCTGGTGAT | TTTATCAAGT | CAAAATGGAC | | |
| msa31912.2{338_CJB110} | ACACTAAATA | GTCTCATTTT | AGCTGGTGAT | TTTATCAAGT | CAAAATGGAC | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa31912.2{338_18RS21} | 501 | TACaAACCAT | TTTCAAATGC | TTGAGCACIT | AATACTTCAA | 550 | GATAAATTATC |
| msa31912.2{338_2603} | TACaAACCAT | TTTCAAATGC | TTGAGCACIT | AATACTTCAA | GATAAATTATC | | |
| msa31912.2{338_A909} | TACaAACCAT | TTTCAAATGC | TTGAGCACIT | AATACTTCAA | GATAAATTATC | | |
| msa31912.2{338_H36B} | TACaAACCAT | TTTCAAATGC | TTGAGCACIT | AATACTTCAA | GATAAATTATC | | |
| msa31912.2{338_JM9130013} | TACaAACCAT | TTTCAAATGC | TTGAGCACIT | AATACTTCAA | GATAAATTATC | | |
| msa31912.2{338_COH1} | TACaAACCAT | TTTCAAATGC | TTGAGCACIT | AATACTTCAA | GATAAATTATC | | |
| msa31912.2{338_M732} | TACaAACCAT | TTTCAAATGC | TTGAGCACIT | AATACTTCAA | GATAAATTATC | | |
| msa31912.2{338_M781} | TACaAACCAT | TTTCAAATGC | TTGAGCACIT | AATACTTCAA | GATAAATTATC | | |
| msa31912.2{338_090} | TACaAACCAT | TTTCAAATGC | TTGAGCACIT | AATACTTCAA | GATAAATTATC | | |
| msa31912.2{338_CJB110} | TACaAACCAT | TTTCAAATGC | TTGAGCACIT | AATACTTCAA | GATAAATTATC | | |
| Consensus | ***-***** | ***** | ***** | ***** | ***** | | |
| msa31912.2{338_18RS21} | 551 | AAGAACAATT | TCAACATCAA | AAGTTAGCCC | AAGTTAGCCC | 600 | TATTGAACCT |
| msa31912.2{338_2603} | AAGAACAATT | TCAACATCAA | AAGTTAGCCC | AAGTTAGCCC | TATTGAACCT | | |
| msa31912.2{338_A909} | AAGAACAATT | TCAACATCAA | AAGTTAGCCC | AAGTTAGCCC | TATTGAACCT | | |
| msa31912.2{338_H36B} | AAGAACAATT | TCAACATCAA | AAGTTAGCCC | AAGTTAGCCC | TATTGAACCT | | |
| msa31912.2{338_JM9130013} | AAGAACAATT | TCAACATCAA | AAGTTAGCCC | AAGTTAGCCC | TATTGAACCT | | |
| msa31912.2{338_COH1} | AAGAACAATT | TCAACATCAA | AAGTTAGCCC | AAGTTAGCCC | TATTGAACCT | | |
| msa31912.2{338_M732} | AAGAACAATT | TCAACATCAA | AAGTTAGCCC | AAGTTAGCCC | TATTGAACCT | | |

Table 73: Comparative Sequences relating to SAG0981

| | | | | | |
|--|------------|------------|------------|------------|-------------|
| msa31912.2{338_M781} | AAGAACAATT | TCAACATCAA | AAGTTAGCCC | AACTGGAAAA | TATTGAACCT |
| msa31912.2{338_090} | AAGAACAATT | TCAACATCAA | AAGTTAGCCC | AACTGGAAAA | TATTGAACCT |
| msa31912.2{338_CJB110} | AAGAACAATT | TCAACATCAA | AAGTTAGCCC | AACTGGAAAA | TATTGAACCT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31912.2{338_18RS21} | AGTGCGCTGA | CTAAACGCCT | TAAAGCAAGC | GGTCTGAAGA | TTTACTTAAG |
| msa31912.2{338_2603} | AGTGCGCTGA | CTAAACGCCT | TAAAGCAAGC | GGTCTGAAGA | TTTACTTAAG |
| msa31912.2{338_A909} | AGTGCGCTGA | CTAAACGCCT | TAAAGCAAGC | GGTCTGAAGA | TTTACTTAAG |
| msa31912.2{338_H36B} | AGTGCGCTGA | CTAAACGCCT | TAAAGCAAGC | GGTCTGAAGA | TTTACTTAAG |
| msa31912.2{338_JM9130013} | AGTGCGCTGA | CTAAACGCCT | TAAAGCAAGC | GGTCTGAAGA | TTTACTTAAG |
| msa31912.2{338_COH1} | AGTGCGCTGA | CTAAACGCCT | TAAAGCAAGC | GGTCTGAAGA | TTTACTTAAG |
| msa31912.2{338_M732} | AGTGCGCTGA | CTAAACGCCT | TAAAGCAAGC | GGTCTGAAGA | TTTACTTAAG |
| msa31912.2{338_M781} | AGTGCGCTGA | CTAAACGCCT | TAAAGCAAGC | GGTCTGAAGA | TTTACTTAAG |
| msa31912.2{338_090} | AGTGCGCTGA | CTAAACGCCT | TAAAGCAAGC | GGTCTGAAGA | TTTACTTAAG |
| msa31912.2{338_CJB110} | AGTGCGCTGA | CTAAACGCCT | TAAAGCAAGC | GGTCTGAAGA | TTTACTTAAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31912.2{338_18RS21} | AACGAGAACA | CAGGCAGCCG | ATCTATTAGT | TAAAAGTTGC | ACTCAAACCTA |
| msa31912.2{338_2603} | AACGAGAACA | CAGGCAGCCG | ATCTATTAGT | TAAAAGTTGC | ACTCAAACCTA |
| msa31912.2{338_A909} | AACGAGAACA | CAGGCAGCCG | ATCTATTAGT | TAAAAGTTGC | ACTCAAACCTA |
| msa31912.2{338_H36B} | AACGAGAACA | CAGGCAGCCG | ATCTATTAGT | TAAAAGTTGC | ACTCAAACCTA |
| msa31912.2{338_JM9130013} | AACGAGAACA | CAGGCAGCCG | ATCTATTAGT | TAAAAGTTGC | ACTCAAACCTA |
| msa31912.2{338_COH1} | AACGAGAACA | CAGGCAGCCG | ATCTATTAGT | TAAAAGTTGC | ACTCAAACCTA |
| msa31912.2{338_M732} | AACGAGAACA | CAGGCAGCCG | ATCTATTAGT | TAAAAGTTGC | ACTCAAACCTA |
| msa31912.2{338_M781} | AACGAGAACA | CAGGCAGCCG | ATCTATTAGT | TAAAAGTTGC | ACTCAAACCTA |
| msa31912.2{338_090} | AACGAGAACA | CAGGCAGCCG | ATCTATTAGT | TAAAAGTTGC | ACTCAAACCTA |
| msa31912.2{338_CJB110} | AACGAGAACA | CAGGCAGCCG | ATCTATTAGT | TAAAAGTTGC | ACTCAAACCTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa31912.2{338_18RS21} | AAGGGGGAAG | CTATGATTTC | | | |
| msa31912.2{338_2603} | AAGGGGGAAG | CTATGATTTC | | | |
| msa31912.2{338_A909} | AAGGGGGAAG | CTATGATTTC | | | |
| msa31912.2{338_H36B} | AAGGGGGAAG | CTATGATTTC | | | |
| msa31912.2{338_JM9130013} | AAGGGGGAAG | CTATGATTTC | | | |
| msa31912.2{338_COH1} | AAGGGGGAAG | CTATGATTTC | | | |
| msa31912.2{338_M732} | AAGGGGGAAG | CTATGATTTC | | | |
| msa31912.2{338_M781} | AAGGGGGAAG | CTATGATTTC | | | |
| msa31912.2{338_090} | AAGGGGGAAG | CTATGATTTC | | | |
| msa31912.2{338_CJB110} | AAGGGGGAAG | CTATGATTTC | | | |
| Consensus | ***** | ***** | | | |
| SEQ ID NO. 7311 | | | | | |
| STRAIN 2603 frame: 1 | | | | | |
| LSAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFITITA | | | | | |
| GDEFQALLKPSKVFQIIDHIQLALKPVNVRFG LGTGNIIITSINSNESIGADGPAYWHAR | | | | | |
| SAINHIDKNDYGTGVQVAICLDDQNLLETLNLSI SAGDFIKSKWTNNHFQMLEHLILQ | | | | | |
| DNYQEQQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCTQT KGGSYDF | | | | | |
| SEQ ID NO. 7312 | | | | | |
| STRAIN 090 frame: 1 | | | | | |
| SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFITITAG | | | | | |
| DEFQALLKPSKVFQIIDHIQLALKPVNVRFG LGTGNIIITSINL NESIGADGPAYWHARS | | | | | |
| AINHIHDKNDYGTGVQVAICLDDQNLLETLNLSI SAGDFIKSKWTNNHFQMLEHLILQD | | | | | |
| NYQEQQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCTQT KGGSYDF | | | | | |
| SEQ ID NO. 7313 | | | | | |
| STRAIN A909 frame: 1 | | | | | |
| SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFITITAG | | | | | |
| DEFQALLKPSKVFQIIDHIQLALKPVNVRFG LGTGNIIITSINSNESIGADGPAYWHARS | | | | | |
| AINHIHDKNDYGTGVQVAICLDDQNLLETLNLSI SAGDFIKSKWTNNHFQMLEHLILQD | | | | | |
| NYQEQQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCTQT KGGSYDF | | | | | |
| SEQ ID NO. 7314 | | | | | |
| STRAIN H36B frame: 1 | | | | | |
| SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFITITAG | | | | | |
| DEFQALLKPSKVFQIIDHIQLALKPVNVRFG LGTGNIIITSINSNESIGADGPAYWHARS | | | | | |
| AINHIHDKNDYGTGVQVAICLDDQNLLETLNLSI SAGDFIKSKWTNNHFQMLEHLILQD | | | | | |
| NYQEQQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCTQT KGGSYDF | | | | | |
| SEQ ID NO. 7315 | | | | | |
| STRAIN 18RS21 frame: 1 | | | | | |
| SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFITITAG | | | | | |
| DEFQALLKPSKVFQIIDHIQLALKPVNVRFG LGTGNIIITSINSNESIGADGPAYWHARS | | | | | |
| AINHIHDKNDYGTGVQVAICLDDQNLLETLNLSI SAGDFIKSKWTNNHFQMLEHLILQD | | | | | |
| NYQEQQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCTQT KGGSYDF | | | | | |
| SEQ ID NO. 7316 | | | | | |
| STRAIN M732 frame: 1 | | | | | |
| SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFITITAG | | | | | |

Table 73: Comparative Sequences relating to SAG0981

DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRKLKASGLKIYLRTRTQAADLLVKSCQTQKGGSYDF

SEQ ID NO. 7317

STRAIN COH1 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERETFQQS FQQLMTELS DVYGEELIS PFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRKLKASGLKIYLRTRTQAADLLVKSCQTQKGGSYDF

SEQ ID NO. 7318

STRAIN M781 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERETFQQS FQQLMTELS DVYGEELIS PFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRKLKASGLKIYLRTRTQAADLLVKSCQTQKGGSYDF

SEQ ID NO. 7319

STRAIN CJB110 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERETFQQS FQQLMTELS DVYGEELIS PFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRKLKASGLKIYLRTRTQAADLLVKSCQTQKGGSYDF

SEQ ID NO. 7320

STRAIN JM9130013 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERETFQQS FQQLMTELS DVYGEELIS PFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRKLKASGLKIYLRTRTQAADLLVKSCQTQKGGSYDF

PRETTY of: /biotmp/msa32053.2{*} February 18, 2003 08:25 ..

| | | | |
|---------------------------|------------|------------|-------------|
| | 1 | | 50 |
| msa32053.2{338_18RS21} | ~SAIIDKKVV | iFMYLALIGD | I INSKQILER |
| msa32053.2{338_2603} | 1SAIIDKKVV | iFMYLALIGD | I INSKQILER |
| msa32053.2{338_A909} | ~SAIIDKKVV | iFMYLALIGD | I INSKQILER |
| msa32053.2{338_CJB110} | ~SAIIDKKVV | vFMYLALIGD | I INSKQILER |
| msa32053.2{338_COH1} | ~SAIIDKKVV | iFMYLALIGD | I INSKQILER |
| msa32053.2{338_H36B} | ~SAIIDKKVV | iFMYLALIGD | I INSKQILER |
| msa32053.2{338_JM9130013} | ~SAIIDKKVV | iFMYLALIGD | I INSKQILER |
| msa32053.2{338_M732} | ~SAIIDKKVV | iFMYLALIGD | I INSKQILER |
| msa32053.2{338_M781} | ~SAIIDKKVV | iFMYLALIGD | I INSKQILER |
| msa32053.2{338_090} | ~SAIIDKKVV | iFMYLALIGD | I INSKQILER |
| Consensus | ***** | -***** | ***** |

| | | | |
|---------------------------|------------|------------|------------|
| | 51 | | 100 |
| msa32053.2{338_18RS21} | ELISpFTITA | GDEFQALLKp | SKKVFQIIDH |
| msa32053.2{338_2603} | ELISpFTITA | GDEFQALLKp | SKKVFQIIDH |
| msa32053.2{338_A909} | ELISpFTITA | GDEFQALLKp | SKKVFQIIDH |
| msa32053.2{338_CJB110} | ELISpFTITA | GDEFQALLKp | SKKVFQIIDH |
| msa32053.2{338_COH1} | ELISpFTITA | GDEFQALLKq | SKKVFQIIDH |
| msa32053.2{338_H36B} | ELISpFTITA | GDEFQALLKp | SKKVFQIIDH |
| msa32053.2{338_JM9130013} | ELISpFTITA | GDEFQALLKp | SKKVFQIIDH |
| msa32053.2{338_M732} | ELISpFTITA | GDEFQALLKq | SKKVFQIIDH |
| msa32053.2{338_M781} | ELISpFTITA | GDEFQALLKq | SKKVFQIIDH |
| msa32053.2{338_090} | ELISpFTITA | GDEFQALLKp | SKKVFQIIDH |
| Consensus | ****-**** | ***** | ***** |

| | | | |
|---------------------------|------------|------------|------------|
| | 101 | | 150 |
| msa32053.2{338_18RS21} | TSINsNESIG | ADGPAYWHAR | SAINHIHDKN |
| msa32053.2{338_2603} | TSINsNESIG | ADGPAYWHAR | SAINHIHDKN |
| msa32053.2{338_A909} | TSINsNESIG | ADGPAYWHAR | SAINHIHDKN |
| msa32053.2{338_CJB110} | TSINsNESIG | ADGPAYWHAR | SAINHIHDKN |
| msa32053.2{338_COH1} | TSINsNESIG | ADGPAYWHAR | SAINHIHDKN |
| msa32053.2{338_H36B} | TSINsNESIG | ADGPAYWHAR | SAINHIHDKN |
| msa32053.2{338_JM9130013} | TSINsNESIG | ADGPAYWHAR | SAINHIHDKN |
| msa32053.2{338_M732} | TSINsNESIG | ADGPAYWHAR | SAINHIHDKN |
| msa32053.2{338_M781} | TSINsNESIG | ADGPAYWHAR | SAINHIHDKN |
| msa32053.2{338_090} | TSINsNESIG | ADGPAYWHAR | SAINHIHDKN |
| Consensus | ****-**** | ***** | ***** |

| | | | |
|---------------------------|-------------|------------|------------|
| | 151 | | 200 |
| msa32053.2{338_18RS21} | TLNSLSISAGD | FIKSKWTTNH | FQMLEHLILQ |
| msa32053.2{338_2603} | TLNSLSISAGD | FIKSKWTTNH | FQMLEHLILQ |
| msa32053.2{338_A909} | TLNSLSISAGD | FIKSKWTTNH | FQMLEHLILQ |
| msa32053.2{338_CJB110} | TLNSLSISAGD | FIKSKWTTNH | FQMLEHLILQ |
| msa32053.2{338_COH1} | TLNSLSISAGD | FIKSKWTTNH | FQMLEHLILQ |
| msa32053.2{338_H36B} | TLNSLSISAGD | FIKSKWTTNH | FQMLEHLILQ |
| msa32053.2{338_JM9130013} | TLNSLSISAGD | FIKSKWTTNH | FQMLEHLILQ |
| msa32053.2{338_M732} | TLNSLSISAGD | FIKSKWTTNH | FQMLEHLILQ |
| msa32053.2{338_M781} | TLNSLSISAGD | FIKSKWTTNH | FQMLEHLILQ |
| Consensus | TLNSLSISAGD | FIKSKWTTNH | FQMLEHLILQ |

Table 73: Comparative Sequences relating to SAG0981

| | | | | | |
|---------------------------|------------|------------|------------|------------|------------|
| msa32053.2{338_090} | TLNSLISAGD | FIKSKWTTNH | FQMLEHLILQ | DNYQEQFQHQ | KLAQLENIEP |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 201 | | | 240 | |
| msa32053.2{338_18RS21} | SALTKRLKAS | GLKIYLRTRT | QAADLLVKSC | TQTKGGSYDF | |
| msa32053.2{338_2603} | SALTKRLKAS | GLKIYLRTRT | QAADLLVKSC | TQTKGGSYDF | |
| msa32053.2{338_A909} | SALTKRLKAS | GLKIYLRTRT | QAADLLVKSC | TQTKGGSYDF | |
| msa32053.2{338_CJB110} | SALTKRLKAS | GLKIYLRTRT | QAADLLVKSC | TQTKGGSYDF | |
| msa32053.2{338_COH1} | SALTKRLKAS | GLKIYLRTRT | QAADLLVKSC | TQTKGGSYDF | |
| msa32053.2{338_H36B} | SALTKRLKAS | GLKIYLRTRT | QAADLLVKSC | TQTKGGSYDF | |
| msa32053.2{338_JM9130013} | SALTKRLKAS | GLKIYLRTRT | QAADLLVKSC | TQTKGGSYDF | |
| msa32053.2{338_M732} | SALTKRLKAS | GLKIYLRTRT | QAADLLVKSC | TQTKGGSYDF | |
| msa32053.2{338_M781} | SALTKRLKAS | GLKIYLRTRT | QAADLLVKSC | TQTKGGSYDF | |
| msa32053.2{338_090} | SALTKRLKAS | GLKIYLRTRT | QAADLLVKSC | TQTKGGSYDF | |
| Consensus | ***** | ***** | ***** | ***** | |

Table 74: Comparative Sequences relating to SAG1572

SEQ ID NO. 7401

STRAIN 2603

ATGGAAATGCAAGTTCAAAAAGTTTAAATCAAATATACATTACGGAACACTCTAT
CTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGGATTTTA
AGAGAAGTTGATTTTATTGTGTCAGAGGATACACGAAATACGGGACTTTTACTCAAGCAC
TTTGATATTACTACTAAACAAATTAGTTTTCACGAAACAAATGCTTACGATAAAATCTCT
GGGTTAATTGATTTGTTAAAAGAAGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATG
CCCTCTATTTCGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGTTTAGCT
CCACAACCTCATATTTTATTGGCTTCTTACCTCGTAAGAAAGGTCAACAAATAACTTTC
TTTGAAACAAAGCAAGATTACCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTC
TCTGATACGCTAAACACATGAAAGAGATTTCGGAGATCGCCAAGTTGTTTATGACGC
GAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACCAATTAGTCAACTTTTAGAGCAT
ATTGAAAGAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAAGAGATACC
GAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAGTATTAGTAAAGAATATATCGCT
AATGGTGATAAACTAATCAAGCGATAAAAAAGTAGCAAAAGAATTTAATCTCAATAGA
CAAGAACTCTATGCTAGTTCCATGATTTA

SEQ ID NO. 7402

STRAIN 090

GAAATGCAAGTTCAAAAAGTTTAAATCAAATACACATTACGGGACACT
CTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTG
CCATTAGGATTTTAAGAGAAGTTGATTTTATTGTGTCAGAGGATACACGA
AATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAG
TTTTACGAAACAAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGT
TAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCT
ATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGAT
CCCGTCTGATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCG
CTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACCGCGT
AAGAAAGGTCAACAAATAACTTTTGTGAAACAAAGAAAGATTACCCCTGa
AACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAAC
ACATGAAGAGATTACGGAGATCGCCAAGTTGTTTATGACGCGAATTG
ACGAACTCTATGAAGAGTATCAAAGAGGAACCAATTAGTCAACTTTTAGG
GCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATG
GTAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTA
GTATTAGTAA

SEQ ID NO. 7403

STRAIN A909

AGTTCAAAAAAGTTTAAATCAAATATACATTACGGAACACTCTATCTAG
TCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGG
ATTTTAAAGAGAAGTTGATTTTATTGTGTCAGAGGATACACGAAATACGGG
ACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGTTTTCAGC
AACAATATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTTAAAAGAA
GGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTCTGA
CCCGAGCATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCAAGTTG
TATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGG
TTAGCTCCACAACCTCATATTTTATGGCTTCTTACCACGTAAGAAAGG
TCAACAAATAACTTTCTTTGAACAAAGCAAGATTACCTGAAACACAAA
TCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAACACATGAAA
GAGATTACCGAGATCGCCAAGTTGTTTATGACGCGAATTGACGAAACT
CTATGAAGAGTATCAAAGAGGAACCAATTAGTCAACTTTTAGAGCATATTG
AAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAAGAGA
GATACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAGTATTAGT
AA

SEQ ID NO. 7404

STRAIN H36B

GAAATGCAAGTTCAAAAAGTTTAAATCAAATACACATT
ACGGGACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAAGAGAAGTTGATTTTATTGTGTCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTTA
ATTGATTGTGTTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGG
AATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCCGTCTATCTATACCAAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTT
CTTACCGGTAAGCAAGGTCAACAAATAACTTTTGTGAAACAAAGAAAG
ATTACCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTCTCTGAT
ACGCTAAACACATGAAAGAGATTATGGAGATCGCCAAGTTGTTTATGAT
ACCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACCAATTAGTCA
AACTTTTAGGGCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAAGAGATATCTGAGCGAGTGAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7405

STRAIN 18RS21

GAAATGCAAGTTCAAAAAGTTTAAATCAAATATACATT
ACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAAGAGAAGTTGATTTTATTGTGTCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTA
ATTGATTGTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGG

Table 74: Comparative Sequences relating to SAG1572

AATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGTTTGTCTCCACACCTCATATTTTTTATGGCTT
CTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTGAAACAAAGCAAG
ATTACCCCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTCTCTGAT
ACGCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTGTTTAGT
ACGCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTC
AACTTTTAGAGCATATTGAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7406

STRAIN M732

GAAATGCAAGTTCAAAAAAGTTTAAATCAAAT
ATACATTACGGAACACTCTATCTAGTCCCACTCCAATTGGTAATCTAGA
TGATATGACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTT
GTGAGAGGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATT
ACTACTAAACAAATTAGTTTTCACGAACCAATGCTTACGATAAAATCTC
TGGGTTAATTGATTTGTAAAGAAGGGAAATCTTTAGCCCAAGTATCTG
ATGACGGAATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCT
GCTATTGAAGGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGG
TATTACTGCTCTCATCGCTTCAGTTTACTCTCCCAACCTCATATTTTTT
ATGGCTTCTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACA
AAGCAAGATTACCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGT
CTCTGATACGCTAAAACACATGAAAGAGATTACGGAGATCGCCAAGTTG
TTTTAGTACGCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACC
ATTAGTCAACTTTTAGAGCATATTGAAAGGTCCCTCTCAAAGGTGAATG
CTTAATTATGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTA
GCCAACAGATCCACTAGTATTAGTAA

SEQ ID NO. 7407

STRAIN COH1

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATATACATTAC
GGAACACTCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGAC
TTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGAGAGG
ATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAA
CAAAATAGTTTTCACGAACCAATGCTTACGATAAAATCTCTGGGTTAAT
TGATTTGTGTAAGAAGGGGAAATCTTTAGCCCAAGTATCTGATGACGAGAA
TGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAA
GGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGC
TCTCATCGCTTCAGGTTTAGCTCCCAACCTCATATTTTTTATGGCTTCT
TACCAGTTAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGAT
TACCCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATAC
GCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTGTTTATGATC
GCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAA
CTTTTAGAGCATATTGAAAGGTCCCTCTCAAAGGTGAATGCTTAATTAT
TGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAG
ATCCACTAGTATTAGTAA

SEQ ID NO. 7408

STRAIN M781

AAATGCAAGTTCAAAAAAGTTTAAATCAAATATACATTACGGAACACTC
TATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGC
CATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGAGAGGATACACGAA
ATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGT
TTTCACGAACCAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTT
AAAAAGAGGGAAATCTTTAGCCCAAGTATCTGATGACGGAATGCCCTCTA
TTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATC
CCAGTTGTATCTATACAGGAGCTAGCGCTGGTATTACTGCTCTCATCGC
TTCAGGTTTAGCTCCCAACCTCATATTTTTTATGGCTTCTTACCAGTA
AGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGATTACCCTGAA
ACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAACAC
CATGAAAGAGATTACGGAGATCGCCAAGTTGTTTATGATACGGAATTGA
CGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAG
CATATTGAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATGTTGATGG
TAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAG
TATTAGTAA

A

SEQ ID NO. 7409

STRAIN CJB110

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACATTACGGGACAC
TCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGT
GCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGAGAGGATACACG
AAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTA
GTTTTACGAACCAATGCTTACGATAAAATCTCTGGGTTAATTGATTTG
TTAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGACGGAATGCCCTC
TATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGA
TCCCGGTGCTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATC
GCTTCAGGTTTAGCTCCCAACCTCATATTTTTTATGGCTTCTTACCAGG
TAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGAAAGATTACCCTG
AAACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAAA
CATGAAAGAGATTACGGAGATCGCCAAGTTGTTTATGATACGGAATT

Table 74: Comparative Sequences relating to SAG1572

GACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAG
GGCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGAT
GGTAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACAGATCCACT
AGTATTAGTAA

SEQ ID NO. 7410

STRAIN 1169NT

TGCAAGTTCAAAAAAGTTTAAATCAAATACACATTATGGGACACTCTAT
CTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCAT
TAGGATTTTAAGAGAGTTGaTTTATTGTGTCAGAGGATACAGAAATA
CGGCACITTTACTCAAGCCTTTGATaTTACTACTAAACAAATTAGtTTT
cACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTtGTTAAA
AGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATT
CTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTC
AGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACCACGTAAGA
AAGGTCAACAAATAACTTTTGTGAAACAAGCAAGATTATCTGAAACA
CAAATCTTTTATGAGTCAACCGtTTGAGTCTCTGATACGCTAAACACAT
GAAAGAGATTTACGGAGATCGCCAAGTTGTTTATGACGCAATTGACgA
AACTCTATGAAGAGTATCAAAGAGGAACCATTaGTCAACTTTTAGAGCAT
ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGtTGATGGTAA
GAGAGATaCCGAGCGAGTGAAGACAGTAGCCAACAGATCCACTAGTAT
TAGTAA

SEQ ID NO. 7411

STRAIN JM9130013

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACACATTACGGGA
CACTCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTT
CGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTGTGTCAGAGGATAC
ACGAAATACGGGACTTTTACTCAAGCCTTTGATATTACTACTAAACAA
TTGATTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTTAATTGAT
TTGTTAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCC
CTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGG
ATATCCCGGTGCTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTC
ATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACC
GCGTAAGCAAGTCAACAAATAACTTTTGTGAAACAAGAAAGATTACC
CTGAAACACAATCTTTTATGAGTCAACCGTTTCGAGTCTCTGATACGCTA
AAACACATGAAGAGATTTATGGAGATCGCCAAGTTGTTTATGACGCGA
ATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTT
TAGGGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTT
GATGGTAAAGAGATACTAGCGAGTGAAGACAGTAGCCAACAGATCC
AGTAGTATTAGTAA

PRETTY of: /biotmp/msa323014.2{*} March 28, 2003 02:40 ..

| | | | |
|----------------------------|------------|------------|------------|
| | 1 | | 50 |
| msa323014.2{343_18RS21} | ---gaaatgc | aAGTTCAAAA | AAGTTTTAAA |
| msa323014.2{343_A909} | ----- | -AGTTCAAAA | AAGTTTTAAA |
| msa323014.2{343_COH1} | ---gaaatgc | aAGTTCAAAA | AAGTTTTAAA |
| msa323014.2{343_M732} | ---gaaatgc | aAGTTCAAAA | AAGTTTTAAA |
| msa323014.2{343_M781} | ---aaatgc | aAGTTCAAAA | AAGTTTTAAA |
| msa323014.2{343_2603} | atggaaatgc | aAGTTCAAAA | AAGTTTTAAA |
| msa323014.2{343_1169NT} | ----- | atggaaatgc | aAGTTCAAAA |
| msa323014.2{343_090} | ---gaaatgc | aAGTTCAAAA | AAGTTTTAAA |
| msa323014.2{343_CJB110} | ---gaaatgc | aAGTTCAAAA | AAGTTTTAAA |
| msa323014.2{343_H36B} | ---gaaatgc | aAGTTCAAAA | AAGTTTTAAA |
| msa323014.2{343_JM9130013} | ---gaaatgc | aAGTTCAAAA | AAGTTTTAAA |
| Consensus | ***** | ***** | ***** |

| | | | |
|----------------------------|------------|------------|------------|
| | 51 | | 100 |
| msa323014.2{343_18RS21} | ACTCTATCTA | GTCCCAACTC | CAATTGGTAA |
| msa323014.2{343_A909} | ACTCTATCTA | GTCCCAACTC | CAATTGGTAA |
| msa323014.2{343_COH1} | ACTCTATCTA | GTCCCAACTC | CAATTGGTAA |
| msa323014.2{343_M732} | ACTCTATCTA | GTCCCAACTC | CAATTGGTAA |
| msa323014.2{343_M781} | ACTCTATCTA | GTCCCAACTC | CAATTGGTAA |
| msa323014.2{343_2603} | ACTCTATCTA | GTCCCAACTC | CAATTGGTAA |
| msa323014.2{343_1169NT} | ACTCTATCTA | GTCCCAACTC | CAATTGGTAA |
| msa323014.2{343_090} | ACTCTATCTA | GTCCCAACTC | CAATTGGTAA |
| msa323014.2{343_CJB110} | ACTCTATCTA | GTCCCAACTC | CAATTGGTAA |
| msa323014.2{343_H36B} | ACTCTATCTA | GTCCCAACTC | CAATTGGTAA |
| msa323014.2{343_JM9130013} | ACTCTATCTA | GTCCCAACTC | CAATTGGTAA |
| Consensus | ***** | ***** | ***** |

| | | | |
|-------------------------|------------|------------|------------|
| | 101 | | 150 |
| msa323014.2{343_18RS21} | GTGCCATTAG | GATTTTAAGA | GAAGTTGATT |
| msa323014.2{343_A909} | GTGCCATTAG | GATTTTAAGA | GAAGTTGATT |
| msa323014.2{343_COH1} | GTGCCATTAG | GATTTTAAGA | GAAGTTGATT |
| msa323014.2{343_M732} | GTGCCATTAG | GATTTTAAGA | GAAGTTGATT |
| msa323014.2{343_M781} | GTGCCATTAG | GATTTTAAGA | GAAGTTGATT |
| msa323014.2{343_2603} | GTGCCATTAG | GATTTTAAGA | GAAGTTGATT |
| msa323014.2{343_1169NT} | GTGCCATTAG | GATTTTAAGA | GAAGTTGATT |
| msa323014.2{343_090} | GTGCCATTAG | GATTTTAAGA | GAAGTTGATT |

Table 74: Comparative Sequences relating to SAG1572

| | | | | | |
|----------------------------|------------|-------------|-------------|------------|------------|
| msa323014.2{343_CJB110} | GTGCCATTAG | GATTTTAAGA | GAAGTTGATT | TTATTGTGTC | AGAGGATACA |
| msa323014.2{343_H36B} | GTGCCATTAG | GATTTTAAGA | GAAGTTGATT | TTATTGTGTC | AGAGGATACA |
| msa323014.2{343_JM9130013} | GTGCCATTAG | GATTTTAAGA | GAAGTTGATT | TTATTGTGTC | AGAGGATACA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa323014.2{343_18RS21} | 151 | | | | 200 |
| msa323014.2{343_A909} | CGAAATACGG | GACTTTTACT | CAAGCACITTT | GATATTACTA | CTAAACAAAT |
| msa323014.2{343_COH1} | CGAAATACGG | GACTTTTACT | CAAGCACITTT | GATATTACTA | CTAAACAAAT |
| msa323014.2{343_M732} | CGAAATACGG | GACTTTTACT | CAAGCACITTT | GATATTACTA | CTAAACAAAT |
| msa323014.2{343_M781} | CGAAATACGG | GACTTTTACT | CAAGCACITTT | GATATTACTA | CTAAACAAAT |
| msa323014.2{343_2603} | CGAAATACGG | GACTTTTACT | CAAGCACITTT | GATATTACTA | CTAAACAAAT |
| msa323014.2{343_1169NT} | CGAAATACGG | GACTTTTACT | CAAGCACITTT | GATATTACTA | CTAAACAAAT |
| msa323014.2{343_090} | CGAAATACGG | GACTTTTACT | CAAGCACITTT | GATATTACTA | CTAAACAAAT |
| msa323014.2{343_CJB110} | CGAAATACGG | GACTTTTACT | CAAGCACITTT | GATATTACTA | CTAAACAAAT |
| msa323014.2{343_H36B} | CGAAATACGG | GACTTTTACT | CAAGCACITTT | GATATTACTA | CTAAACAAAT |
| msa323014.2{343_JM9130013} | CGAAATACGG | GACTTTTACT | CAAGCACITTT | GATATTACTA | CTAAACAAAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa323014.2{343_18RS21} | 201 | | | | 250 |
| msa323014.2{343_A909} | TAGTTTTTAC | GAACACAATG | CTTAcGATAA | AATCTCTGGG | TTAATTGATT |
| msa323014.2{343_COH1} | TAGTTTTTAC | GAACACAATG | CTTAcGATAA | AATCTCTGGG | TTAATTGATT |
| msa323014.2{343_M732} | TAGTTTTTAC | GAACACAATG | CTTAcGATAA | AATCTCTGGG | TTAATTGATT |
| msa323014.2{343_M781} | TAGTTTTTAC | GAACACAATG | CTTAcGATAA | AATCTCTGGG | TTAATTGATT |
| msa323014.2{343_2603} | TAGTTTTTAC | GAACACAATG | CTTAcGATAA | AATCTCTGGG | TTAATTGATT |
| msa323014.2{343_1169NT} | TAGTTTTTAC | GAACACAATG | CTTAcGATAA | AATCTCTGGG | TTAATTGATT |
| msa323014.2{343_090} | TAGTTTTTAC | GAACACAATG | CTTAcGATAA | AATCTCTGGG | TTAATTGATT |
| msa323014.2{343_CJB110} | TAGTTTTTAC | GAACACAATG | CTTAcGATAA | AATCTCTGGG | TTAATTGATT |
| msa323014.2{343_H36B} | TAGTTTTTAC | GAACACAATG | CTTAcGATAA | AATCTCTGGG | TTAATTGATT |
| msa323014.2{343_JM9130013} | TAGTTTTTAC | GAACACAATG | CTTAcGATAA | AATCTCTGGG | TTAATTGATT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa323014.2{343_18RS21} | 251 | | | | 300 |
| msa323014.2{343_A909} | TGTTAAAAGA | AGGGGaaATCT | TTAGCCCAAG | TATCTGATGC | AGGAATGCCC |
| msa323014.2{343_COH1} | TGTTAAAAGA | AGGGGaaATCT | TTAGCCCAAG | TATCTGATGC | AGGAATGCCC |
| msa323014.2{343_M732} | TGTTAAAAGA | AGGGGaaATCT | TTAGCCCAAG | TATCTGATGC | AGGAATGCCC |
| msa323014.2{343_M781} | TGTTAAAAGA | AGGGGaaATCT | TTAGCCCAAG | TATCTGATGC | AGGAATGCCC |
| msa323014.2{343_2603} | TGTTAAAAGA | AGGGGaaATCT | TTAGCCCAAG | TATCTGATGC | AGGAATGCCC |
| msa323014.2{343_1169NT} | TGTTAAAAGA | AGGGGaaATCT | TTAGCCCAAG | TATCTGATGC | AGGAATGCCC |
| msa323014.2{343_090} | TGTTAAAAGA | AGGGGaaATCT | TTAGCCCAAG | TATCTGATGC | AGGAATGCCC |
| msa323014.2{343_CJB110} | TGTTAAAAGA | AGGGGaaATCT | TTAGCCCAAG | TATCTGATGC | AGGAATGCCC |
| msa323014.2{343_H36B} | TGTTAAAAGA | AGGGGaaATCT | TTAGCCCAAG | TATCTGATGC | AGGAATGCCC |
| msa323014.2{343_JM9130013} | TGTTAAAAGA | AGGGGaaATCT | TTAGCCCAAG | TATCTGATGC | AGGAATGCCC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa323014.2{343_18RS21} | 301 | | | | 350 |
| msa323014.2{343_A909} | TCTATTTCTG | ACCCAGGACA | TGACCTTGTC | AAGGCTGCTA | TTGAAGGGGg |
| msa323014.2{343_COH1} | TCTATTTCTG | ACCCAGGACA | TGACCTTGTC | AAGGCTGCTA | TTGAAGGGGg |
| msa323014.2{343_M732} | TCTATTTCTG | ACCCAGGACA | TGACCTTGTC | AAGGCTGCTA | TTGAAGGGGg |
| msa323014.2{343_M781} | TCTATTTCTG | ACCCAGGACA | TGACCTTGTC | AAGGCTGCTA | TTGAAGGGGg |
| msa323014.2{343_2603} | TCTATTTCTG | ACCCAGGACA | TGACCTTGTC | AAGGCTGCTA | TTGAAGGGGg |
| msa323014.2{343_1169NT} | TCTATTTCTG | ACCCAGGACA | TGACCTTGTC | AAGGCTGCTA | TTGAAGGGGg |
| msa323014.2{343_090} | TCTATTTCTG | ACCCAGGACA | TGACCTTGTC | AAGGCTGCTA | TTGAAGGGGg |
| msa323014.2{343_CJB110} | TCTATTTCTG | ACCCAGGACA | TGACCTTGTC | AAGGCTGCTA | TTGAAGGGGg |
| msa323014.2{343_H36B} | TCTATTTCTG | ACCCAGGACA | TGACCTTGTC | AAGGCTGCTA | TTGAAGGGGg |
| msa323014.2{343_JM9130013} | TCTATTTCTG | ACCCAGGACA | TGACCTTGTC | AAGGCTGCTA | TTGAAGGGGg |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa323014.2{343_18RS21} | 351 | | | | 400 |
| msa323014.2{343_A909} | tATCCCaGtT | GTATCTATAC | CAGGAGCTAG | CGCTGGTATT | ACTGCTCTCA |
| msa323014.2{343_COH1} | tATCCCaGtT | GTATCTATAC | CAGGAGCTAG | CGCTGGTATT | ACTGCTCTCA |
| msa323014.2{343_M732} | tATCCCaGtT | GTATCTATAC | CAGGAGCTAG | CGCTGGTATT | ACTGCTCTCA |
| msa323014.2{343_M781} | tATCCCaGtT | GTATCTATAC | CAGGAGCTAG | CGCTGGTATT | ACTGCTCTCA |
| msa323014.2{343_2603} | tATCCCaGtT | GTATCTATAC | CAGGAGCTAG | CGCTGGTATT | ACTGCTCTCA |
| msa323014.2{343_1169NT} | tATCCCaGtT | GTATCTATAC | CAGGAGCTAG | CGCTGGTATT | ACTGCTCTCA |
| msa323014.2{343_090} | gATCCCGtTc | GTATCTATAC | CAGGAGCTAG | CGCTGGTATT | ACTGCTCTCA |
| msa323014.2{343_CJB110} | gATCCCGtTc | GTATCTATAC | CAGGAGCTAG | CGCTGGTATT | ACTGCTCTCA |
| msa323014.2{343_H36B} | tATCCCGtTc | GTATCTATAC | CAGGAGCTAG | CGCTGGTATT | ACTGCTCTCA |
| msa323014.2{343_JM9130013} | tATCCCGtTc | GTATCTATAC | CAGGAGCTAG | CGCTGGTATT | ACTGCTCTCA |
| Consensus | -*****- | ***** | ***** | ***** | ***** |
| msa323014.2{343_18RS21} | 401 | | | | 450 |
| msa323014.2{343_A909} | TCGCTTCAGG | TTTAGCTCCA | CAACCTCATA | TTTTTTATGG | CTTCTTACCa |
| msa323014.2{343_COH1} | TCGCTTCAGG | TTTAGCTCCA | CAACCTCATA | TTTTTTATGG | CTTCTTACCa |
| msa323014.2{343_M732} | TCGCTTCAGG | TTTAGCTCCA | CAACCTCATA | TTTTTTATGG | CTTCTTACCa |
| msa323014.2{343_M781} | TCGCTTCAGG | TTTAGCTCCA | CAACCTCATA | TTTTTTATGG | CTTCTTACCa |
| msa323014.2{343_2603} | TCGCTTCAGG | TTTAGCTCCA | CAACCTCATA | TTTTTTATGG | CTTCTTACCa |
| msa323014.2{343_1169NT} | TCGCTTCAGG | TTTAGCTCCA | CAACCTCATA | TTTTTTATGG | CTTCTTACCa |

Table 74: Comparative Sequences relating to SAG1572

| | | | | | | | |
|----------------------------|------------|------------|-------------|-------------|------------|------------|-----|
| msa323014.2{343_090} | TCGCTTCAGG | TTTAGCTCCA | CAACCTCATA | TTTTTTATGG | CTTCTTACCg | | |
| msa323014.2{343_CJB110} | TCGCTTCAGG | TTTAGCTCCA | CAACCTCATA | TTTTTTATGG | CTTCTTACCg | | |
| msa323014.2{343_H36B} | TCGCTTCAGG | TTTAGCTCCA | CAACCTCATA | TTTTTTATGG | CTTCTTACCg | | |
| msa323014.2{343_JM9130013} | TCGCTTCAGG | TTTAGCTCCA | CAACCTCATA | TTTTTTATGG | CTTCTTACCg | | |
| Consensus | ***** | ***** | ***** | ***** | *****- | | |
| msa323014.2{343_18RS21} | 451 | CGTAAGaAAG | GTCAACAAAT | AACITTTcTTT | GAAACAAAGc | AAGATTacCC | 500 |
| msa323014.2{343_A909} | CGTAAGaAAG | GTCAACAAAT | AACITTTcTTT | GAAACAAAGc | AAGATTacCC | | |
| msa323014.2{343_COH1} | CGTAAGaAAG | GTCAACAAAT | AACITTTcTTT | GAAACAAAGc | AAGATTacCC | | |
| msa323014.2{343_M732} | CGTAAGaAAG | GTCAACAAAT | AACITTTcTTT | GAAACAAAGc | AAGATTacCC | | |
| msa323014.2{343_M781} | CGTAAGaAAG | GTCAACAAAT | AACITTTcTTT | GAAACAAAGc | AAGATTacCC | | |
| msa323014.2{343_2603} | CGTAAGaAAG | GTCAACAAAT | AACITTTcTTT | GAAACAAAGc | AAGATTacCC | | |
| msa323014.2{343_1169NT} | CGTAAGaAAG | GTCAACAAAT | AACITTTcTTT | GAAACAAAGc | AAGATTacCC | | |
| msa323014.2{343_090} | CGTAAGaAAG | GTCAACAAAT | AACITTTcTTT | GAAACAAAGc | AAGATTacCC | | |
| msa323014.2{343_CJB110} | CGTAAGaAAG | GTCAACAAAT | AACITTTcTTT | GAAACAAAGc | AAGATTacCC | | |
| msa323014.2{343_H36B} | CGTAAGcAAG | GTCAACAAAT | AACITTTcTTT | GAAACAAAGc | AAGATTacCC | | |
| msa323014.2{343_JM9130013} | CGTAAGcAAG | GTCAACAAAT | AACITTTcTTT | GAAACAAAGc | AAGATTacCC | | |
| Consensus | *****-*** | ***** | *****-*** | ***** | ***** | *****-*** | |
| msa323014.2{343_18RS21} | 501 | TGAAACACAA | ATCTTTTATG | AGTCACCGTT | TCGAGTCTCT | GATACGCTAA | 550 |
| msa323014.2{343_A909} | TGAAACACAA | ATCTTTTATG | AGTCACCGTT | TCGAGTCTCT | GATACGCTAA | | |
| msa323014.2{343_COH1} | TGAAACACAA | ATCTTTTATG | AGTCACCGTT | TCGAGTCTCT | GATACGCTAA | | |
| msa323014.2{343_M732} | TGAAACACAA | ATCTTTTATG | AGTCACCGTT | TCGAGTCTCT | GATACGCTAA | | |
| msa323014.2{343_M781} | TGAAACACAA | ATCTTTTATG | AGTCACCGTT | TCGAGTCTCT | GATACGCTAA | | |
| msa323014.2{343_2603} | TGAAACACAA | ATCTTTTATG | AGTCACCGTT | TCGAGTCTCT | GATACGCTAA | | |
| msa323014.2{343_1169NT} | TGAAACACAA | ATCTTTTATG | AGTCACCGTT | TCGAGTCTCT | GATACGCTAA | | |
| msa323014.2{343_090} | TGAAACACAA | ATCTTTTATG | AGTCACCGTT | TCGAGTCTCT | GATACGCTAA | | |
| msa323014.2{343_CJB110} | TGAAACACAA | ATCTTTTATG | AGTCACCGTT | TCGAGTCTCT | GATACGCTAA | | |
| msa323014.2{343_H36B} | TGAAACACAA | ATCTTTTATG | AGTCACCGTT | TCGAGTCTCT | GATACGCTAA | | |
| msa323014.2{343_JM9130013} | TGAAACACAA | ATCTTTTATG | AGTCACCGTT | TCGAGTCTCT | GATACGCTAA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | |
| msa323014.2{343_18RS21} | 551 | AACACATGAA | AGAGATTTAc | GGAGATCGCC | AAGTTGTTTT | AGTACGCGAA | 600 |
| msa323014.2{343_A909} | AACACATGAA | AGAGATTTAc | GGAGATCGCC | AAGTTGTTTT | AGTACGCGAA | | |
| msa323014.2{343_COH1} | AACACATGAA | AGAGATTTAc | GGAGATCGCC | AAGTTGTTTT | AGTACGCGAA | | |
| msa323014.2{343_M732} | AACACATGAA | AGAGATTTAc | GGAGATCGCC | AAGTTGTTTT | AGTACGCGAA | | |
| msa323014.2{343_M781} | AACACATGAA | AGAGATTTAc | GGAGATCGCC | AAGTTGTTTT | AGTACGCGAA | | |
| msa323014.2{343_2603} | AACACATGAA | AGAGATTTAc | GGAGATCGCC | AAGTTGTTTT | AGTACGCGAA | | |
| msa323014.2{343_1169NT} | AACACATGAA | AGAGATTTAc | GGAGATCGCC | AAGTTGTTTT | AGTACGCGAA | | |
| msa323014.2{343_090} | AACACATGAA | AGAGATTTAc | GGAGATCGCC | AAGTTGTTTT | AGTACGCGAA | | |
| msa323014.2{343_CJB110} | AACACATGAA | AGAGATTTAc | GGAGATCGCC | AAGTTGTTTT | AGTACGCGAA | | |
| msa323014.2{343_H36B} | AACACATGAA | AGAGATTTAc | GGAGATCGCC | AAGTTGTTTT | AGTACGCGAA | | |
| msa323014.2{343_JM9130013} | AACACATGAA | AGAGATTTAc | GGAGATCGCC | AAGTTGTTTT | AGTACGCGAA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | |
| msa323014.2{343_18RS21} | 601 | TTGACGAAAC | TCTATGAAGA | GTATCAAAGA | GGAACCATTA | GTCAACTTTT | 650 |
| msa323014.2{343_A909} | TTGACGAAAC | TCTATGAAGA | GTATCAAAGA | GGAACCATTA | GTCAACTTTT | | |
| msa323014.2{343_COH1} | TTGACGAAAC | TCTATGAAGA | GTATCAAAGA | GGAACCATTA | GTCAACTTTT | | |
| msa323014.2{343_M732} | TTGACGAAAC | TCTATGAAGA | GTATCAAAGA | GGAACCATTA | GTCAACTTTT | | |
| msa323014.2{343_M781} | TTGACGAAAC | TCTATGAAGA | GTATCAAAGA | GGAACCATTA | GTCAACTTTT | | |
| msa323014.2{343_2603} | TTGACGAAAC | TCTATGAAGA | GTATCAAAGA | GGAACCATTA | GTCAACTTTT | | |
| msa323014.2{343_1169NT} | TTGACGAAAC | TCTATGAAGA | GTATCAAAGA | GGAACCATTA | GTCAACTTTT | | |
| msa323014.2{343_090} | TTGACGAAAC | TCTATGAAGA | GTATCAAAGA | GGAACCATTA | GTCAACTTTT | | |
| msa323014.2{343_CJB110} | TTGACGAAAC | TCTATGAAGA | GTATCAAAGA | GGAACCATTA | GTCAACTTTT | | |
| msa323014.2{343_H36B} | TTGACGAAAC | TCTATGAAGA | GTATCAAAGA | GGAACCATTA | GTCAACTTTT | | |
| msa323014.2{343_JM9130013} | TTGACGAAAC | TCTATGAAGA | GTATCAAAGA | GGAACCATTA | GTCAACTTTT | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | |
| msa323014.2{343_18RS21} | 651 | AGaGCATATT | GAAAAGGTCC | CTCTCAAAGG | TGAATGCTTA | ATTATTGTTG | 700 |
| msa323014.2{343_A909} | AGaGCATATT | GAAAAGGTCC | CTCTCAAAGG | TGAATGCTTA | ATTATTGTTG | | |
| msa323014.2{343_COH1} | AGaGCATATT | GAAAAGGTCC | CTCTCAAAGG | TGAATGCTTA | ATTATTGTTG | | |
| msa323014.2{343_M732} | AGaGCATATT | GAAAAGGTCC | CTCTCAAAGG | TGAATGCTTA | ATTATTGTTG | | |
| msa323014.2{343_M781} | AGaGCATATT | GAAAAGGTCC | CTCTCAAAGG | TGAATGCTTA | ATTATTGTTG | | |
| msa323014.2{343_2603} | AGaGCATATT | GAAAAGGTCC | CTCTCAAAGG | TGAATGCTTA | ATTATTGTTG | | |
| msa323014.2{343_1169NT} | AGaGCATATT | GAAAAGGTCC | CTCTCAAAGG | TGAATGCTTA | ATTATTGTTG | | |
| msa323014.2{343_090} | AGgGCATATT | GAAAAGGTCC | CTCTCAAAGG | TGAATGCTTA | ATTATTGTTG | | |
| msa323014.2{343_CJB110} | AGgGCATATT | GAAAAGGTCC | CTCTCAAAGG | TGAATGCTTA | ATTATTGTTG | | |
| msa323014.2{343_H36B} | AGgGCATATT | GAAAAGGTCC | CTCTCAAAGG | TGAATGCTTA | ATTATTGTTG | | |
| msa323014.2{343_JM9130013} | AGgGCATATT | GAAAAGGTCC | CTCTCAAAGG | TGAATGCTTA | ATTATTGTTG | | |
| Consensus | **-***** | *****-**** | ***** | ***** | ***** | ***** | |
| msa323014.2{343_18RS21} | 701 | ATGGTAAGAG | AGATACcGAG | CGAGTGAAG | ACAGTAGCCA | ACAAGATCCA | 750 |
| msa323014.2{343_A909} | ATGGTAAGAG | AGATACcGAG | CGAGTGAAG | ACAGTAGCCA | ACAAGATCCA | | |
| msa323014.2{343_COH1} | ATGGTAAGAG | AGATACcGAG | CGAGTGAAG | ACAGTAGCCA | ACAAGATCCA | | |
| msa323014.2{343_M732} | ATGGTAAGAG | AGATACcGAG | CGAGTGAAG | ACAGTAGCCA | ACAAGATCCA | | |
| msa323014.2{343_M781} | ATGGTAAGAG | AGATACcGAG | CGAGTGAAG | ACAGTAGCCA | ACAAGATCCA | | |
| msa323014.2{343_2603} | ATGGTAAGAG | AGATACcGAG | CGAGTGAAG | ACAGTAGCCA | ACAAGATCCA | | |

Table 74: Comparative Sequences relating to SAG1572

| | | | | | |
|----------------------------|------------|-------------|-------------|------------|-------------|
| msa323014.2{343_1169NT} | ATGGTAAGAG | AGATACCGAG | CGAGTGAAAG | ACAGTAGCCA | ACAAGATCCA |
| msa323014.2{343_090} | ATGGTAAGAG | AGATACCGAG | CGAGTGAAAG | ACAGTAGCCA | ACAAGATCCA |
| msa323014.2{343_CJB110} | ATGGTAAGAG | AGATACCGAG | CGAGTGAAAG | ACAGTAGCCA | ACAAGATCCA |
| msa323014.2{343_H36B} | ATGGTAAGAG | AGATACCGAG | CGAGTGAAAG | ACAGTAGCCA | ACAAGATCCA |
| msa323014.2{343_JM9130013} | ATGGTAAGAG | AGATACCGAG | CGAGTGAAAG | ACAGTAGCCA | ACAAGATCCA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 751 | | | | 800 |
| msa323014.2{343_18RS21} | cTAGTATTAG | TAA----- | ----- | ----- | ----- |
| msa323014.2{343_A909} | cTAGTATTAG | TAA----- | ----- | ----- | ----- |
| msa323014.2{343_COH1} | cTAGTATTAG | TAA----- | ----- | ----- | ----- |
| msa323014.2{343_M732} | cTAGTATTAG | TAA----- | ----- | ----- | ----- |
| msa323014.2{343_M781} | cTAGTATTAG | TAAA----- | ----- | ----- | ----- |
| msa323014.2{343_2603} | cTAGTATTAG | TAAAagaata | tatcgctaata | ggtgataaaa | ctaatacaagc |
| msa323014.2{343_1169NT} | cTAGTATTAG | TAA----- | ----- | ----- | ----- |
| msa323014.2{343_090} | cTAGTATTAG | TAA----- | ----- | ----- | ----- |
| msa323014.2{343_CJB110} | cTAGTATTAG | TAA----- | ----- | ----- | ----- |
| msa323014.2{343_H36B} | cTAGTATTAG | TAA----- | ----- | ----- | ----- |
| msa323014.2{343_JM9130013} | gTAGTATTAG | TAA----- | ----- | ----- | ----- |
| Consensus | -***** | ***** | ***** | ***** | ***** |
| | 801 | | | | 850 |
| msa323014.2{343_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_A909} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_M732} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_M781} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_2603} | gataaaaaaa | gtagcaaaaag | aatttaattct | caatagacaa | gaactctatg |
| msa323014.2{343_1169NT} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_090} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_CJB110} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_H36B} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 851 | | 867 | | |
| msa323014.2{343_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_A909} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_M732} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_M781} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_2603} | ctagtttcca | tgattta | ----- | ----- | ----- |
| msa323014.2{343_1169NT} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_090} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_CJB110} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_H36B} | ----- | ----- | ----- | ----- | ----- |
| msa323014.2{343_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ----- | ----- | ----- |

SEQ ID NO. 7412

STRAIN 2603 frame: 1

MEMQVQKSFKSNHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 DITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPISIDPGHDLVKAAIEGDI PV
 VSI PGASAGITALIASGLAPQPHIFYGFLPRKKGQITFFETKQDYPETQIFYESPFRVSD
 TLKHKMEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDT
 RVDSSQDPLVLV

SEQ ID NO. 7413

STRAIN 090 frame: 1

EMQVQKSFKSNHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPISIDPGHDLVKAAIEGGI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQITFFETKQDYPETQIFYESPFRVSD
 TLKHKMEIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDT
 RVDSSQDPLVLV

SEQ ID NO. 7414

STRAIN A909 frame: 2

VQKSFKSNHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDIT
 KQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPISIDPGHDLVKAAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQITFFETKQDYPETQIFYESPFRVSD
 TLKHKMEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDT
 RVDSSQDPLVLV

SEQ ID NO. 7415

STRAIN H36B frame: 1

EMQVQKSFKSNHYGTYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPISIDPGHDLVKAAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQITFFETKQDYPETQIFYESPFRVSD
 TLKHKMEIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDT
 RVDSSQDPLVLV

SEQ ID NO. 7416

Table 74: Comparative Sequences relating to SAG1572

STRAIN 18RS21 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQTFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLEHIEKVPLKGECLIIVDGKRDTTER
 VKDSSQDDPLVLV

SEQ ID NO. 7417
 STRAIN M732 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQTFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLEHIEKVPLKGECLIIVDGKRDTTER
 VKDSSQDDPLVLV

SEQ ID NO. 7418
 STRAIN COH1 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQTFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLEHIEKVPLKGECLIIVDGKRDTTER
 VKDSSQDDPLVLV

SEQ ID NO. 7419
 STRAIN M781 frame: 3
 MQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDI
 TTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVVS
 IPGASAGITALIASGLAPQPHIFYGFLPRKKGQQTFFETKQDYPETQIFYESPFRVSDT
 LKHMKEIYGDRQVVLVRELTKLYEYQRTISQLEHIEKVPLKGECLIIVDGKRDTTERV
 KDSSQDDPLVLV

SEQ ID NO. 7420
 STRAIN CJB110 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGGI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQTFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLGHIKVPLKGECLIIVDGKRDTTER
 VKDSSQDDPLVLV

SEQ ID NO. 7421
 STRAIN 1169NT frame: 3
 QVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDIT
 TKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVVSI
 PGASAGITALIASGLAPQPHIFYGFLPRKKGQQTFFETKQDYPETQIFYESPFRVSDTL
 KHMKEIYGDRQVVLVRELTKLYEYQRTISQLEHIEKVPLKGECLIIVDGKRDTTERVK
 DSSQDDPLVLV

SEQ ID NO. 7422
 STRAIN JM9130013 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQTFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLGHIKVPLKGECLIIVDGKRDTTER
 VKDSSQDDPVVLV

| | | |
|----------------------------|--|-----|
| msa324064.2{343_18RS21} | 1 | 50 |
| msa324064.2{343_A909} | ~emqVQKSFK SNIHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT | |
| msa324064.2{343_M781} | ----VQKSFK SNIHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT | |
| msa324064.2{343_2603} | ~mqVQKSFK SNIHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT | |
| msa324064.2{343_COH1} | memqVQKSFK SNIHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT | |
| msa324064.2{343_M732} | ~emqVQKSFK SNIHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT | |
| msa324064.2{343_1169NT} | ---qVQKSFK SNCHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT | |
| msa324064.2{343_090} | ~emqVQKSFK SNCHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT | |
| msa324064.2{343_CJB110} | ~emqVQKSFK SNCHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT | |
| msa324064.2{343_H36B} | ~emqVQKSFK SNCHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT | |
| msa324064.2{343_JM9130013} | ~emqVQKSFK SNCHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT | |
| Consensus | *--***** **-***** ***** ***** ***** | |
| msa324064.2{343_18RS21} | 51 | 100 |
| msa324064.2{343_A909} | RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP | |
| msa324064.2{343_M781} | RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP | |
| msa324064.2{343_2603} | RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP | |
| msa324064.2{343_COH1} | RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP | |
| msa324064.2{343_M732} | RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP | |
| msa324064.2{343_1169NT} | RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP | |
| msa324064.2{343_090} | RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP | |
| msa324064.2{343_CJB110} | RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP | |
| msa324064.2{343_H36B} | RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP | |
| msa324064.2{343_JM9130013} | RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP | |
| Consensus | ***** ***** ***** ***** ***** | |

Table 74: Comparative Sequences relating to SAG1572

| | | | | | |
|----------------------------|------------|-------------|------------|------------|------------|
| | 101 | | | | 150 |
| msa324064.2{343_18RS21} | SISDPGHDLV | KAAIEGdIPV | VSIPGASAGI | TALIASGLAP | QPHIFYGFLP |
| msa324064.2{343_A909} | SISDPGHDLV | KAAIEGdIPV | VSIPGASAGI | TALIASGLAP | QPHIFYGFLP |
| msa324064.2{343_M781} | SISDPGHDLV | KAAIEGdIPV | VSIPGASAGI | TALIASGLAP | QPHIFYGFLP |
| msa324064.2{343_2603} | SISDPGHDLV | KAAIEGdIPV | VSIPGASAGI | TALIASGLAP | QPHIFYGFLP |
| msa324064.2{343_COH1} | SISDPGHDLV | KAAIEGdIPV | VSIPGASAGI | TALIASGLAP | QPHIFYGFLP |
| msa324064.2{343_M732} | SISDPGHDLV | KAAIEGdIPV | VSIPGASAGI | TALIASGLAP | QPHIFYGFLP |
| msa324064.2{343_1169NT} | SISDPGHDLV | KAAIEGdIPV | VSIPGASAGI | TALIASGLAP | QPHIFYGFLP |
| msa324064.2{343_090} | SISDPGHDLV | KAAIEGgIPV | VSIPGASAGI | TALIASGLAP | QPHIFYGFLP |
| msa324064.2{343_CJB110} | SISDPGHDLV | KAAIEGdIPV | VSIPGASAGI | TALIASGLAP | QPHIFYGFLP |
| msa324064.2{343_H36B} | SISDPGHDLV | KAAIEGdIPV | VSIPGASAGI | TALIASGLAP | QPHIFYGFLP |
| msa324064.2{343_JM9130013} | SISDPGHDLV | KAAIEGdIPV | VSIPGASAGI | TALIASGLAP | QPHIFYGFLP |
| Consensus | ***** | *****_*** | ***** | ***** | ***** |
| | 151 | | | | 200 |
| msa324064.2{343_18RS21} | RKkGQQITFF | ETKqDYPETQ | IFYESPFRVS | DTLKHMKIY | GDRQVVLVRE |
| msa324064.2{343_A909} | RKkGQQITFF | ETKqDYPETQ | IFYESPFRVS | DTLKHMKIY | GDRQVVLVRE |
| msa324064.2{343_M781} | RKkGQQITFF | ETKqDYPETQ | IFYESPFRVS | DTLKHMKIY | GDRQVVLVRE |
| msa324064.2{343_2603} | RKkGQQITFF | ETKqDYPETQ | IFYESPFRVS | DTLKHMKIY | GDRQVVLVRE |
| msa324064.2{343_COH1} | RKkGQQITFF | ETKqDYPETQ | IFYESPFRVS | DTLKHMKIY | GDRQVVLVRE |
| msa324064.2{343_M732} | RKkGQQITFF | ETKqDYPETQ | IFYESPFRVS | DTLKHMKIY | GDRQVVLVRE |
| msa324064.2{343_1169NT} | RKkGQQITFF | ETKqDYPETQ | IFYESPFRVS | DTLKHMKIY | GDRQVVLVRE |
| msa324064.2{343_090} | RKkGQQITFF | ETKkDYPETQ | IFYESPFRVS | DTLKHMKIY | GDRQVVLVRE |
| msa324064.2{343_CJB110} | RKkGQQITFF | ETKkDYPETQ | IFYESPFRVS | DTLKHMKIY | GDRQVVLVRE |
| msa324064.2{343_H36B} | RKkGQQITFF | ETKkDYPETQ | IFYESPFRVS | DTLKHMKIY | GDRQVVLVRE |
| msa324064.2{343_JM9130013} | RKkGQQITFF | ETKkDYPETQ | IFYESPFRVS | DTLKHMKIY | GDRQVVLVRE |
| Consensus | **_***** | ***_***** | ***** | ***** | ***** |
| | 201 | | | | 250 |
| msa324064.2{343_18RS21} | LTKLYEEYQR | GTISQLLeHI | EKVPLKGECL | IIVDGKRDTE | RVKDSSQQDP |
| msa324064.2{343_A909} | LTKLYEEYQR | GTISQLLeHI | EKVPLKGECL | IIVDGKRDTE | RVKDSSQQDP |
| msa324064.2{343_M781} | LTKLYEEYQR | GTISQLLeHI | EKVPLKGECL | IIVDGKRDTE | RVKDSSQQDP |
| msa324064.2{343_2603} | LTKLYEEYQR | GTISQLLeHI | EKVPLKGECL | IIVDGKRDTE | RVKDSSQQDP |
| msa324064.2{343_COH1} | LTKLYEEYQR | GTISQLLeHI | EKVPLKGECL | IIVDGKRDTE | RVKDSSQQDP |
| msa324064.2{343_M732} | LTKLYEEYQR | GTISQLLeHI | EKVPLKGECL | IIVDGKRDTE | RVKDSSQQDP |
| msa324064.2{343_1169NT} | LTKLYEEYQR | GTISQLLeHI | EKVPLKGECL | IIVDGKRDTE | RVKDSSQQDP |
| msa324064.2{343_090} | LTKLYEEYQR | GTISQLLgHI | EKVPLKGECL | IIVDGKRDTE | RVKDSSQQDP |
| msa324064.2{343_CJB110} | LTKLYEEYQR | GTISQLLgHI | EKVPLKGECL | IIVDGKRDTE | RVKDSSQQDP |
| msa324064.2{343_H36B} | LTKLYEEYQR | GTISQLLgHI | EKVPLKGECL | IIVDGKRDTE | RVKDSSQQDP |
| msa324064.2{343_JM9130013} | LTKLYEEYQR | GTISQLLgHI | EKVPLKGECL | IIVDGKRDTE | RVKDSSQQDP |
| Consensus | ***** | *****_** | ***** | ***** | ***** |
| | 251 | | | | 289 |
| msa324064.2{343_18RS21} | LVLV~----- | ----- | ----- | ----- | ----- |
| msa324064.2{343_A909} | LVLV~----- | ----- | ----- | ----- | ----- |
| msa324064.2{343_M781} | LVLV~----- | ----- | ----- | ----- | ----- |
| msa324064.2{343_2603} | LVLVkeyian | gdktngaiikk | vakefnlnrq | elyasfhdI | ----- |
| msa324064.2{343_COH1} | LVLV~----- | ----- | ----- | ----- | ----- |
| msa324064.2{343_M732} | LVLV~----- | ----- | ----- | ----- | ----- |
| msa324064.2{343_1169NT} | LVLV~----- | ----- | ----- | ----- | ----- |
| msa324064.2{343_090} | LVLV~----- | ----- | ----- | ----- | ----- |
| msa324064.2{343_CJB110} | LVLV~----- | ----- | ----- | ----- | ----- |
| msa324064.2{343_H36B} | LVLV~----- | ----- | ----- | ----- | ----- |
| msa324064.2{343_JM9130013} | vVLV~----- | ----- | ----- | ----- | ----- |
| Consensus | -***** | ***** | ***** | ***** | ***** |

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7501
STRAIN 2603
ATGAGCGTATATGTTAGTGGAAATAGGAATTATT
TCTTCTTTGGGAAAGAATTATAGCGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGA
ATTCTTAAACATTTATATAAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATA
ACTAGTGACCCAGAGGTTCTCTGAGCAATACAAAGATGAGACACGTAATTTTAAATTTGCT
TTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAAAGCTTATCATAT
ATTGCTGTGTGTTTAGGACCTCACTTGGGGGAAAGAGTGTGGTCAAATGCCTTGTAT
CAATTTGAAGAAGGAGAGCGTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTAC
CATATTGCTGATGAATTTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTC
ACCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGATGGC
GATTGTGATTTAGCTATTTTGGTGGCTGTGATGAGTTAAGTGATATTTCTTTAGCAGGC
TTCACATCACTAGGAGCTATTAATACAGAAATGGCATGTGAGCCCTATTCTCTGGAAAA
GGAATCAATTTGGGTGAGGGCGCTGGTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCT
AAATATGAAAAAATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCT
AAGCCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGTATT
GACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGGTACTCAAGCTAATGATAAA
ATGAAAAAAATATGATGTTAAGTTTTCGCCACAACGACATTGATCAGCAGTACCAAG
GGGCAACGGGTCATACCTCTAGGGGCTGCAGGTATTATCGAATTGATTAAATGTTTAGCG
GCAATAGAGGAACAGACTGTACCGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCA
GAAAAATTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTTTTCG
TTTGTCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTTTAGATTCACTCTAGAA
ACATTACCTGCTAGAGAAAAATCTTAAATGGCTATCTTATCATCTGTGCTTCCATTCT
AAGAATGAATCAGTTCTTCTATAAACCCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAA
GCATTACGCTTTTAAAGGGGCTAGACCACCAAACTGTCAACCCAGCACAAATTTAGGAAA
ATGATGATTTTTCCAAAATGGTTGCCGTAAACAGCTCAAGCACTAATAGAAAGCAAT
ATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTTGATTTTACAACACTTTCTGGA
CCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAATCAACAAGAGGATATGCACATGTT
TCTGCTTCAGCATTCGCTTTACGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATT
TTTAAAAATAACAGGTCTTTTATCTGTCTTTTCGACAAATAGTGGAGCGCTTGATGGTATA
CAATATGCCAAGGAATGATCGCTAACGATAATCTAGACTATGTGATTCTTGTCTCTGCT
AATCAGTGGACAGACAGATTTTATGTGGTGGCAACAATTAACATATGATAGTCAAATG
TTTGTGCTTCTGATTATTGTTTCAGCACAAAGTCTCTCTCGTCAAGCATTTGGATAATCT
CCTATAATATTAGGTAGTAAACAATTAATAATAGCCATAAAACATTACAGATGTGATG
ACTATTTTGTGCTGCTGCTTCAAATTTATTTATCAGACTTAGGACTAACCATAAAAGAT
ATCAAAGGTTTCTGTTTGAATGAGCGGAAGAGGAGGAGTTAGTTTCAAGATTATGATTTCTTA
GCGAATCTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGGTCAGTTTGGATTTTCA
TCTAATGCTGCTGGTGAAGAAGTGGACTATACCTGTTAATGAAAGTATAGAAAAGGCTAT
TATTAGTCTATCTTATCGATCTTCGGTGGTATCTCTTTGTCTATTATTGAAAAAGG

SEQ ID NO. 7502
STRAIN 090
ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGaATTAT
AGCGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACA
TTTATATAAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAA
CTAGTGACCCAGAGGTTCTCTGAGCAATACAAAGATGAGACACGTAATTTT
AAATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAA
TTTAAAGCTTTATCATAATATGCTGTGTGTTTAGGGACCTCACTTGGGG
GAAAGAGTGTGCTCAAATGCCCTGTATCAATTTGAAGAAGGAGAGCGT
CAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGA
TGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAA
CCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTT
CAAGATGGCGAATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAG
TGATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAA
TGGCATGTGAGCCCTATTCTCTGAAAAAGGAATCAATTTGGGTGAGGGC
GCTGGTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAATATGGAAA
AATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTA
AGCCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAA
GCAGGTATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGG
TACTCAAGCTAATGATAAAATGGAAGAAAAATATGATGGTAAGTTTTC
CGACAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCACTACTA
GGGGCTGCAAGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGA
ACAGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTTCCAG
AAAAATTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTA
AATTTTCTGTTTGTCTTTGGTGAATAATAGTGGTATCTTATTGTCTATC
TTTAGATTCACTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATG
CTATCTTATCATCTGTGCTTCCATTCTAAGAAATGAATCACTTTCTATA
ACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTT
TAAAGGGGCTAGACCACCAAACTGTCAACCCAGCACAATTTAGGAAAA
TGGATGATTTTCCAAAATGGTTGCCGTAAACAAGCTCAAGCACTAATA
GAAAGCAATATTAACTAAAAAACAAGTACTTCAAAGTAGGAATTTGT
ATTTACAACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAAGC
AAATCACAACAGAGGATATGCACATGTTTCTGCTTCAGGATTCCTGTTT
ACAGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAAAATAAC
AGGTCCTTTATCTGCTATTTGACAAATAGTGGAGCGCTTGATGGTATAC
AATATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTT
GTTTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAAT
AAACTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAGCACAAG
TCCTCTCTGCTCAAGCATTTGGATAATTTCTCTATAATATTAGGTAGTAAA
CAATTAAAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGA
TGCTGCGCTTCAAATTTATTTATCAGACTTAGGACTAACCATAAAAGATA
TCAAAGGTTTCTGTTTGAATGAGCGGAAGAGGAGGAGTTAGTTCAAGATTAT
GATTTCTTAGCGAATCTGTGAGTATTATAATATGCCAAACCTTGCTTC

Table 75: Comparative Sequences relating to SAG0671

TGGTCAGTTTGGATTTTCATCTAATGGTGTGGTGAAGAACTGGACTATA
CTGTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATTTCG
ATCTTTGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

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STRAIN A909

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATT
ATAGCGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAA
CATTTATATATAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCAT
AACTAGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATT
TTAAATTTGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTT
AATTTAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGG
GGGAAAGAGTGTGGTCAAAATGCCCTTGATCAATTTGAAGAAGGAGAGC
GTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCT
GATGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTT
AACCCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTAC
TTCAGAGATGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTA
AGTGATATTTCTTTAGCAGGCTTCACTACCTAGGAGCTATTAATACAGA
AATGGCATGTGAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGG
GCGCTGGTTTGTGTTCTTGTCAAAGATCAGTCTTCTAGCTAAATATGGA
AAAATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACC
TAAGCCAACAGGTGAAGGGGCGGCACAGATTGCAAGCAGCTAGTGACTC
AAGCAGGTATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACA
GGTACTCAAGCTAATGATAAATGGAATAAATATGTATGGTAAGTTT
CCCGACAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCT
TAGGGGCTGCGAGTATTATCGAATTGATTAAATTGTTTAGCGGCAATAGAG
GAACAGACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTCC
AGAAAATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTT
TAAATTTTTCGTTTGTCTTTTGGTGAATAATAGTGGTGTCTTATTGTCA
TCTTTAGATTCACTCTAGAAAACATTACCTGCTAGAGAAAACTTAAAAAT
GGCTATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTA
TAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGC
TTTAAAGGGGCTAGACCACCCAAACTGTCAACCCAGCACATTTAGGAA
AATGGATGATTTTCCAAAATGGTTGCCGTAAACAGCTCAAGCACTAA
TAGAAAGCAATAATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAATT
GTATTTACAAACATTTCTGACCAGTTGAGGTTGTTGAAGGTATTGAAAA
GCAAAATCAACAACGAAGGATATGCATGTTTCTGCTTACAGATTCCCGT
TTACAGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAATA
ACAGGTCCTTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGATGGTAT
ACAAATATGCAAGGAAATGATGCGTAAACGATAATCTAGACTATGTGATTC
TTGTTTCTGCTAATCAGTGGACAGACATGAGTTTATGTGTGGCAACA
TTAACTATGATAGTCAAAATGTTTGTCCGTTCTGATTATTGTTCAAGACA
AGTCTCTCTCTCGTCAAGCATTGGATAAATCTCTATAATATTAGGTAGTA
AACAAATAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTT
GATGCTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAGA
TATCAAGGTTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTCAAGATT
ATGATTTCTTAGCGAACTTGTCTGAGTATTATATATGCCAAACCTTGCT
TCTGGTCAGTTTGGATTTCATCTAATGGTGTCTGGTGAAGAACTGGACTA
TACTGTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTTATT
CGATCTTCGGTGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7504

STRAIN H36B

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGA
GCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTAT
ATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACTAGT
GACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAAATT
TGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAA
AAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAG
AGTGTGGTCAAAATGCCCTTGATCAATTTGAAGAAGGAGAGCGTCAAGT
AGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGAAT
TGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCC
TGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGA
TGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTGATA
TTTCTTTAGCAGGCTTCACTACCTAGGAGCTATTAATACAGAAATGGCA
TGTCAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGGGCGCTGG
TTTTGTGTTCTTGTCAAAGATCAGTCTTCTAGCTAAATATGGAATAATTA
TCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGCCA
ACAGGTGAAGGGGCGGCACAGATTGCAAGCAGCTAGTGACTCAAGCAGG
TATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGGTACTC
AAGCTAATGATAAATGGAATAAATATGTATGGTAAGTTTTCCTCGACA
ACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGGGGC
TGCAGGTATTATCGAATTGATTAAATTGTTTAGCGGCAATAGAGGAACAGA
CTGTACCAAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAAAAT
TTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTT
TTCGTTTGTCTTTGGTGAATAAATAGTGGTGTCTTATTGTCTATCTTTAG
ATTCACTCTAGAAAAATTACCTGCTAGAGAAAACTTAAATAGGCTATC
TTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTA
TGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAAAG
GGGCTAGACCAACCAAACTGTCAACCCAGCACAAATTTAGGAAAAATGGAT
GATTTTTCAAAAATGGTTGCCGTAAACAGCTCAAGCACTAATAGAAAG
CAATATTAACTCAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATTTA
CAACACTTTCTGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAATC

Table 75: Comparative Sequences relating to SAG0671

ACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACAGT
AATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAATAACAGGTC
CTTTATCTGTCTATTTCCGACAAATAGTGGAGCGCTTGATGGTATACAAAT
GCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCCTGTTTC
TGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAACCT
ATGATAGTCAAAATGTTTGTGCGTTCTGATTATTGTTCCAGCACAAGTCCTC
TCTCGTCAAGCATTTGGATAATTCTCTATAATATTAGGTAGTAAACAATT
AAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATGCTG
CGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAGATATCAAA
GGTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTAGATTATGATTT
CTTAGCGAATCTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGGTC
AGTTTGGATTTTCATCTAATGGTGTGCTGGTGAAGAACTGGACTATCTGTT
AATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATTTCGATCTT
CGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7505

STRAIN 18RS21

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATTT
ATATATAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
GTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
AAAAGCTTATCATAATATTGCTGTGTGTTAGGGACCTCAGTTGGGGGA
AGAGTGTGCTGCTCAAAATGCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
GTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGA
ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
CCTGTTCTGCAAGTAATAATGCGTAATAATTAGGAACACAATTACTTCAA
GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAAATACAGAAATGG
CATGTCAGCCCTATTCTTCTGGAAGGAATCAATTTGGGTGAGGGCGCT
GGTTTGTGTTCTTGTCAAAGATCAGTCCCTAGCTAAATATGGAATAAT
TATCGGTGCTTATTACTTTCAGATGGTTATCATATAACAGCACCTTAAGC
CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
GGTATTGACTACAGTGAGATTGACTATTTAAACGGTACCGGTACAGGTAC
TCAAGCTAATGATAAAATGGAATAAATATGTATGGTAAGTTTTCCTCGA
CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGGG
GCTGCAAGTATTATCGAATTGATTAAATGTTTACGGCAATAGAGGAACA
GACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAAA
ATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
TTTTGCTTTGCTTTTGGTGAATAATAGTGGTGTCTTATTGTCTATCTTT
AGATTACCTCTAGAAACATTACCTGCTAGAGAAATCTTAAATGGCTA
TCTTATCATCTGTGCTTCCATTTCTAAGAAATGAATCACTTTCTATAACC
TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
AGGGGCTAGACCCCAAACTGTCAACCCAGCACAATTTAGGAAAATGG
ATGATTTTTCCAAAATGGTTGCGGTAAACAGCTCAAGCACTAATAGAA
AGCAATATTAACTTAAAAAACAAGTACTTCAAAAGTAGGAATTGTATT
TACAACACTTTCTGGACAGTTGAGGTGTTGAAGGTATTGAAAAGCAAA
TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCGTTTACA
GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAATAACAGG
TCCTTTATCTGTCTTTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
TCTGTCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTA
CTATGATGATCAAAATGTTTGTGCGTTCTGATTATTGTTTCAGCACAAGTCC
TCTCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAACAA
TTAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATGCT
TGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAGATATCA
AAGGTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTAGATTATGAT
TTCTTAGCGAATCTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGG
TCAGTTTGGATTTTCATCTAATGGTGTGCTGGTGAAGAACTGGACTATCTG
TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATTTCGATCT
TTCGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7506

STRAIN M732

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAG
CGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
TATATAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACT
AGTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
TAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCAGTTGGGGGA
AAGAGTGTGCTGCTCAAAATGCTTGTATCAATTTGAAGAAGGAGAGCGTCA
AGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATG
AATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACC
GCCTGTTCTGCAAGTAATAATGCCGTAATAATTAGGAACACAATTACTTCA
AGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTG
ATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAAATACAGAAATG
GCATGTCAGCCCTATTCTTCTGGAAGGAATCAATTTGGGTGAGGGCGC
TGGTTTGTGTTCTTGTCAAAGATCAGTCCCTAGCTAAATATGGAATAAT
TTATCGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTAAG
CCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGC
AGGTATTGACTACAGTGAGATTGACTATTTAAACGGTACCGGTACAGGTA
CTCAAGCTAATGATAAAATGGAATAAATATGTATGGTAAGTTTTCCTCG
ACAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGG

Table 75: Comparative Sequences relating to SAG0671

GGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAAC
 AGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTCCAGAA
 AATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAA
 TTTTTCGTTTGGCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCT
 TAGATTACCTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAAC
 CTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTA
 AAGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAATTTAGGAAAATG
 GATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
 AAGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTAT
 TTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 ATCACAACAGAAGGATATGCACATGTTTCTGCTTCAAGATTCCCGTTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAATAACAG
 GTCCTTTATCTGTCATTTTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 TATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 ACTATGATAGTCAAAATGTTTGTGCGTTCTGATTATGTTGAGCACAAGTC
 CTCTCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAACA
 ATTAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGGATG
 CTGCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATC
 AAAGGTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTGAGATTATGA
 TTTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTG
 GTCAGTTTGGATTTCATCTAATGGTGTGCTGTTGAAGAACTGGACTataCT
 GTTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCTCTATCTTATTCGAT
 CTTCCGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7507

STRAIN COH1

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
 ATATAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTTAGCAGGCTTCACTCACTAGGAGCTATTAATACAGAAATGG
 CATGTCTAGCCCTATTCTCTGGAAGGAATCAATTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGAAAAAT
 TATCGGTGGTCTTATTAATTAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTACCGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAAGAAATATGTTATGGTAAGTTTTCCTCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCTACTCTAGGG
 GCTGCAAGTATTATCGAATTGATTAAATTGTTTAGCGGCAATAGAGGAACA
 GACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTT
 AGATTACCTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTATT
 TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCAAGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAATAACAGG
 TCCTTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAAATGTTTGTGCGTTCTGATTATTGTTGAGCACAAGTCC
 TCTCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAACAA
 TTAATAATAGCCATAAAACATTACAGATGTGATGACTATTTTGTGTC
 TGGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
 AAGGTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTGAGATTATGAT
 TTTCTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTGCTGTTGAAGAACTGGACTATCTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCTCTATCTTATTCGATC
 TTCCGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7508

STRAIN M781

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
 ATATAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA

Table 75: Comparative Sequences relating to SAG0671

ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGG
 CATGTACAGCCCTATTCTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAATAAT
 TATCGGTGGTCTTATTAATCTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAATAAATATGTATGGTAAGTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTACATACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAAATGTTTGTAGCGCAATAGAGGAACA
 GACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGTCTTTTGGTGGAAATAATAGTGGTATCTTATTGTCACTTT
 AGATTCACTCTAGAAAACATTACCTGTCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTCTATAACC
 TATGAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACCAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATGTATT
 TACAACACTTTCTGGACCGTTGAGGTTGTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCTCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAATAACAGG
 TCCCTTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAATGTTTGTGGTCTGATTATTGTTTCAACAGTCC
 TCTCTCGTCAAGCATTGGGATAATCTCCTATAATATTAGGTAGTAAACAA
 TTAATAATATAGCCATAAAACATTCAAGATGTGATGACTATTTTGTATGC
 TGGCCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAGATATCA
 AAGGTTTCTGTTTGAATGAGCGGAAGAAGGCAGTTAGTTTCAAGTTATGAT
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGG
 TCAGTTTGGATTTTCTATTAATGGTGTGGTGAAGAACTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTATTTCGATC
 TTTGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7509

STRAIN CJB110

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAAATTATAGC
 GAGCATAAAGCAGCATCTCTCGACTTAAAGAAAGGAATTTCTAAACATTT
 ATATAAATAACAGCATCTATTTTGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCCTTCTCAGGTGTTAATTT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAAATGCCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTATAACAGAAATGG
 CATGTACAGCCCTATTCTCTGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAATAAT
 TATCGGTGGTCTTATTAATCTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAATAAATATGTATGGTAAGTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTACATACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAAATGTTTGTAGCGCAATAGAGGAACA
 GACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGTCTTTTGGTGGAAATAATAGTGGTATCTTATTGTCTATCTT
 AGATTCACTCTAGAAAACATTACCTGTCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTCTATAACC
 TATGAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACCAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATGTATT
 TACAACACTTTCTGGACCGTTGAGGTTGTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCTCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAATAACAGG
 TCCCTTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAATGTTTGTGGTCTGATTATTGTTTCAACAGTCC
 TCTCTCGTCAAGCATTGGGATAATCTCCTATAATATTAGGTAGTAAACAA
 TTAATAATATAGCCATAAAACATTCAAGATGTGATGACTATTTTGTATGC
 TGGCCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAGATATCA
 AAGGTTTCTGTTTGAATGAGCGGAAGAAGGCAGTTAGTTTCAAGTTATGAT
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGG
 TCAGTTTGGATTTTCTATTAATGGTGTGGTGAAGAACTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTATTTCGATC
 TTTGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7510

STRAIN 1169NT

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAG
 CGAGCATAAACAGCATCTCTTCGACTTAAAGAAAGGAATTTCTAAACATT
 TATATAAAAATCAGGACTCTATTTTGAATCTTATACAGGAAGCATAACT
 AGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAA
 ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
 TAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGA
 AAGAGTGTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCA
 AGTAGATGCTAGTTTATAGAAAAAGCATCTGTTTACCATATTGCTGATG
 AATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACC
 GCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCA
 AGATGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTG
 ATATTTCTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATG
 GCATGTGAGCCCTATTCTTCTGGAAGAAAGGAATCAATTTGGGTGAGGCGC
 TGGTTTGTGTGTTCTTGTCAAAGATCAGTCCCTAGCTAAATATGGAAAAA
 TTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAG
 CCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGC
 AGGTATTGACTACAGTGAGATTGACTATATTACGGTCACGGTACAGGTA
 CTCAAGCTAATGATAAAATGGAAAAAATATGTATGGTAAGTTTTCCTCG
 ACAACGACATTGATCAGCAGTACCAAGGGGCAACCGGTCATACTTAGG
 GGCTGCAGGTATTATCGAATTGATTAAATTGTTTAGCGCAATAGAGGAAC
 AGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTCCAGAA
 AATTTTGTCTATCATCAAAGAGAGAATACCCATAAGAAATGCTTTAA
 TTTTTCGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATGTCTATCTT
 TAGATTCACTCTAGAAACATTACCTGCTAGAGAAAAATCTTAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTTCTATAAC
 CTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCAATTACGCTTTA
 AAGGGGCTAGACCACCCAAACTGTCAACCCAGCACAAATTTAGGAAAAATG
 GATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
 AAGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTAT
 TTACAACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAAAGCAA
 ATCACAACAGAAAGGATATGCACATGTTCTGCTTCACGATTCCCGTTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAAAATAACAG
 GTCCTTTATCTGTCAATTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 TATGCCAAGGAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTA
 ACTATGATAGTCAAATGTTTGTGGTTCTGATTATTGTTTCAACAGATC
 CTCTCTCGTCAAGCATGGATAATTCTCTATAATATTAGGTAGTAAACA
 ATTTAAAAATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATG
 CTGCGCTTCAAATTTTATTATCAGACTTAGGACTAACCATAAAAGATATC
 AAAGGTTTCTGTTGGAAATGAGCGGAAGAAGGCAGTTAGTTCAAGATTATGA
 TTTCTTAGCGAATCTGTCTGAGTATTATAATATGCCAACCTTGCTCTG
 GTCAGTTTGGATTTCATCTAATGGTGCTGGTGAAGAACTGGACTATACT
 GTTAATGAAGTATAGAAAAGGGCTATTATTAGTCTTATCTTATTCGAT
 CTTTGGTGGTATCTCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7511

STRAIN JM9130013

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGAG
 CATAAACAGCATCTCTTCGACTTAAAGAAAGGAATTTCTAAACATTATATA
 TAAAAATCAGGACTCTATTTTGAATCTTATACAGGAAGCATAACTAGTG
 ACCGAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAAATTT
 GCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAAA
 AGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGAAAGA
 GTGCTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAAGTA
 GATGCTAGTTTATAGAAAAAGCATCTGTTTACCATATTGCTGATGAATT
 GATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCTT
 GTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGAT
 GGCGATTGTGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGATAT
 TTCTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATGGCAT
 GTCAGCCCTATTCTTCTGGAAGAAAGGAATCAATTTGGGTGAGGCGCTGGT
 TTTGTGTTCTTGTCAAAGATCAGTCCCTAGCTAAATATGGAAAAATTTAT
 CGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGCCAA
 CAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGT
 ATTGACTACAGTGAGATTGACTATATTACGGTCACGGTACAGGTACTCA
 AGCTAATGATAAAATGGAAAAAATATGTATGGTAAGTTTTCCTCGACAA
 CGACATTGATCAGCAGTACCAAGGGGCAACCGGTCATACTCTAGGGGCT
 GCAGGTATTATCGAATTGATTAAATTGTTTAGCGGCAATAGAGGAACAGAC
 TGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAAAATTT
 TTGTCTATCATCAAAGAGAGAATAACCAATAAGAAATGCTTTAAATTTT
 TCGTTTGTCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCTCTTTAGA
 TTCACCTCTAGAAACATTACCTGCTAGAGAAAAATCTTAAATGGCTATCT
 TATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTAT
 GAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCAATTACGCTTTAAAGG
 GGCTAGACCCCAAACTGTCAACCCAGCACAAATTTAGGAAAAATGGATG
 ATTTTTCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAAAGC
 AATATTAAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTATTAC
 AACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAAAGCAATCA
 CAACAGAGGATATGCACATGTTCTGCTTCAAGATTCCCGTTTACAGTA
 ATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAAAATAACAGGTCC
 TTTATCTGTCATTTTCGACAAATAGTGGAGCGCTTGATGGTATACAAATATG

Table 75: Comparative Sequences relating to SAG0671

CCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTTCCT
 GCTAATCAGTGGACAGACATGAGTTTATGTTGGTGGCAACAATTAACCTA
 TGATAGTCAAATCTTTGTCGGTCTGATTATTGTTACGACACAGTCCTCT
 CTCGTCAAGCATGGATAAATCTCCTATAATATTAGGTAGTAAACAATTA
 AAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTGCTGC
 GCTTCAAATTTTATATCAGACTTAGGACTAACCATAAAGATATCAAG
 GTTTCGTTTGAATGAGCGGAAGAGGCAGTTAGTTTCAAGATTATGATTTC
 TTAGCGAAGCTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGGTCA
 GTTTGGATTTCATCTAATGGTGTCTGGTGAAGAACTGGACTATACGTGA
 ATGAAAGTATAGAAAAGGGCTATTATTAGTCCTATCTTATTCGATCTTC
 GGTGTATCTCTTTGCTATTATTGAAAAAAGG

PRETTY of: /biotmp/msal18688.2{*} April 9, 2003 02:55 ..

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| | 1 | | | | 50 |
| msal18688.2{361_18RS21} | ----- | ATGTTAGTGG | AATAGGAATT | ATTTCTTCTT | TGGGAAAGAA |
| msal18688.2{361_A909} | ----- | ATGTTAGTGG | AATAGGAATT | ATTTCTTCTT | TGGGAAAGAA |
| msal18688.2{361_COH1} | ----- | ATGTTAGTGG | AATAGGAATT | ATTTCTTCTT | TGGGAAAGAA |
| msal18688.2{361_H36B} | ----- | ATGTTAGTGG | AATAGGAATT | ATTTCTTCTT | TGGGAAAGAA |
| msal18688.2{361_JM9130013} | ----- | ATGTTAGTGG | AATAGGAATT | ATTTCTTCTT | TGGGAAAGAA |
| msal18688.2{361_M732} | ----- | ATGTTAGTGG | AATAGGAATT | ATTTCTTCTT | TGGGAAAGAA |
| msal18688.2{GBS361_2603} | atgagcgtat | ATGTTAGTGG | AATAGGAATT | ATTTCTTCTT | TGGGAAAGAA |
| msal18688.2{361_090} | ----- | ATGTTAGTGG | AATAGGAATT | ATTTCTTCTT | TGGGAAAGAA |
| msal18688.2{361_1169NT} | ----- | ATGTTAGTGG | AATAGGAATT | ATTTCTTCTT | TGGGAAAGAA |
| msal18688.2{361_CJB110} | ----- | ATGTTAGTGG | AATAGGAATT | ATTTCTTCTT | TGGGAAAGAA |
| msal18688.2{361_M781} | ----- | ATGTTAGTGG | AATAGGAATT | ATTTCTTCTT | TGGGAAAGAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 51 | | | | 100 |
| msal18688.2{361_18RS21} | TTATAGCGAG | CATAAACAGC | ATCTCTTCGA | CTTAAAAGAA | GGAATTTCTA |
| msal18688.2{361_A909} | TTATAGCGAG | CATAAACAGC | ATCTCTTCGA | CTTAAAAGAA | GGAATTTCTA |
| msal18688.2{361_COH1} | TTATAGCGAG | CATAAACAGC | ATCTCTTCGA | CTTAAAAGAA | GGAATTTCTA |
| msal18688.2{361_H36B} | TTATAGCGAG | CATAAACAGC | ATCTCTTCGA | CTTAAAAGAA | GGAATTTCTA |
| msal18688.2{361_JM9130013} | TTATAGCGAG | CATAAACAGC | ATCTCTTCGA | CTTAAAAGAA | GGAATTTCTA |
| msal18688.2{361_M732} | TTATAGCGAG | CATAAACAGC | ATCTCTTCGA | CTTAAAAGAA | GGAATTTCTA |
| msal18688.2{GBS361_2603} | TTATAGCGAG | CATAAACAGC | ATCTCTTCGA | CTTAAAAGAA | GGAATTTCTA |
| msal18688.2{361_090} | TTATAGCGAG | CATAAACAGC | ATCTCTTCGA | CTTAAAAGAA | GGAATTTCTA |
| msal18688.2{361_1169NT} | TTATAGCGAG | CATAAACAGC | ATCTCTTCGA | CTTAAAAGAA | GGAATTTCTA |
| msal18688.2{361_CJB110} | TTATAGCGAG | CATAAACAGC | ATCTCTTCGA | CTTAAAAGAA | GGAATTTCTA |
| msal18688.2{361_M781} | TTATAGCGAG | CATAAACAGC | ATCTCTTCGA | CTTAAAAGAA | GGAATTTCTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 101 | | | | 150 |
| msal18688.2{361_18RS21} | AACATTTATA | TAAAAATCAC | GACTCTATTT | TAGAATCTTA | TACAGGAAGC |
| msal18688.2{361_A909} | AACATTTATA | TAAAAATCAC | GACTCTATTT | TAGAATCTTA | TACAGGAAGC |
| msal18688.2{361_COH1} | AACATTTATA | TAAAAATCAC | GACTCTATTT | TAGAATCTTA | TACAGGAAGC |
| msal18688.2{361_H36B} | AACATTTATA | TAAAAATCAC | GACTCTATTT | TAGAATCTTA | TACAGGAAGC |
| msal18688.2{361_JM9130013} | AACATTTATA | TAAAAATCAC | GACTCTATTT | TAGAATCTTA | TACAGGAAGC |
| msal18688.2{361_M732} | AACATTTATA | TAAAAATCAC | GACTCTATTT | TAGAATCTTA | TACAGGAAGC |
| msal18688.2{GBS361_2603} | AACATTTATA | TAAAAATCAC | GACTCTATTT | TAGAATCTTA | TACAGGAAGC |
| msal18688.2{361_090} | AACATTTATA | TAAAAATCAC | GACTCTATTT | TAGAATCTTA | TACAGGAAGC |
| msal18688.2{361_1169NT} | AACATTTATA | TAAAAATCAC | GACTCTATTT | TAGAATCTTA | TACAGGAAGC |
| msal18688.2{361_CJB110} | AACATTTATA | TAAAAATCAC | GACTCTATTT | TAGAATCTTA | TACAGGAAGC |
| msal18688.2{361_M781} | AACATTTATA | TAAAAATCAC | GACTCTATTT | TAGAATCTTA | TACAGGAAGC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 151 | | | | 200 |
| msal18688.2{361_18RS21} | ATAACTAGTG | ACCCAGAGGT | TCCTGAGCAA | TACAAAGATG | AGACACGTAA |
| msal18688.2{361_A909} | ATAACTAGTG | ACCCAGAGGT | TCCTGAGCAA | TACAAAGATG | AGACACGTAA |
| msal18688.2{361_COH1} | ATAACTAGTG | ACCCAGAGGT | TCCTGAGCAA | TACAAAGATG | AGACACGTAA |
| msal18688.2{361_H36B} | ATAACTAGTG | ACCCAGAGGT | TCCTGAGCAA | TACAAAGATG | AGACACGTAA |
| msal18688.2{361_JM9130013} | ATAACTAGTG | ACCCAGAGGT | TCCTGAGCAA | TACAAAGATG | AGACACGTAA |
| msal18688.2{361_M732} | ATAACTAGTG | ACCCAGAGGT | TCCTGAGCAA | TACAAAGATG | AGACACGTAA |
| msal18688.2{GBS361_2603} | ATAACTAGTG | ACCCAGAGGT | TCCTGAGCAA | TACAAAGATG | AGACACGTAA |
| msal18688.2{361_090} | ATAACTAGTG | ACCCAGAGGT | TCCTGAGCAA | TACAAAGATG | AGACACGTAA |
| msal18688.2{361_1169NT} | ATAACTAGTG | ACCCAGAGGT | TCCTGAGCAA | TACAAAGATG | AGACACGTAA |
| msal18688.2{361_CJB110} | ATAACTAGTG | ACCCAGAGGT | TCCTGAGCAA | TACAAAGATG | AGACACGTAA |
| msal18688.2{361_M781} | ATAACTAGTG | ACCCAGAGGT | TCCTGAGCAA | TACAAAGATG | AGACACGTAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 201 | | | | 250 |
| msal18688.2{361_18RS21} | TTTTAAATTT | GCTTTTACCG | CTTTTGAAGA | GGCTCTTGCT | TCCTCAGGTG |
| msal18688.2{361_A909} | TTTTAAATTT | GCTTTTACCG | CTTTTGAAGA | GGCTCTTGCT | TCCTCAGGTG |
| msal18688.2{361_COH1} | TTTTAAATTT | GCTTTTACCG | CTTTTGAAGA | GGCTCTTGCT | TCCTCAGGTG |
| msal18688.2{361_H36B} | TTTTAAATTT | GCTTTTACCG | CTTTTGAAGA | GGCTCTTGCT | TCCTCAGGTG |
| msal18688.2{361_JM9130013} | TTTTAAATTT | GCTTTTACCG | CTTTTGAAGA | GGCTCTTGCT | TCCTCAGGTG |
| msal18688.2{361_M732} | TTTTAAATTT | GCTTTTACCG | CTTTTGAAGA | GGCTCTTGCT | TCCTCAGGTG |
| msal18688.2{GBS361_2603} | TTTTAAATTT | GCTTTTACCG | CTTTTGAAGA | GGCTCTTGCT | TCCTCAGGTG |
| msal18688.2{361_090} | TTTTAAATTT | GCTTTTACCG | CTTTTGAAGA | GGCTCTTGCT | TCCTCAGGTG |
| msal18688.2{361_1169NT} | TTTTAAATTT | GCTTTTACCG | CTTTTGAAGA | GGCTCTTGCT | TCCTCAGGTG |
| msal18688.2{361_CJB110} | TTTTAAATTT | GCTTTTACCG | CTTTTGAAGA | GGCTCTTGCT | TCCTCAGGTG |
| msal18688.2{361_M781} | TTTTAAATTT | GCTTTTACCG | CTTTTGAAGA | GGCTCTTGCT | TCCTCAGGTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |

Table 75: Comparative Sequences relating to SAG0671

| | 251 | | 300 |
|----------------------------|-----------------------|------------|-----------------------|
| msa118688.2{361_18RS21} | TTAATTTAAA AGCTTATCAT | AATATTGCTG | TGTGTTTAGG GACCTCACTT |
| msa118688.2{361_A909} | TTAATTTAAA AGCTTATCAT | AATATTGCTG | TGTGTTTAGG GACCTCACTT |
| msa118688.2{361_COH1} | TTAATTTAAA AGCTTATCAT | AATATTGCTG | TGTGTTTAGG GACCTCACTT |
| msa118688.2{361_H36B} | TTAATTTAAA AGCTTATCAT | AATATTGCTG | TGTGTTTAGG GACCTCACTT |
| msa118688.2{361_JM9130013} | TTAATTTAAA AGCTTATCAT | AATATTGCTG | TGTGTTTAGG GACCTCACTT |
| msa118688.2{361_M732} | TTAATTTAAA AGCTTATCAT | AATATTGCTG | TGTGTTTAGG GACCTCACTT |
| msa118688.2{GBS361_2603} | TTAATTTAAA AGCTTATCAT | AATATTGCTG | TGTGTTTAGG GACCTCACTT |
| msa118688.2{361_090} | TTAATTTAAA AGCTTATCAT | AATATTGCTG | TGTGTTTAGG GACCTCACTT |
| msa118688.2{361_1169NT} | TTAATTTAAA AGCTTATCAT | AATATTGCTG | TGTGTTTAGG GACCTCACTT |
| msa118688.2{361_CJB110} | TTAATTTAAA AGCTTATCAT | AATATTGCTG | TGTGTTTAGG GACCTCACTT |
| msa118688.2{361_M781} | TTAATTTAAA AGCTTATCAT | AATATTGCTG | TGTGTTTAGG GACCTCACTT |
| Consensus | ***** | ***** | ***** |
| msa118688.2{361_18RS21} | GGGGGAAAGA GTGCTGGTCA | AAATGCCTTG | TATCAATTTG AAGAAGGAGA |
| msa118688.2{361_A909} | GGGGGAAAGA GTGCTGGTCA | AAATGCCTTG | TATCAATTTG AAGAAGGAGA |
| msa118688.2{361_COH1} | GGGGGAAAGA GTGCTGGTCA | AAATGCCTTG | TATCAATTTG AAGAAGGAGA |
| msa118688.2{361_H36B} | GGGGGAAAGA GTGCTGGTCA | AAATGCCTTG | TATCAATTTG AAGAAGGAGA |
| msa118688.2{361_JM9130013} | GGGGGAAAGA GTGCTGGTCA | AAATGCCTTG | TATCAATTTG AAGAAGGAGA |
| msa118688.2{361_M732} | GGGGGAAAGA GTGCTGGTCA | AAATGCCTTG | TATCAATTTG AAGAAGGAGA |
| msa118688.2{GBS361_2603} | GGGGGAAAGA GTGCTGGTCA | AAATGCCTTG | TATCAATTTG AAGAAGGAGA |
| msa118688.2{361_090} | GGGGGAAAGA GTGCTGGTCA | AAATGCCTTG | TATCAATTTG AAGAAGGAGA |
| msa118688.2{361_1169NT} | GGGGGAAAGA GTGCTGGTCA | AAATGCCTTG | TATCAATTTG AAGAAGGAGA |
| msa118688.2{361_CJB110} | GGGGGAAAGA GTGCTGGTCA | AAATGCCTTG | TATCAATTTG AAGAAGGAGA |
| msa118688.2{361_M781} | GGGGGAAAGA GTGCTGGTCA | AAATGCCTTG | TATCAATTTG AAGAAGGAGA |
| Consensus | ***** | ***** | ***** |
| msa118688.2{361_18RS21} | GCGTCAAGTA GATGCTAGTT | TATTAGAAAA | AGCATCTGTT TACCATATTG |
| msa118688.2{361_A909} | GCGTCAAGTA GATGCTAGTT | TATTAGAAAA | AGCATCTGTT TACCATATTG |
| msa118688.2{361_COH1} | GCGTCAAGTA GATGCTAGTT | TATTAGAAAA | AGCATCTGTT TACCATATTG |
| msa118688.2{361_H36B} | GCGTCAAGTA GATGCTAGTT | TATTAGAAAA | AGCATCTGTT TACCATATTG |
| msa118688.2{361_JM9130013} | GCGTCAAGTA GATGCTAGTT | TATTAGAAAA | AGCATCTGTT TACCATATTG |
| msa118688.2{361_M732} | GCGTCAAGTA GATGCTAGTT | TATTAGAAAA | AGCATCTGTT TACCATATTG |
| msa118688.2{GBS361_2603} | GCGTCAAGTA GATGCTAGTT | TATTAGAAAA | AGCATCTGTT TACCATATTG |
| msa118688.2{361_090} | GCGTCAAGTA GATGCTAGTT | TATTAGAAAA | AGCATCTGTT TACCATATTG |
| msa118688.2{361_1169NT} | GCGTCAAGTA GATGCTAGTT | TATTAGAAAA | AGCATCTGTT TACCATATTG |
| msa118688.2{361_CJB110} | GCGTCAAGTA GATGCTAGTT | TATTAGAAAA | AGCATCTGTT TACCATATTG |
| msa118688.2{361_M781} | GCGTCAAGTA GATGCTAGTT | TATTAGAAAA | AGCATCTGTT TACCATATTG |
| Consensus | ***** | ***** | ***** |
| msa118688.2{361_18RS21} | CTGATGAATT GATGGCTTAT | CATGATATTG | TGGGAGCTTC GTATGTTATT |
| msa118688.2{361_A909} | CTGATGAATT GATGGCTTAT | CATGATATTG | TGGGAGCTTC GTATGTTATT |
| msa118688.2{361_COH1} | CTGATGAATT GATGGCTTAT | CATGATATTG | TGGGAGCTTC GTATGTTATT |
| msa118688.2{361_H36B} | CTGATGAATT GATGGCTTAT | CATGATATTG | TGGGAGCTTC GTATGTTATT |
| msa118688.2{361_JM9130013} | CTGATGAATT GATGGCTTAT | CATGATATTG | TGGGAGCTTC GTATGTTATT |
| msa118688.2{361_M732} | CTGATGAATT GATGGCTTAT | CATGATATTG | TGGGAGCTTC GTATGTTATT |
| msa118688.2{GBS361_2603} | CTGATGAATT GATGGCTTAT | CATGATATTG | TGGGAGCTTC GTATGTTATT |
| msa118688.2{361_090} | CTGATGAATT GATGGCTTAT | CATGATATTG | TGGGAGCTTC GTATGTTATT |
| msa118688.2{361_1169NT} | CTGATGAATT GATGGCTTAT | CATGATATTG | TGGGAGCTTC GTATGTTATT |
| msa118688.2{361_CJB110} | CTGATGAATT GATGGCTTAT | CATGATATTG | TGGGAGCTTC GTATGTTATT |
| msa118688.2{361_M781} | CTGATGAATT GATGGCTTAT | CATGATATTG | TGGGAGCTTC GTATGTTATT |
| Consensus | ***** | ***** | ***** |
| msa118688.2{361_18RS21} | TCAACCGCCT GTTCTGCAAG | TAATAATGCC | GTAATATTAG GAACACAATT |
| msa118688.2{361_A909} | TCAACCGCCT GTTCTGCAAG | TAATAATGCC | GTAATATTAG GAACACAATT |
| msa118688.2{361_COH1} | TCAACCGCCT GTTCTGCAAG | TAATAATGCC | GTAATATTAG GAACACAATT |
| msa118688.2{361_H36B} | TCAACCGCCT GTTCTGCAAG | TAATAATGCC | GTAATATTAG GAACACAATT |
| msa118688.2{361_JM9130013} | TCAACCGCCT GTTCTGCAAG | TAATAATGCC | GTAATATTAG GAACACAATT |
| msa118688.2{361_M732} | TCAACCGCCT GTTCTGCAAG | TAATAATGCC | GTAATATTAG GAACACAATT |
| msa118688.2{GBS361_2603} | TCAACCGCCT GTTCTGCAAG | TAATAATGCC | GTAATATTAG GAACACAATT |
| msa118688.2{361_090} | TCAACCGCCT GTTCTGCAAG | TAATAATGCC | GTAATATTAG GAACACAATT |
| msa118688.2{361_1169NT} | TCAACCGCCT GTTCTGCAAG | TAATAATGCC | GTAATATTAG GAACACAATT |
| msa118688.2{361_CJB110} | TCAACCGCCT GTTCTGCAAG | TAATAATGCC | GTAATATTAG GAACACAATT |
| msa118688.2{361_M781} | TCAACCGCCT GTTCTGCAAG | TAATAATGCC | GTAATATTAG GAACACAATT |
| Consensus | ***** | ***** | ***** |
| msa118688.2{361_18RS21} | ACTTCAAGAT GCGGATTGTG | ATTTAGCTAT | TTGTGGTGGC TGTGATGAGT |
| msa118688.2{361_A909} | ACTTCAAGAT GCGGATTGTG | ATTTAGCTAT | TTGTGGTGGC TGTGATGAGT |
| msa118688.2{361_COH1} | ACTTCAAGAT GCGGATTGTG | ATTTAGCTAT | TTGTGGTGGC TGTGATGAGT |
| msa118688.2{361_H36B} | ACTTCAAGAT GCGGATTGTG | ATTTAGCTAT | TTGTGGTGGC TGTGATGAGT |
| msa118688.2{361_JM9130013} | ACTTCAAGAT GCGGATTGTG | ATTTAGCTAT | TTGTGGTGGC TGTGATGAGT |
| msa118688.2{361_M732} | ACTTCAAGAT GCGGATTGTG | ATTTAGCTAT | TTGTGGTGGC TGTGATGAGT |
| msa118688.2{GBS361_2603} | ACTTCAAGAT GCGGATTGTG | ATTTAGCTAT | TTGTGGTGGC TGTGATGAGT |
| msa118688.2{361_090} | ACTTCAAGAT GCGGATTGTG | ATTTAGCTAT | TTGTGGTGGC TGTGATGAGT |
| msa118688.2{361_1169NT} | ACTTCAAGAT GCGGATTGTG | ATTTAGCTAT | TTGTGGTGGC TGTGATGAGT |
| msa118688.2{361_CJB110} | ACTTCAAGAT GCGGATTGTG | ATTTAGCTAT | TTGTGGTGGC TGTGATGAGT |
| msa118688.2{361_M781} | ACTTCAAGAT GCGGATTGTG | ATTTAGCTAT | TTGTGGTGGC TGTGATGAGT |
| Consensus | ***** | ***** | ***** |

Table 75: Comparative Sequences relating to SAG0671

| Consensus | ***** | ***** | ***** | ***** | ***** |
|----------------------------|------------|------------|------------|------------|------------|
| | 551 | | | | 600 |
| msa118688.2{361_18RS21} | TAAGTGATAT | TTCTTTAGCA | GGCTTCACAT | CACTAGGAGC | TATTAATACA |
| msa118688.2{361_A909} | TAAGTGATAT | TTCTTTAGCA | GGCTTCACAT | CACTAGGAGC | TATTAATACA |
| msa118688.2{361_COH1} | TAAGTGATAT | TTCTTTAGCA | GGCTTCACAT | CACTAGGAGC | TATTAATACA |
| msa118688.2{361_H36B} | TAAGTGATAT | TTCTTTAGCA | GGCTTCACAT | CACTAGGAGC | TATTAATACA |
| msa118688.2{361_JM9130013} | TAAGTGATAT | TTCTTTAGCA | GGCTTCACAT | CACTAGGAGC | TATTAATACA |
| msa118688.2{361_M732} | TAAGTGATAT | TTCTTTAGCA | GGCTTCACAT | CACTAGGAGC | TATTAATACA |
| msa118688.2{GBS361_2603} | TAAGTGATAT | TTCTTTAGCA | GGCTTCACAT | CACTAGGAGC | TATTAATACA |
| msa118688.2{361_090} | TAAGTGATAT | TTCTTTAGCA | GGCTTCACAT | CACTAGGAGC | TATTAATACA |
| msa118688.2{361_1169NT} | TAAGTGATAT | TTCTTTAGCA | GGCTTCACAT | CACTAGGAGC | TATTAATACA |
| msa118688.2{361_CJB110} | TAAGTGATAT | TTCTTTAGCA | GGCTTCACAT | CACTAGGAGC | TATTAATACA |
| msa118688.2{361_M781} | TAAGTGATAT | TTCTTTAGCA | GGCTTCACAT | CACTAGGAGC | TATTAATACA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 601 | | | | 650 |
| msa118688.2{361_18RS21} | GAAATGGCAT | GTCAGCCCTA | TTCTTCTGGA | AAAGGAATCA | ATTTGGGTGA |
| msa118688.2{361_A909} | GAAATGGCAT | GTCAGCCCTA | TTCTTCTGGA | AAAGGAATCA | ATTTGGGTGA |
| msa118688.2{361_COH1} | GAAATGGCAT | GTCAGCCCTA | TTCTTCTGGA | AAAGGAATCA | ATTTGGGTGA |
| msa118688.2{361_H36B} | GAAATGGCAT | GTCAGCCCTA | TTCTTCTGGA | AAAGGAATCA | ATTTGGGTGA |
| msa118688.2{361_JM9130013} | GAAATGGCAT | GTCAGCCCTA | TTCTTCTGGA | AAAGGAATCA | ATTTGGGTGA |
| msa118688.2{361_M732} | GAAATGGCAT | GTCAGCCCTA | TTCTTCTGGA | AAAGGAATCA | ATTTGGGTGA |
| msa118688.2{GBS361_2603} | GAAATGGCAT | GTCAGCCCTA | TTCTTCTGGA | AAAGGAATCA | ATTTGGGTGA |
| msa118688.2{361_090} | GAAATGGCAT | GTCAGCCCTA | TTCTTCTGGA | AAAGGAATCA | ATTTGGGTGA |
| msa118688.2{361_1169NT} | GAAATGGCAT | GTCAGCCCTA | TTCTTCTGGA | AAAGGAATCA | ATTTGGGTGA |
| msa118688.2{361_CJB110} | GAAATGGCAT | GTCAGCCCTA | TTCTTCTGGA | AAAGGAATCA | ATTTGGGTGA |
| msa118688.2{361_M781} | GAAATGGCAT | GTCAGCCCTA | TTCTTCTGGA | AAAGGAATCA | ATTTGGGTGA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 651 | | | | 700 |
| msa118688.2{361_18RS21} | GGGCGCTGGT | TTTGTGTGTC | TTGTCAAAGA | TCAGTCCTTA | GCTAAATATG |
| msa118688.2{361_A909} | GGGCGCTGGT | TTTGTGTGTC | TTGTCAAAGA | TCAGTCCTTA | GCTAAATATG |
| msa118688.2{361_COH1} | GGGCGCTGGT | TTTGTGTGTC | TTGTCAAAGA | TCAGTCCTTA | GCTAAATATG |
| msa118688.2{361_H36B} | GGGCGCTGGT | TTTGTGTGTC | TTGTCAAAGA | TCAGTCCTTA | GCTAAATATG |
| msa118688.2{361_JM9130013} | GGGCGCTGGT | TTTGTGTGTC | TTGTCAAAGA | TCAGTCCTTA | GCTAAATATG |
| msa118688.2{361_M732} | GGGCGCTGGT | TTTGTGTGTC | TTGTCAAAGA | TCAGTCCTTA | GCTAAATATG |
| msa118688.2{GBS361_2603} | GGGCGCTGGT | TTTGTGTGTC | TTGTCAAAGA | TCAGTCCTTA | GCTAAATATG |
| msa118688.2{361_090} | GGGCGCTGGT | TTTGTGTGTC | TTGTCAAAGA | TCAGTCCTTA | GCTAAATATG |
| msa118688.2{361_1169NT} | GGGCGCTGGT | TTTGTGTGTC | TTGTCAAAGA | TCAGTCCTTA | GCTAAATATG |
| msa118688.2{361_CJB110} | GGGCGCTGGT | TTTGTGTGTC | TTGTCAAAGA | TCAGTCCTTA | GCTAAATATG |
| msa118688.2{361_M781} | GGGCGCTGGT | TTTGTGTGTC | TTGTCAAAGA | TCAGTCCTTA | GCTAAATATG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 701 | | | | 750 |
| msa118688.2{361_18RS21} | GAAAAATTAT | CGGTGGTCTT | ATTACTTCAG | ATGGTTATCA | TATAACAGCA |
| msa118688.2{361_A909} | GAAAAATTAT | CGGTGGTCTT | ATTACTTCAG | ATGGTTATCA | TATAACAGCA |
| msa118688.2{361_COH1} | GAAAAATTAT | CGGTGGTCTT | ATTACTTCAG | ATGGTTATCA | TATAACAGCA |
| msa118688.2{361_H36B} | GAAAAATTAT | CGGTGGTCTT | ATTACTTCAG | ATGGTTATCA | TATAACAGCA |
| msa118688.2{361_JM9130013} | GAAAAATTAT | CGGTGGTCTT | ATTACTTCAG | ATGGTTATCA | TATAACAGCA |
| msa118688.2{361_M732} | GAAAAATTAT | CGGTGGTCTT | ATTACTTCAG | ATGGTTATCA | TATAACAGCA |
| msa118688.2{GBS361_2603} | GAAAAATTAT | CGGTGGTCTT | ATTACTTCAG | ATGGTTATCA | TATAACAGCA |
| msa118688.2{361_090} | GAAAAATTAT | CGGTGGTCTT | ATTACTTCAG | ATGGTTATCA | TATAACAGCA |
| msa118688.2{361_1169NT} | GAAAAATTAT | CGGTGGTCTT | ATTACTTCAG | ATGGTTATCA | TATAACAGCA |
| msa118688.2{361_CJB110} | GAAAAATTAT | CGGTGGTCTT | ATTACTTCAG | ATGGTTATCA | TATAACAGCA |
| msa118688.2{361_M781} | GAAAAATTAT | CGGTGGTCTT | ATTACTTCAG | ATGGTTATCA | TATAACAGCA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 751 | | | | 800 |
| msa118688.2{361_18RS21} | CCTAAGCCAA | CAGGTGAAGG | GGCGGCACAG | ATTGCAAAGC | AGCTAGTGAC |
| msa118688.2{361_A909} | CCTAAGCCAA | CAGGTGAAGG | GGCGGCACAG | ATTGCAAAGC | AGCTAGTGAC |
| msa118688.2{361_COH1} | CCTAAGCCAA | CAGGTGAAGG | GGCGGCACAG | ATTGCAAAGC | AGCTAGTGAC |
| msa118688.2{361_H36B} | CCTAAGCCAA | CAGGTGAAGG | GGCGGCACAG | ATTGCAAAGC | AGCTAGTGAC |
| msa118688.2{361_JM9130013} | CCTAAGCCAA | CAGGTGAAGG | GGCGGCACAG | ATTGCAAAGC | AGCTAGTGAC |
| msa118688.2{361_M732} | CCTAAGCCAA | CAGGTGAAGG | GGCGGCACAG | ATTGCAAAGC | AGCTAGTGAC |
| msa118688.2{GBS361_2603} | CCTAAGCCAA | CAGGTGAAGG | GGCGGCACAG | ATTGCAAAGC | AGCTAGTGAC |
| msa118688.2{361_090} | CCTAAGCCAA | CAGGTGAAGG | GGCGGCACAG | ATTGCAAAGC | AGCTAGTGAC |
| msa118688.2{361_1169NT} | CCTAAGCCAA | CAGGTGAAGG | GGCGGCACAG | ATTGCAAAGC | AGCTAGTGAC |
| msa118688.2{361_CJB110} | CCTAAGCCAA | CAGGTGAAGG | GGCGGCACAG | ATTGCAAAGC | AGCTAGTGAC |
| msa118688.2{361_M781} | CCTAAGCCAA | CAGGTGAAGG | GGCGGCACAG | ATTGCAAAGC | AGCTAGTGAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 801 | | | | 850 |
| msa118688.2{361_18RS21} | TCAAGCAGGT | ATTGACTACA | GTGAGATTGA | CTATATTAAc | GGTCACGGTA |
| msa118688.2{361_A909} | TCAAGCAGGT | ATTGACTACA | GTGAGATTGA | CTATATTAAc | GGTCACGGTA |
| msa118688.2{361_COH1} | TCAAGCAGGT | ATTGACTACA | GTGAGATTGA | CTATATTAAc | GGTCACGGTA |
| msa118688.2{361_H36B} | TCAAGCAGGT | ATTGACTACA | GTGAGATTGA | CTATATTAAc | GGTCACGGTA |
| msa118688.2{361_JM9130013} | TCAAGCAGGT | ATTGACTACA | GTGAGATTGA | CTATATTAAc | GGTCACGGTA |
| msa118688.2{361_M732} | TCAAGCAGGT | ATTGACTACA | GTGAGATTGA | CTATATTAAc | GGTCACGGTA |
| msa118688.2{GBS361_2603} | TCAAGCAGGT | ATTGACTACA | GTGAGATTGA | CTATATTAAc | GGTCACGGTA |
| msa118688.2{361_090} | TCAAGCAGGT | ATTGACTACA | GTGAGATTGA | CTATATTAAc | GGTCACGGTA |
| msa118688.2{361_1169NT} | TCAAGCAGGT | ATTGACTACA | GTGAGATTGA | CTATATTAAc | GGTCACGGTA |
| msa118688.2{361_CJB110} | TCAAGCAGGT | ATTGACTACA | GTGAGATTGA | CTATATTAAc | GGTCACGGTA |

Table 75: Comparative Sequences relating to SAG0671

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| msa118688.2{361_M781} | TCAAGCAGGT | ATTGACTACA | GTGAGATTGA | CTATATTAAT | GGTCACGGTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 851 | | | | 900 |
| msa118688.2{361_18RS21} | CAGGTACTCA | AGCTAATGAT | AAAATGGAAA | AAAATATGTA | TGGTAAGTTT |
| msa118688.2{361_A909} | CAGGTACTCA | AGCTAATGAT | AAAATGGAAA | AAAATATGTA | TGGTAAGTTT |
| msa118688.2{361_COH1} | CAGGTACTCA | AGCTAATGAT | AAAATGGAAA | AAAATATGTA | TGGTAAGTTT |
| msa118688.2{361_H36B} | CAGGTACTCA | AGCTAATGAT | AAAATGGAAA | AAAATATGTA | TGGTAAGTTT |
| msa118688.2{361_JM9130013} | CAGGTACTCA | AGCTAATGAT | AAAATGGAAA | AAAATATGTA | TGGTAAGTTT |
| msa118688.2{361_M732} | CAGGTACTCA | AGCTAATGAT | AAAATGGAAA | AAAATATGTA | TGGTAAGTTT |
| msa118688.2{GBS361_2603} | CAGGTACTCA | AGCTAATGAT | AAAATGGAAA | AAAATATGTA | TGGTAAGTTT |
| msa118688.2{361_090} | CAGGTACTCA | AGCTAATGAT | AAAATGGAAA | AAAATATGTA | TGGTAAGTTT |
| msa118688.2{361_1169NT} | CAGGTACTCA | AGCTAATGAT | AAAATGGAAA | AAAATATGTA | TGGTAAGTTT |
| msa118688.2{361_CJB110} | CAGGTACTCA | AGCTAATGAT | AAAATGGAAA | AAAATATGTA | TGGTAAGTTT |
| msa118688.2{361_M781} | CAGGTACTCA | AGCTAATGAT | AAAATGGAAA | AAAATATGTA | TGGTAAGTTT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 901 | | | | 950 |
| msa118688.2{361_18RS21} | TTCCCGACAA | CGACATTGAT | CAGCAGTACC | AAGGGGCAAA | CGGGTCATAC |
| msa118688.2{361_A909} | TTCCCGACAA | CGACATTGAT | CAGCAGTACC | AAGGGGCAAA | CGGGTCATAC |
| msa118688.2{361_COH1} | TTCCCGACAA | CGACATTGAT | CAGCAGTACC | AAGGGGCAAA | CGGGTCATAC |
| msa118688.2{361_H36B} | TTCCCGACAA | CGACATTGAT | CAGCAGTACC | AAGGGGCAAA | CGGGTCATAC |
| msa118688.2{361_JM9130013} | TTCCCGACAA | CGACATTGAT | CAGCAGTACC | AAGGGGCAAA | CGGGTCATAC |
| msa118688.2{361_M732} | TTCCCGACAA | CGACATTGAT | CAGCAGTACC | AAGGGGCAAA | CGGGTCATAC |
| msa118688.2{GBS361_2603} | TTCCCGACAA | CGACATTGAT | CAGCAGTACC | AAGGGGCAAA | CGGGTCATAC |
| msa118688.2{361_090} | TTCCCGACAA | CGACATTGAT | CAGCAGTACC | AAGGGGCAAA | CGGGTCATAC |
| msa118688.2{361_1169NT} | TTCCCGACAA | CGACATTGAT | CAGCAGTACC | AAGGGGCAAA | CGGGTCATAC |
| msa118688.2{361_CJB110} | TTCCCGACAA | CGACATTGAT | CAGCAGTACC | AAGGGGCAAA | CGGGTCATAC |
| msa118688.2{361_M781} | TTCCCGACAA | CGACATTGAT | CAGCAGTACC | AAGGGGCAAA | CGGGTCATAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 951 | | | | 1000 |
| msa118688.2{361_18RS21} | TCTAGGGGCT | GCAGGTATTA | TCGAATTGAT | TAATTGTTTA | GCGGCAATAG |
| msa118688.2{361_A909} | TCTAGGGGCT | GCAGGTATTA | TCGAATTGAT | TAATTGTTTA | GCGGCAATAG |
| msa118688.2{361_COH1} | TCTAGGGGCT | GCAGGTATTA | TCGAATTGAT | TAATTGTTTA | GCGGCAATAG |
| msa118688.2{361_H36B} | TCTAGGGGCT | GCAGGTATTA | TCGAATTGAT | TAATTGTTTA | GCGGCAATAG |
| msa118688.2{361_JM9130013} | TCTAGGGGCT | GCAGGTATTA | TCGAATTGAT | TAATTGTTTA | GCGGCAATAG |
| msa118688.2{361_M732} | TCTAGGGGCT | GCAGGTATTA | TCGAATTGAT | TAATTGTTTA | GCGGCAATAG |
| msa118688.2{GBS361_2603} | TCTAGGGGCT | GCAGGTATTA | TCGAATTGAT | TAATTGTTTA | GCGGCAATAG |
| msa118688.2{361_090} | TCTAGGGGCT | GCAGGTATTA | TCGAATTGAT | TAATTGTTTA | GCGGCAATAG |
| msa118688.2{361_1169NT} | TCTAGGGGCT | GCAGGTATTA | TCGAATTGAT | TAATTGTTTA | GCGGCAATAG |
| msa118688.2{361_CJB110} | TCTAGGGGCT | GCAGGTATTA | TCGAATTGAT | TAATTGTTTA | GCGGCAATAG |
| msa118688.2{361_M781} | TCTAGGGGCT | GCAGGTATTA | TCGAATTGAT | TAATTGTTTA | GCGGCAATAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 1001 | | | | 1050 |
| msa118688.2{361_18RS21} | AGGAACAGAC | TGTACCAGCA | ACTAAAAATG | AGATTGGGAT | AGAAGGTTTT |
| msa118688.2{361_A909} | AGGAACAGAC | TGTACCAGCA | ACTAAAAATG | AGATTGGGAT | AGAAGGTTTT |
| msa118688.2{361_COH1} | AGGAACAGAC | TGTACCAGCA | ACTAAAAATG | AGATTGGGAT | AGAAGGTTTT |
| msa118688.2{361_H36B} | AGGAACAGAC | TGTACCAGCA | ACTAAAAATG | AGATTGGGAT | AGAAGGTTTT |
| msa118688.2{361_JM9130013} | AGGAACAGAC | TGTACCAGCA | ACTAAAAATG | AGATTGGGAT | AGAAGGTTTT |
| msa118688.2{361_M732} | AGGAACAGAC | TGTACCAGCA | ACTAAAAATG | AGATTGGGAT | AGAAGGTTTT |
| msa118688.2{GBS361_2603} | AGGAACAGAC | TGTACCAGCA | ACTAAAAATG | AGATTGGGAT | AGAAGGTTTT |
| msa118688.2{361_090} | AGGAACAGAC | TGTACCAGCA | ACTAAAAATG | AGATTGGGAT | AGAAGGTTTT |
| msa118688.2{361_1169NT} | AGGAACAGAC | TGTACCAGCA | ACTAAAAATG | AGATTGGGAT | AGAAGGTTTT |
| msa118688.2{361_CJB110} | AGGAACAGAC | TGTACCAGCA | ACTAAAAATG | AGATTGGGAT | AGAAGGTTTT |
| msa118688.2{361_M781} | AGGAACAGAC | TGTACCAGCA | ACTAAAAATG | AGATTGGGAT | AGAAGGTTTT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 1051 | | | | 1100 |
| msa118688.2{361_18RS21} | CCAGAAAAAT | TTGTCTATCA | TCAAAAGAGA | GAATACCCAA | TAAGAAATGC |
| msa118688.2{361_A909} | CCAGAAAAAT | TTGTCTATCA | TCAAAAGAGA | GAATACCCAA | TAAGAAATGC |
| msa118688.2{361_COH1} | CCAGAAAAAT | TTGTCTATCA | TCAAAAGAGA | GAATACCCAA | TAAGAAATGC |
| msa118688.2{361_H36B} | CCAGAAAAAT | TTGTCTATCA | TCAAAAGAGA | GAATACCCAA | TAAGAAATGC |
| msa118688.2{361_JM9130013} | CCAGAAAAAT | TTGTCTATCA | TCAAAAGAGA | GAATACCCAA | TAAGAAATGC |
| msa118688.2{361_M732} | CCAGAAAAAT | TTGTCTATCA | TCAAAAGAGA | GAATACCCAA | TAAGAAATGC |
| msa118688.2{GBS361_2603} | CCAGAAAAAT | TTGTCTATCA | TCAAAAGAGA | GAATACCCAA | TAAGAAATGC |
| msa118688.2{361_090} | CCAGAAAAAT | TTGTCTATCA | TCAAAAGAGA | GAATACCCAA | TAAGAAATGC |
| msa118688.2{361_1169NT} | CCAGAAAAAT | TTGTCTATCA | TCAAAAGAGA | GAATACCCAA | TAAGAAATGC |
| msa118688.2{361_CJB110} | CCAGAAAAAT | TTGTCTATCA | TCAAAAGAGA | GAATACCCAA | TAAGAAATGC |
| msa118688.2{361_M781} | CCAGAAAAAT | TTGTCTATCA | TCAAAAGAGA | GAATACCCAA | TAAGAAATGC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 1101 | | | | 1150 |
| msa118688.2{361_18RS21} | TTTAAATTTT | TCGTTTGCTT | TTGGTGGAAA | TAATAGTGGT | GTCTTATTGT |
| msa118688.2{361_A909} | TTTAAATTTT | TCGTTTGCTT | TTGGTGGAAA | TAATAGTGGT | GTCTTATTGT |
| msa118688.2{361_COH1} | TTTAAATTTT | TCGTTTGCTT | TTGGTGGAAA | TAATAGTGGT | GTCTTATTGT |
| msa118688.2{361_H36B} | TTTAAATTTT | TCGTTTGCTT | TTGGTGGAAA | TAATAGTGGT | GTCTTATTGT |
| msa118688.2{361_JM9130013} | TTTAAATTTT | TCGTTTGCTT | TTGGTGGAAA | TAATAGTGGT | GTCTTATTGT |
| msa118688.2{361_M732} | TTTAAATTTT | TCGTTTGCTT | TTGGTGGAAA | TAATAGTGGT | GTCTTATTGT |
| msa118688.2{GBS361_2603} | TTTAAATTTT | TCGTTTGCTT | TTGGTGGAAA | TAATAGTGGT | GTCTTATTGT |
| msa118688.2{361_090} | TTTAAATTTT | TCGTTTGCTT | TTGGTGGAAA | TAATAGTGGT | GTCTTATTGT |
| msa118688.2{361_1169NT} | TTTAAATTTT | TCGTTTGCTT | TTGGTGGAAA | TAATAGTGGT | GTCTTATTGT |
| msa118688.2{361_M781} | TTTAAATTTT | TCGTTTGCTT | TTGGTGGAAA | TAATAGTGGT | GTCTTATTGT |
| Consensus | ***** | ***** | ***** | ***** | ***** |

Table 75: Comparative Sequences relating to SAG0671

| | | | | | | | |
|----------------------------|------------|------------|------------|------------|------------|------------|------|
| msa118688.2{361_CJB110} | TTTAAATTTT | TCGTTTGCTT | TTGGTGGAAA | TAATAGTGGT | aTCTTATTGT | | |
| msa118688.2{361_M781} | TTTAAATTTT | TCGTTTGCTT | TTGGTGGAAA | TAATAGTGGT | aTCTTATTGT | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa118688.2{361_18RS21} | 1151 | CATCTTTAGA | TTCACCTCTA | GAAACATTAC | CTGCTAGAGA | AAATCTTAAA | 1200 |
| msa118688.2{361_A909} | CATCTTTAGA | TTCACCTCTA | GAAACATTAC | CTGCTAGAGA | AAATCTTAAA | | |
| msa118688.2{361_COH1} | CATCTTTAGA | TTCACCTCTA | GAAACATTAC | CTGCTAGAGA | AAATCTTAAA | | |
| msa118688.2{361_H36B} | CATCTTTAGA | TTCACCTCTA | GAAACATTAC | CTGCTAGAGA | AAATCTTAAA | | |
| msa118688.2{361_JM9130013} | CATCTTTAGA | TTCACCTCTA | GAAACATTAC | CTGCTAGAGA | AAATCTTAAA | | |
| msa118688.2{361_M732} | CATCTTTAGA | TTCACCTCTA | GAAACATTAC | CTGCTAGAGA | AAATCTTAAA | | |
| msa118688.2{GBS361_2603} | CATCTTTAGA | TTCACCTCTA | GAAACATTAC | CTGCTAGAGA | AAATCTTAAA | | |
| msa118688.2{361_090} | CATCTTTAGA | TTCACCTCTA | GAAACATTAC | CTGCTAGAGA | AAATCTTAAA | | |
| msa118688.2{361_1169NT} | CATCTTTAGA | TTCACCTCTA | GAAACATTAC | CTGCTAGAGA | AAATCTTAAA | | |
| msa118688.2{361_CJB110} | CATCTTTAGA | TTCACCTCTA | GAAACATTAC | CTGCTAGAGA | AAATCTTAAA | | |
| msa118688.2{361_M781} | CATCTTTAGA | TTCACCTCTA | GAAACATTAC | CTGCTAGAGA | AAATCTTAAA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa118688.2{361_18RS21} | 1201 | ATGGCTATCT | TATCATCTGT | TGCTTCCATT | TCTAAGAATG | AATCACTTTC | 1250 |
| msa118688.2{361_A909} | ATGGCTATCT | TATCATCTGT | TGCTTCCATT | TCTAAGAATG | AATCACTTTC | | |
| msa118688.2{361_COH1} | ATGGCTATCT | TATCATCTGT | TGCTTCCATT | TCTAAGAATG | AATCACTTTC | | |
| msa118688.2{361_H36B} | ATGGCTATCT | TATCATCTGT | TGCTTCCATT | TCTAAGAATG | AATCACTTTC | | |
| msa118688.2{361_JM9130013} | ATGGCTATCT | TATCATCTGT | TGCTTCCATT | TCTAAGAATG | AATCACTTTC | | |
| msa118688.2{361_M732} | ATGGCTATCT | TATCATCTGT | TGCTTCCATT | TCTAAGAATG | AATCACTTTC | | |
| msa118688.2{GBS361_2603} | ATGGCTATCT | TATCATCTGT | TGCTTCCATT | TCTAAGAATG | AATCACTTTC | | |
| msa118688.2{361_090} | ATGGCTATCT | TATCATCTGT | TGCTTCCATT | TCTAAGAATG | AATCACTTTC | | |
| msa118688.2{361_1169NT} | ATGGCTATCT | TATCATCTGT | TGCTTCCATT | TCTAAGAATG | AATCACTTTC | | |
| msa118688.2{361_CJB110} | ATGGCTATCT | TATCATCTGT | TGCTTCCATT | TCTAAGAATG | AATCACTTTC | | |
| msa118688.2{361_M781} | ATGGCTATCT | TATCATCTGT | TGCTTCCATT | TCTAAGAATG | AATCACTTTC | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa118688.2{361_18RS21} | 1251 | TATAACCTAT | GAAAAAGTTG | CTAGTAATTT | CAACGACTTT | GAAGCATTAC | 1300 |
| msa118688.2{361_A909} | TATAACCTAT | GAAAAAGTTG | CTAGTAATTT | CAACGACTTT | GAAGCATTAC | | |
| msa118688.2{361_COH1} | TATAACCTAT | GAAAAAGTTG | CTAGTAATTT | CAACGACTTT | GAAGCATTAC | | |
| msa118688.2{361_H36B} | TATAACCTAT | GAAAAAGTTG | CTAGTAATTT | CAACGACTTT | GAAGCATTAC | | |
| msa118688.2{361_JM9130013} | TATAACCTAT | GAAAAAGTTG | CTAGTAATTT | CAACGACTTT | GAAGCATTAC | | |
| msa118688.2{361_M732} | TATAACCTAT | GAAAAAGTTG | CTAGTAATTT | CAACGACTTT | GAAGCATTAC | | |
| msa118688.2{GBS361_2603} | TATAACCTAT | GAAAAAGTTG | CTAGTAATTT | CAACGACTTT | GAAGCATTAC | | |
| msa118688.2{361_090} | TATAACCTAT | GAAAAAGTTG | CTAGTAATTT | CAACGACTTT | GAAGCATTAC | | |
| msa118688.2{361_1169NT} | TATAACCTAT | GAAAAAGTTG | CTAGTAATTT | CAACGACTTT | GAAGCATTAC | | |
| msa118688.2{361_CJB110} | TATAACCTAT | GAAAAAGTTG | CTAGTAATTT | CAACGACTTT | GAAGCATTAC | | |
| msa118688.2{361_M781} | TATAACCTAT | GAAAAAGTTG | CTAGTAATTT | CAACGACTTT | GAAGCATTAC | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa118688.2{361_18RS21} | 1301 | GCTTTAAAGG | GGCTAGACCA | CCCAAACTG | TCAACCCAGC | ACAATTTAGG | 1350 |
| msa118688.2{361_A909} | GCTTTAAAGG | GGCTAGACCA | CCCAAACTG | TCAACCCAGC | ACAATTTAGG | | |
| msa118688.2{361_COH1} | GCTTTAAAGG | GGCTAGACCA | CCCAAACTG | TCAACCCAGC | ACAATTTAGG | | |
| msa118688.2{361_H36B} | GCTTTAAAGG | GGCTAGACCA | CCCAAACTG | TCAACCCAGC | ACAATTTAGG | | |
| msa118688.2{361_JM9130013} | GCTTTAAAGG | GGCTAGACCA | CCCAAACTG | TCAACCCAGC | ACAATTTAGG | | |
| msa118688.2{361_M732} | GCTTTAAAGG | GGCTAGACCA | CCCAAACTG | TCAACCCAGC | ACAATTTAGG | | |
| msa118688.2{GBS361_2603} | GCTTTAAAGG | GGCTAGACCA | CCCAAACTG | TCAACCCAGC | ACAATTTAGG | | |
| msa118688.2{361_090} | GCTTTAAAGG | GGCTAGACCA | CCCAAACTG | TCAACCCAGC | ACAATTTAGG | | |
| msa118688.2{361_1169NT} | GCTTTAAAGG | GGCTAGACCA | CCCAAACTG | TCAACCCAGC | ACAATTTAGG | | |
| msa118688.2{361_CJB110} | GCTTTAAAGG | GGCTAGACCA | CCCAAACTG | TCAACCCAGC | ACAATTTAGG | | |
| msa118688.2{361_M781} | GCTTTAAAGG | GGCTAGACCA | CCCAAACTG | TCAACCCAGC | ACAATTTAGG | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa118688.2{361_18RS21} | 1351 | AAAATGGATG | ATTTTTCCTA | AATGGTTGCC | GTAACAACAG | CTCAAGCACT | 1400 |
| msa118688.2{361_A909} | AAAATGGATG | ATTTTTCCTA | AATGGTTGCC | GTAACAACAG | CTCAAGCACT | | |
| msa118688.2{361_COH1} | AAAATGGATG | ATTTTTCCTA | AATGGTTGCC | GTAACAACAG | CTCAAGCACT | | |
| msa118688.2{361_H36B} | AAAATGGATG | ATTTTTCCTA | AATGGTTGCC | GTAACAACAG | CTCAAGCACT | | |
| msa118688.2{361_JM9130013} | AAAATGGATG | ATTTTTCCTA | AATGGTTGCC | GTAACAACAG | CTCAAGCACT | | |
| msa118688.2{361_M732} | AAAATGGATG | ATTTTTCCTA | AATGGTTGCC | GTAACAACAG | CTCAAGCACT | | |
| msa118688.2{GBS361_2603} | AAAATGGATG | ATTTTTCCTA | AATGGTTGCC | GTAACAACAG | CTCAAGCACT | | |
| msa118688.2{361_090} | AAAATGGATG | ATTTTTCCTA | AATGGTTGCC | GTAACAACAG | CTCAAGCACT | | |
| msa118688.2{361_1169NT} | AAAATGGATG | ATTTTTCCTA | AATGGTTGCC | GTAACAACAG | CTCAAGCACT | | |
| msa118688.2{361_CJB110} | AAAATGGATG | ATTTTTCCTA | AATGGTTGCC | GTAACAACAG | CTCAAGCACT | | |
| msa118688.2{361_M781} | AAAATGGATG | ATTTTTCCTA | AATGGTTGCC | GTAACAACAG | CTCAAGCACT | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa118688.2{361_18RS21} | 1401 | AATAGAAAGC | AATATTAATC | TAAAAAACA | AGATACTTCA | AAAGTAGGAA | 1450 |
| msa118688.2{361_A909} | AATAGAAAGC | AATATTAATC | TAAAAAACA | AGATACTTCA | AAAGTAGGAA | | |
| msa118688.2{361_COH1} | AATAGAAAGC | AATATTAATC | TAAAAAACA | AGATACTTCA | AAAGTAGGAA | | |
| msa118688.2{361_H36B} | AATAGAAAGC | AATATTAATC | TAAAAAACA | AGATACTTCA | AAAGTAGGAA | | |
| msa118688.2{361_JM9130013} | AATAGAAAGC | AATATTAATC | TAAAAAACA | AGATACTTCA | AAAGTAGGAA | | |
| msa118688.2{361_M732} | AATAGAAAGC | AATATTAATC | TAAAAAACA | AGATACTTCA | AAAGTAGGAA | | |
| msa118688.2{GBS361_2603} | AATAGAAAGC | AATATTAATC | TAAAAAACA | AGATACTTCA | AAAGTAGGAA | | |
| msa118688.2{361_090} | AATAGAAAGC | AATATTAATC | TAAAAAACA | AGATACTTCA | AAAGTAGGAA | | |

Table 75: Comparative Sequences relating to SAG0671

| | | | | | | | |
|----------------------------|-------------|-------------|------------|------------|------------|------------|------|
| msa118688.2{361_1169NT} | AATAGAAAGC | AATATTAATC | TAAAAAAACA | AGATACTTCA | AAAGTAGGAA | | |
| msa118688.2{361_CJB110} | AATAGAAAGC | AATATTAATC | TAAAAAAACA | AGATACTTCA | AAAGTAGGAA | | |
| msa118688.2{361_M781} | AATAGAAAGC | AATATTAATC | TAAAAAAACA | AGATACTTCA | AAAGTAGGAA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | | | | | | |
| msa118688.2{361_18RS21} | 1451 | TTGTATTAC | AACACTTTCT | GGACCAGTTG | AGGTTGTTGA | AGGTATTGAA | 1500 |
| msa118688.2{361_A909} | TTGTATTAC | AACACTTTCT | GGACCAGTTG | AGGTTGTTGA | AGGTATTGAA | | |
| msa118688.2{361_COH1} | TTGTATTAC | AACACTTTCT | GGACCAGTTG | AGGTTGTTGA | AGGTATTGAA | | |
| msa118688.2{361_H36B} | TTGTATTAC | AACACTTTCT | GGACCAGTTG | AGGTTGTTGA | AGGTATTGAA | | |
| msa118688.2{361_JM9130013} | TTGTATTAC | AACACTTTCT | GGACCAGTTG | AGGTTGTTGA | AGGTATTGAA | | |
| msa118688.2{361_M732} | TTGTATTAC | AACACTTTCT | GGACCAGTTG | AGGTTGTTGA | AGGTATTGAA | | |
| msa118688.2{GBS361_2603} | TTGTATTAC | AACACTTTCT | GGACCAGTTG | AGGTTGTTGA | AGGTATTGAA | | |
| msa118688.2{361_090} | TTGTATTAC | AACACTTTCT | GGACCAGTTG | AGGTTGTTGA | AGGTATTGAA | | |
| msa118688.2{361_1169NT} | TTGTATTAC | AACACTTTCT | GGACCAGTTG | AGGTTGTTGA | AGGTATTGAA | | |
| msa118688.2{361_CJB110} | TTGTATTAC | AACACTTTCT | GGACCAGTTG | AGGTTGTTGA | AGGTATTGAA | | |
| msa118688.2{361_M781} | TTGTATTAC | AACACTTTCT | GGACCAGTTG | AGGTTGTTGA | AGGTATTGAA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | | | | | | |
| msa118688.2{361_18RS21} | 1501 | AAGCAAATCA | CAACAGAAGG | ATATGCACAT | GTTTCTGCTT | CACGATTCCC | 1550 |
| msa118688.2{361_A909} | AAGCAAATCA | CAACAGAAGG | ATATGCACAT | GTTTCTGCTT | CACGATTCCC | | |
| msa118688.2{361_COH1} | AAGCAAATCA | CAACAGAAGG | ATATGCACAT | GTTTCTGCTT | CACGATTCCC | | |
| msa118688.2{361_H36B} | AAGCAAATCA | CAACAGAAGG | ATATGCACAT | GTTTCTGCTT | CACGATTCCC | | |
| msa118688.2{361_JM9130013} | AAGCAAATCA | CAACAGAAGG | ATATGCACAT | GTTTCTGCTT | CACGATTCCC | | |
| msa118688.2{361_M732} | AAGCAAATCA | CAACAGAAGG | ATATGCACAT | GTTTCTGCTT | CACGATTCCC | | |
| msa118688.2{GBS361_2603} | AAGCAAATCA | CAACAGAAGG | ATATGCACAT | GTTTCTGCTT | CACGATTCCC | | |
| msa118688.2{361_090} | AAGCAAATCA | CAACAGAAGG | ATATGCACAT | GTTTCTGCTT | CACGATTCCC | | |
| msa118688.2{361_1169NT} | AAGCAAATCA | CAACAGAAGG | ATATGCACAT | GTTTCTGCTT | CACGATTCCC | | |
| msa118688.2{361_CJB110} | AAGCAAATCA | CAACAGAAGG | ATATGCACAT | GTTTCTGCTT | CACGATTCCC | | |
| msa118688.2{361_M781} | AAGCAAATCA | CAACAGAAGG | ATATGCACAT | GTTTCTGCTT | CACGATTCCC | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | | | | | | |
| msa118688.2{361_18RS21} | 1551 | GTTTACAGTA | ATGAATGCAG | CAGCTGGTAT | GCTTCTATC | ATTTTAAAAA | 1600 |
| msa118688.2{361_A909} | GTTTACAGTA | ATGAATGCAG | CAGCTGGTAT | GCTTCTATC | ATTTTAAAAA | | |
| msa118688.2{361_COH1} | GTTTACAGTA | ATGAATGCAG | CAGCTGGTAT | GCTTCTATC | ATTTTAAAAA | | |
| msa118688.2{361_H36B} | GTTTACAGTA | ATGAATGCAG | CAGCTGGTAT | GCTTCTATC | ATTTTAAAAA | | |
| msa118688.2{361_JM9130013} | GTTTACAGTA | ATGAATGCAG | CAGCTGGTAT | GCTTCTATC | ATTTTAAAAA | | |
| msa118688.2{361_M732} | GTTTACAGTA | ATGAATGCAG | CAGCTGGTAT | GCTTCTATC | ATTTTAAAAA | | |
| msa118688.2{GBS361_2603} | GTTTACAGTA | ATGAATGCAG | CAGCTGGTAT | GCTTCTATC | ATTTTAAAAA | | |
| msa118688.2{361_090} | GTTTACAGTA | ATGAATGCAG | CAGCTGGTAT | GCTTCTATC | ATTTTAAAAA | | |
| msa118688.2{361_1169NT} | GTTTACAGTA | ATGAATGCAG | CAGCTGGTAT | GCTTCTATC | ATTTTAAAAA | | |
| msa118688.2{361_CJB110} | GTTTACAGTA | ATGAATGCAG | CAGCTGGTAT | GCTTCTATC | ATTTTAAAAA | | |
| msa118688.2{361_M781} | GTTTACAGTA | ATGAATGCAG | CAGCTGGTAT | GCTTCTATC | ATTTTAAAAA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | | | | | | |
| msa118688.2{361_18RS21} | 1601 | TAACAGGTCC | TTTATCTGTC | ATTTCGACAA | ATAGTGGAGC | GCTTGATGGT | 1650 |
| msa118688.2{361_A909} | TAACAGGTCC | TTTATCTGTC | ATTTCGACAA | ATAGTGGAGC | GCTTGATGGT | | |
| msa118688.2{361_COH1} | TAACAGGTCC | TTTATCTGTC | ATTTCGACAA | ATAGTGGAGC | GCTTGATGGT | | |
| msa118688.2{361_H36B} | TAACAGGTCC | TTTATCTGTC | ATTTCGACAA | ATAGTGGAGC | GCTTGATGGT | | |
| msa118688.2{361_JM9130013} | TAACAGGTCC | TTTATCTGTC | ATTTCGACAA | ATAGTGGAGC | GCTTGATGGT | | |
| msa118688.2{361_M732} | TAACAGGTCC | TTTATCTGTC | ATTTCGACAA | ATAGTGGAGC | GCTTGATGGT | | |
| msa118688.2{GBS361_2603} | TAACAGGTCC | TTTATCTGTC | ATTTCGACAA | ATAGTGGAGC | GCTTGATGGT | | |
| msa118688.2{361_090} | TAACAGGTCC | TTTATCTGTC | ATTTCGACAA | ATAGTGGAGC | GCTTGATGGT | | |
| msa118688.2{361_1169NT} | TAACAGGTCC | TTTATCTGTC | ATTTCGACAA | ATAGTGGAGC | GCTTGATGGT | | |
| msa118688.2{361_CJB110} | TAACAGGTCC | TTTATCTGTC | ATTTCGACAA | ATAGTGGAGC | GCTTGATGGT | | |
| msa118688.2{361_M781} | TAACAGGTCC | TTTATCTGTC | ATTTCGACAA | ATAGTGGAGC | GCTTGATGGT | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | | | | | | |
| msa118688.2{361_18RS21} | 1651 | ATACAATATG | CCAAGGAAAT | GATGCGTAAC | GATAATCTAG | ACTATGTGAT | 1700 |
| msa118688.2{361_A909} | ATACAATATG | CCAAGGAAAT | GATGCGTAAC | GATAATCTAG | ACTATGTGAT | | |
| msa118688.2{361_COH1} | ATACAATATG | CCAAGGAAAT | GATGCGTAAC | GATAATCTAG | ACTATGTGAT | | |
| msa118688.2{361_H36B} | ATACAATATG | CCAAGGAAAT | GATGCGTAAC | GATAATCTAG | ACTATGTGAT | | |
| msa118688.2{361_JM9130013} | ATACAATATG | CCAAGGAAAT | GATGCGTAAC | GATAATCTAG | ACTATGTGAT | | |
| msa118688.2{361_M732} | ATACAATATG | CCAAGGAAAT | GATGCGTAAC | GATAATCTAG | ACTATGTGAT | | |
| msa118688.2{GBS361_2603} | ATACAATATG | CCAAGGAAAT | GATGCGTAAC | GATAATCTAG | ACTATGTGAT | | |
| msa118688.2{361_090} | ATACAATATG | CCAAGGAAAT | GATGCGTAAC | GATAATCTAG | ACTATGTGAT | | |
| msa118688.2{361_1169NT} | ATACAATATG | CCAAGGAAAT | GATGCGTAAC | GATAATCTAG | ACTATGTGAT | | |
| msa118688.2{361_CJB110} | ATACAATATG | CCAAGGAAAT | GATGCGTAAC | GATAATCTAG | ACTATGTGAT | | |
| msa118688.2{361_M781} | ATACAATATG | CCAAGGAAAT | GATGCGTAAC | GATAATCTAG | ACTATGTGAT | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | | | | | | |
| msa118688.2{361_18RS21} | 1701 | TCTTGTCTTCT | GCTAATCAGT | GGACAGACAT | GAGTTTATG | TGGTGGCAAC | 1750 |
| msa118688.2{361_A909} | TCTTGTCTTCT | GCTAATCAGT | GGACAGACAT | GAGTTTATG | TGGTGGCAAC | | |
| msa118688.2{361_COH1} | TCTTGTCTTCT | GCTAATCAGT | GGACAGACAT | GAGTTTATG | TGGTGGCAAC | | |
| msa118688.2{361_H36B} | TCTTGTCTTCT | GCTAATCAGT | GGACAGACAT | GAGTTTATG | TGGTGGCAAC | | |
| msa118688.2{361_JM9130013} | TCTTGTCTTCT | GCTAATCAGT | GGACAGACAT | GAGTTTATG | TGGTGGCAAC | | |
| msa118688.2{361_M732} | TCTTGTCTTCT | GCTAATCAGT | GGACAGACAT | GAGTTTATG | TGGTGGCAAC | | |
| msa118688.2{GBS361_2603} | TCTTGTCTTCT | GCTAATCAGT | GGACAGACAT | GAGTTTATG | TGGTGGCAAC | | |

Table 75: Comparative Sequences relating to SAG0671

| | | | | | | | |
|----------------------------|------------|------------|-------------|-------------|-------------|-------|-------------|
| msa118688.2{361_090} | TCTTGTTCCT | GCTAATCAGT | GGACAGACAT | GAGTTTATG | TGGTGGCAAC | | |
| msa118688.2{361_1169NT} | TCTTGTTCCT | GCTAATCAGT | GGACAGACAT | GAGTTTATG | TGGTGGCAAC | | |
| msa118688.2{361_CJB110} | TCTTGTTCCT | GCTAATCAGT | GGACAGACAT | GAGTTTATG | TGGTGGCAAC | | |
| msa118688.2{361_M781} | TCTTGTTCCT | GCTAATCAGT | GGACAGACAT | GAGTTTATG | TGGTGGCAAC | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa118688.2{361_18RS21} | 1751 | AATTAAACTA | TGATAGTCAA | ATGTTTGTCTG | GTTCTGATTA | 1800 | TTGTTTCAGCA |
| msa118688.2{361_A909} | AATTAAACTA | TGATAGTCAA | ATGTTTGTCTG | GTTCTGATTA | TTGTTTCAGCA | | |
| msa118688.2{361_COH1} | AATTAAACTA | TGATAGTCAA | ATGTTTGTCTG | GTTCTGATTA | TTGTTTCAGCA | | |
| msa118688.2{361_H36B} | AATTAAACTA | TGATAGTCAA | ATGTTTGTCTG | GTTCTGATTA | TTGTTTCAGCA | | |
| msa118688.2{361_JM9130013} | AATTAAACTA | TGATAGTCAA | ATGTTTGTCTG | GTTCTGATTA | TTGTTTCAGCA | | |
| msa118688.2{361_M732} | AATTAAACTA | TGATAGTCAA | ATGTTTGTCTG | GTTCTGATTA | TTGTTTCAGCA | | |
| msa118688.2{GBS361_2603} | AATTAAACTA | TGATAGTCAA | ATGTTTGTCTG | GTTCTGATTA | TTGTTTCAGCA | | |
| msa118688.2{361_090} | AATTAAACTA | TGATAGTCAA | ATGTTTGTCTG | GTTCTGATTA | TTGTTTCAGCA | | |
| msa118688.2{361_1169NT} | AATTAAACTA | TGATAGTCAA | ATGTTTGTCTG | GTTCTGATTA | TTGTTTCAGCA | | |
| msa118688.2{361_CJB110} | AATTAAACTA | TGATAGTCAA | ATGTTTGTCTG | GTTCTGATTA | TTGTTTCAGCA | | |
| msa118688.2{361_M781} | AATTAAACTA | TGATAGTCAA | ATGTTTGTCTG | GTTCTGATTA | TTGTTTCAGCA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | ***** |
| msa118688.2{361_18RS21} | 1801 | CAAGTCCTCT | CTCGTCAAGC | ATTGGATAAT | TCTCCTATAA | 1850 | TATTAGGTAG |
| msa118688.2{361_A909} | CAAGTCCTCT | CTCGTCAAGC | ATTGGATAAT | TCTCCTATAA | TATTAGGTAG | | |
| msa118688.2{361_COH1} | CAAGTCCTCT | CTCGTCAAGC | ATTGGATAAT | TCTCCTATAA | TATTAGGTAG | | |
| msa118688.2{361_H36B} | CAAGTCCTCT | CTCGTCAAGC | ATTGGATAAT | TCTCCTATAA | TATTAGGTAG | | |
| msa118688.2{361_JM9130013} | CAAGTCCTCT | CTCGTCAAGC | ATTGGATAAT | TCTCCTATAA | TATTAGGTAG | | |
| msa118688.2{361_M732} | CAAGTCCTCT | CTCGTCAAGC | ATTGGATAAT | TCTCCTATAA | TATTAGGTAG | | |
| msa118688.2{GBS361_2603} | CAAGTCCTCT | CTCGTCAAGC | ATTGGATAAT | TCTCCTATAA | TATTAGGTAG | | |
| msa118688.2{361_090} | CAAGTCCTCT | CTCGTCAAGC | ATTGGATAAT | TCTCCTATAA | TATTAGGTAG | | |
| msa118688.2{361_1169NT} | CAAGTCCTCT | CTCGTCAAGC | ATTGGATAAT | TCTCCTATAA | TATTAGGTAG | | |
| msa118688.2{361_CJB110} | CAAGTCCTCT | CTCGTCAAGC | ATTGGATAAT | TCTCCTATAA | TATTAGGTAG | | |
| msa118688.2{361_M781} | CAAGTCCTCT | CTCGTCAAGC | ATTGGATAAT | TCTCCTATAA | TATTAGGTAG | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | ***** |
| msa118688.2{361_18RS21} | 1851 | TAAACAATTA | AAATATAGCC | ATAAAACATT | CACAGATGTG | 1900 | ATGACTATTT |
| msa118688.2{361_A909} | TAAACAATTA | AAATATAGCC | ATAAAACATT | CACAGATGTG | ATGACTATTT | | |
| msa118688.2{361_COH1} | TAAACAATTA | AAATATAGCC | ATAAAACATT | CACAGATGTG | ATGACTATTT | | |
| msa118688.2{361_H36B} | TAAACAATTA | AAATATAGCC | ATAAAACATT | CACAGATGTG | ATGACTATTT | | |
| msa118688.2{361_JM9130013} | TAAACAATTA | AAATATAGCC | ATAAAACATT | CACAGATGTG | ATGACTATTT | | |
| msa118688.2{361_M732} | TAAACAATTA | AAATATAGCC | ATAAAACATT | CACAGATGTG | ATGACTATTT | | |
| msa118688.2{GBS361_2603} | TAAACAATTA | AAATATAGCC | ATAAAACATT | CACAGATGTG | ATGACTATTT | | |
| msa118688.2{361_090} | TAAACAATTA | AAATATAGCC | ATAAAACATT | CACAGATGTG | ATGACTATTT | | |
| msa118688.2{361_1169NT} | TAAACAATTA | AAATATAGCC | ATAAAACATT | CACAGATGTG | ATGACTATTT | | |
| msa118688.2{361_CJB110} | TAAACAATTA | AAATATAGCC | ATAAAACATT | CACAGATGTG | ATGACTATTT | | |
| msa118688.2{361_M781} | TAAACAATTA | AAATATAGCC | ATAAAACATT | CACAGATGTG | ATGACTATTT | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | ***** |
| msa118688.2{361_18RS21} | 1901 | TTGATGCTGC | GCTTCAAAT | TTATTATCAG | ACTTAGGACT | 1950 | AACCATAAAA |
| msa118688.2{361_A909} | TTGATGCTGC | GCTTCAAAT | TTATTATCAG | ACTTAGGACT | AACCATAAAA | | |
| msa118688.2{361_COH1} | TTGATGCTGC | GCTTCAAAT | TTATTATCAG | ACTTAGGACT | AACCATAAAA | | |
| msa118688.2{361_H36B} | TTGATGCTGC | GCTTCAAAT | TTATTATCAG | ACTTAGGACT | AACCATAAAA | | |
| msa118688.2{361_JM9130013} | TTGATGCTGC | GCTTCAAAT | TTATTATCAG | ACTTAGGACT | AACCATAAAA | | |
| msa118688.2{361_M732} | TTGATGCTGC | GCTTCAAAT | TTATTATCAG | ACTTAGGACT | AACCATAAAA | | |
| msa118688.2{GBS361_2603} | TTGATGCTGC | GCTTCAAAT | TTATTATCAG | ACTTAGGACT | AACCATAAAA | | |
| msa118688.2{361_090} | TTGATGCTGC | GCTTCAAAT | TTATTATCAG | ACTTAGGACT | AACCATAAAA | | |
| msa118688.2{361_1169NT} | TTGATGCTGC | GCTTCAAAT | TTATTATCAG | ACTTAGGACT | AACCATAAAA | | |
| msa118688.2{361_CJB110} | TTGATGCTGC | GCTTCAAAT | TTATTATCAG | ACTTAGGACT | AACCATAAAA | | |
| msa118688.2{361_M781} | TTGATGCTGC | GCTTCAAAT | TTATTATCAG | ACTTAGGACT | AACCATAAAA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | ***** |
| msa118688.2{361_18RS21} | 1951 | GATATCAAAG | GTTTCGTTTG | GAATGAGCGG | AAGAAGGCAG | 2000 | TTAGTTTCAGA |
| msa118688.2{361_A909} | GATATCAAAG | GTTTCGTTTG | GAATGAGCGG | AAGAAGGCAG | TTAGTTTCAGA | | |
| msa118688.2{361_COH1} | GATATCAAAG | GTTTCGTTTG | GAATGAGCGG | AAGAAGGCAG | TTAGTTTCAGA | | |
| msa118688.2{361_H36B} | GATATCAAAG | GTTTCGTTTG | GAATGAGCGG | AAGAAGGCAG | TTAGTTTCAGA | | |
| msa118688.2{361_JM9130013} | GATATCAAAG | GTTTCGTTTG | GAATGAGCGG | AAGAAGGCAG | TTAGTTTCAGA | | |
| msa118688.2{361_M732} | GATATCAAAG | GTTTCGTTTG | GAATGAGCGG | AAGAAGGCAG | TTAGTTTCAGA | | |
| msa118688.2{GBS361_2603} | GATATCAAAG | GTTTCGTTTG | GAATGAGCGG | AAGAAGGCAG | TTAGTTTCAGA | | |
| msa118688.2{361_090} | GATATCAAAG | GTTTCGTTTG | GAATGAGCGG | AAGAAGGCAG | TTAGTTTCAGA | | |
| msa118688.2{361_1169NT} | GATATCAAAG | GTTTCGTTTG | GAATGAGCGG | AAGAAGGCAG | TTAGTTTCAGA | | |
| msa118688.2{361_CJB110} | GATATCAAAG | GTTTCGTTTG | GAATGAGCGG | AAGAAGGCAG | TTAGTTTCAGA | | |
| msa118688.2{361_M781} | GATATCAAAG | GTTTCGTTTG | GAATGAGCGG | AAGAAGGCAG | TTAGTTTCAGA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | ***** |
| msa118688.2{361_18RS21} | 2001 | TTATGATTTT | TTAGCGAAGT | TGTCTGAGTA | TTATAATATG | 2050 | CCAAACCTTG |
| msa118688.2{361_A909} | TTATGATTTT | TTAGCGAAGT | TGTCTGAGTA | TTATAATATG | CCAAACCTTG | | |
| msa118688.2{361_COH1} | TTATGATTTT | TTAGCGAAGT | TGTCTGAGTA | TTATAATATG | CCAAACCTTG | | |
| msa118688.2{361_H36B} | TTATGATTTT | TTAGCGAAGT | TGTCTGAGTA | TTATAATATG | CCAAACCTTG | | |
| msa118688.2{361_JM9130013} | TTATGATTTT | TTAGCGAAGT | TGTCTGAGTA | TTATAATATG | CCAAACCTTG | | |
| msa118688.2{361_M732} | TTATGATTTT | TTAGCGAAGT | TGTCTGAGTA | TTATAATATG | CCAAACCTTG | | |

Table 75: Comparative Sequences relating to SAG0671

| | | | | | |
|----------------------------|------------|------------|-------------|------------|------------|
| msa118688.2{GBS361_2603} | TTATGATTTC | TTAGCGAACT | TGCTCTGAGTA | TTATAATATG | CCAAACCTTG |
| msa118688.2{361_090} | TTATGATTTC | TTAGCGAACT | TGCTCTGAGTA | TTATAATATG | CCAAACCTTG |
| msa118688.2{361_1169NT} | TTATGATTTC | TTAGCGAACT | TGCTCTGAGTA | TTATAATATG | CCAAACCTTG |
| msa118688.2{361_CJB110} | TTATGATTTC | TTAGCGAACT | TGCTCTGAGTA | TTATAATATG | CCAAACCTTG |
| msa118688.2{361_M781} | TTATGATTTC | TTAGCGAACT | TGCTCTGAGTA | TTATAATATG | CCAAACCTTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 2051 | | | | | |
| msa118688.2{361_18RS21} | CTTCTGGTCA | GTTTGGATT | TCATCTAATG | GTGCTGGTGA | AGAACTGGAC |
| msa118688.2{361_A909} | CTTCTGGTCA | GTTTGGATT | TCATCTAATG | GTGCTGGTGA | AGAACTGGAC |
| msa118688.2{361_COH1} | CTTCTGGTCA | GTTTGGATT | TCATCTAATG | GTGCTGGTGA | AGAACTGGAC |
| msa118688.2{361_H36B} | CTTCTGGTCA | GTTTGGATT | TCATCTAATG | GTGCTGGTGA | AGAACTGGAC |
| msa118688.2{361_JM9130013} | CTTCTGGTCA | GTTTGGATT | TCATCTAATG | GTGCTGGTGA | AGAACTGGAC |
| msa118688.2{361_M732} | CTTCTGGTCA | GTTTGGATT | TCATCTAATG | GTGCTGGTGA | AGAACTGGAC |
| msa118688.2{GBS361_2603} | CTTCTGGTCA | GTTTGGATT | TCATCTAATG | GTGCTGGTGA | AGAACTGGAC |
| msa118688.2{361_090} | CTTCTGGTCA | GTTTGGATT | TCATCTAATG | GTGCTGGTGA | AGAACTGGAC |
| msa118688.2{361_1169NT} | CTTCTGGTCA | GTTTGGATT | TCATCTAATG | GTGCTGGTGA | AGAACTGGAC |
| msa118688.2{361_CJB110} | CTTCTGGTCA | GTTTGGATT | TCATCTAATG | GTGCTGGTGA | AGAACTGGAC |
| msa118688.2{361_M781} | CTTCTGGTCA | GTTTGGATT | TCATCTAATG | GTGCTGGTGA | AGAACTGGAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 2101 | | | | | |
| msa118688.2{361_18RS21} | TATACTGTGA | ATGAAAGTAT | AGAAAAGGGC | TATTATTTAG | TCCTATCTTA |
| msa118688.2{361_A909} | TATACTGTGA | ATGAAAGTAT | AGAAAAGGGC | TATTATTTAG | TCCTATCTTA |
| msa118688.2{361_COH1} | TATACTGTGA | ATGAAAGTAT | AGAAAAGGGC | TATTATTTAG | TCCTATCTTA |
| msa118688.2{361_H36B} | TATACTGTGA | ATGAAAGTAT | AGAAAAGGGC | TATTATTTAG | TCCTATCTTA |
| msa118688.2{361_JM9130013} | TATACTGTGA | ATGAAAGTAT | AGAAAAGGGC | TATTATTTAG | TCCTATCTTA |
| msa118688.2{361_M732} | TATACTGTGA | ATGAAAGTAT | AGAAAAGGGC | TATTATTTAG | TCCTATCTTA |
| msa118688.2{GBS361_2603} | TATACTGTGA | ATGAAAGTAT | AGAAAAGGGC | TATTATTTAG | TCCTATCTTA |
| msa118688.2{361_090} | TATACTGTGA | ATGAAAGTAT | AGAAAAGGGC | TATTATTTAG | TCCTATCTTA |
| msa118688.2{361_1169NT} | TATACTGTGA | ATGAAAGTAT | AGAAAAGGGC | TATTATTTAG | TCCTATCTTA |
| msa118688.2{361_CJB110} | TATACTGTGA | ATGAAAGTAT | AGAAAAGGGC | TATTATTTAG | TCCTATCTTA |
| msa118688.2{361_M781} | TATACTGTGA | ATGAAAGTAT | AGAAAAGGGC | TATTATTTAG | TCCTATCTTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 2151 | | | | | |
| msa118688.2{361_18RS21} | TTCGATCTTC | GGTGGTATCT | CTTTTGCTAT | TATTGAAAAA | AGG |
| msa118688.2{361_A909} | TTCGATCTTC | GGTGGTATCT | CTTTTGCTAT | TATTGAAAAA | AGG |
| msa118688.2{361_COH1} | TTCGATCTTC | GGTGGTATCT | CTTTTGCTAT | TATTGAAAAA | AGG |
| msa118688.2{361_H36B} | TTCGATCTTC | GGTGGTATCT | CTTTTGCTAT | TATTGAAAAA | AGG |
| msa118688.2{361_JM9130013} | TTCGATCTTC | GGTGGTATCT | CTTTTGCTAT | TATTGAAAAA | AGG |
| msa118688.2{361_M732} | TTCGATCTTC | GGTGGTATCT | CTTTTGCTAT | TATTGAAAAA | AGG |
| msa118688.2{GBS361_2603} | TTCGATCTTC | GGTGGTATCT | CTTTTGCTAT | TATTGAAAAA | AGG |
| msa118688.2{361_090} | TTCGATCTTC | GGTGGTATCT | CTTTTGCTAT | TATTGAAAAA | AGG |
| msa118688.2{361_1169NT} | TTCGATCTTC | GGTGGTATCT | CTTTTGCTAT | TATTGAAAAA | AGG |
| msa118688.2{361_CJB110} | TTCGATCTTC | GGTGGTATCT | CTTTTGCTAT | TATTGAAAAA | AGG |
| msa118688.2{361_M781} | TTCGATCTTC | GGTGGTATCT | CTTTTGCTAT | TATTGAAAAA | AGG |
| Consensus | ***** | ***** | ***** | ***** | *** |

SEQ ID NO. 7512

STRAIN 2603 frame: 1

MSVYVSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQ
 YKDETRNFKAFAFEALASSGVNLKAYHNIACVCLGTSLGKKSAGQNALYQFEEGERQV
 DASLLEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDQDCLDAICGG
 CDELSDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYKGIIGGL
 ITSDGYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKF
 FPTTLISSTKGQTGHTLGAAGIIELINCLAAIEEQTPATKNEIGIEGFENFVYHOKR
 EYPRNALNFSFAFGGNNSGVLLSSLDSPLETLARENLMKMAILSSVASISKNESLSITY
 EKVASNDFEALRFKGRPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTS
 KVGIVFTTSLGPPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSV
 ISTNSGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWQQLNYSQMFVGS DYCSA
 QVLSRQALDNPILGSKQLKYSKHTFTDVTMIFDAALQNLSDGLGTIKDIKGFVWNER
 KKAUSSDYDFLANLSEYNNMPLNASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIF
 GGISFAIIEKR

SEQ ID NO. 7513

STRAIN 090 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
 TRNFKAFAFEALASSGVNLKAYHNIACVCLGTSLGKKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDQDCLDAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFPTT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTPATKNEIGIEGFENFVYHOKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETLARENLMKMAILSSVASISKNESLSITYEYKVA
 SNFNDFEALRFKGRPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVG
 VFTTSLGPPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWQQLNYSQMFVGS DYCSAQVLS
 RQALDNPILGSKQLKYSKHTFTDVTMIFDAALQNLSDGLGTIKDIKGFVWNERKKA
 USSDYDFLANLSEYNNMPLNASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIFGGIS
 FAIIEKR

SEQ ID NO. 7514

STRAIN A909 frame: 3

Table 75: Comparative Sequences relating to SAG0671

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLYKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASASNNAVILGTQLLDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGI IGGITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSI I FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLSDLG LTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYIFGGIS
 FAIEKR

SEQ ID NO. 7515

STRAIN H36B frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLYKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASASNNAVILGTQLLDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGI IGGITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSI I FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLSDLG LTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYIFGGIS
 FAIEKR

SEQ ID NO. 7516

STRAIN 18RS21 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLYKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASASNNAVILGTQLLDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGI IGGITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSI I FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLSDLG LTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYIFGGIS
 FAIEKR

SEQ ID NO. 7517

STRAIN M732 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLYKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASASNNAVILGTQLLDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGI IGGITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSI I FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLSDLG LTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYIFGGIS
 FAIEKR

SEQ ID NO. 7518

STRAIN COH1 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLYKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASASNNAVILGTQLLDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYKGI IGGITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSI I FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLSDLG LTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYIFGGIS
 FAIEKR

SEQ ID NO. 7519

STRAIN M781 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLYKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL

Table 75: Comparative Sequences relating to SAG0671

LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHOKREYPI
RNALNFSFAFGGNNSSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPPIILGSKQLKYSKHTFTDVMITFDAALQNLLSDGLTIKDIKGFVWNERKKA
SSDYDFLANLSEYNNMNPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7520

STRAIN CJB110 frame: 3

VSGIGIISLGNKYNSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHOKREYPI
RNALNFSFAFGGNNSSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPPIILGSKQLKYSKHTFTDVMITFDAALQNLLSDGLTIKDIKGFVWNERKKA
SSDYDFLANLSEYNNMNPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7521

STRAIN 1169NT frame: 3

VSGIGIISLGNKYNSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHOKREYPI
RNALNFSFAFGGNNSSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPPIILGSKQLKYSKHTFTDVMITFDAALQNLLSDGLTIKDIKGFVWNERKKA
SSDYDFLANLSEYNNMNPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7522

STRAIN JM9130013 frame: 3

VSGIGIISLGNKYNSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHOKREYPI
RNALNFSFAFGGNNSSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPPIILGSKQLKYSKHTFTDVMITFDAALQNLLSDGLTIKDIKGFVWNERKKA
SSDYDFLANLSEYNNMNPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIIEKR

PRETTY of: /biotmp/msa118713.2{*} April 9, 2003 02:54 ..

| | | | |
|----------------------------|------------|-----------------------|-----------------------|
| | 1 | | 50 |
| msa118713.2{361_090} | ----VSGIGI | ISSLGKNYSE HKQHLFDLKE | GISKHLYKNH DSILESITGS |
| msa118713.2{361_1169NT} | ----VSGIGI | ISSLGKNYSE HKQHLFDLKE | GISKHLYKNH DSILESITGS |
| msa118713.2{361_CJB110} | ----VSGIGI | ISSLGKNYSE HKQHLFDLKE | GISKHLYKNH DSILESITGS |
| msa118713.2{361_M781} | ----VSGIGI | ISSLGKNYSE HKQHLFDLKE | GISKHLYKNH DSILESITGS |
| msa118713.2{361_18RS21} | ----VSGIGI | ISSLGKNYSE HKQHLFDLKE | GISKHLYKNH DSILESITGS |
| msa118713.2{361_A909} | ----VSGIGI | ISSLGKNYSE HKQHLFDLKE | GISKHLYKNH DSILESITGS |
| msa118713.2{361_COH1} | ----VSGIGI | ISSLGKNYSE HKQHLFDLKE | GISKHLYKNH DSILESITGS |
| msa118713.2{361_H36B} | ----VSGIGI | ISSLGKNYSE HKQHLFDLKE | GISKHLYKNH DSILESITGS |
| msa118713.2{361_JM9130013} | ----VSGIGI | ISSLGKNYSE HKQHLFDLKE | GISKHLYKNH DSILESITGS |
| msa118713.2{361_M732} | ----VSGIGI | ISSLGKNYSE HKQHLFDLKE | GISKHLYKNH DSILESITGS |
| msa118713.2{GBS361_2603} | msvYVSGIGI | ISSLGKNYSE HKQHLFDLKE | GISKHLYKNH DSILESITGS |
| Consensus | ***** | ***** | ***** |
| | 51 | | 100 |
| msa118713.2{361_090} | ITSDPEVPEQ | YKDETRNFKF AFTAFEEALA | SSGVNLKAYH NIAVCLGTSL |
| msa118713.2{361_1169NT} | ITSDPEVPEQ | YKDETRNFKF AFTAFEEALA | SSGVNLKAYH NIAVCLGTSL |
| msa118713.2{361_CJB110} | ITSDPEVPEQ | YKDETRNFKF AFTAFEEALA | SSGVNLKAYH NIAVCLGTSL |
| msa118713.2{361_M781} | ITSDPEVPEQ | YKDETRNFKF AFTAFEEALA | SSGVNLKAYH NIAVCLGTSL |
| msa118713.2{361_18RS21} | ITSDPEVPEQ | YKDETRNFKF AFTAFEEALA | SSGVNLKAYH NIAVCLGTSL |

Table 75: Comparative Sequences relating to SAG0671

| | | | | | |
|----------------------------|------------|------------|------------|------------|-------------|
| msa118713.2{361_A909} | ITSDPEVPEQ | YKDETRNFKF | AFTAFEEALA | SSGVNLKAYH | NIACVCLGTSL |
| msa118713.2{361_COH1} | ITSDPEVPEQ | YKDETRNFKF | AFTAFEEALA | SSGVNLKAYH | NIACVCLGTSL |
| msa118713.2{361_H36B} | ITSDPEVPEQ | YKDETRNFKF | AFTAFEEALA | SSGVNLKAYH | NIACVCLGTSL |
| msa118713.2{361_JM9130013} | ITSDPEVPEQ | YKDETRNFKF | AFTAFEEALA | SSGVNLKAYH | NIACVCLGTSL |
| msa118713.2{361_M732} | ITSDPEVPEQ | YKDETRNFKF | AFTAFEEALA | SSGVNLKAYH | NIACVCLGTSL |
| msa118713.2{GBS361_2603} | ITSDPEVPEQ | YKDETRNFKF | AFTAFEEALA | SSGVNLKAYH | NIACVCLGTSL |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa118713.2{361_090} | GGKSAGQNAL | YQFEEGERQV | DASLLEKASV | YHIADELMAY | HDIVGASYVI |
| msa118713.2{361_1169NT} | GGKSAGQNAL | YQFEEGERQV | DASLLEKASV | YHIADELMAY | HDIVGASYVI |
| msa118713.2{361_CJB110} | GGKSAGQNAL | YQFEEGERQV | DASLLEKASV | YHIADELMAY | HDIVGASYVI |
| msa118713.2{361_M781} | GGKSAGQNAL | YQFEEGERQV | DASLLEKASV | YHIADELMAY | HDIVGASYVI |
| msa118713.2{361_18RS21} | GGKSAGQNAL | YQFEEGERQV | DASLLEKASV | YHIADELMAY | HDIVGASYVI |
| msa118713.2{361_A909} | GGKSAGQNAL | YQFEEGERQV | DASLLEKASV | YHIADELMAY | HDIVGASYVI |
| msa118713.2{361_COH1} | GGKSAGQNAL | YQFEEGERQV | DASLLEKASV | YHIADELMAY | HDIVGASYVI |
| msa118713.2{361_H36B} | GGKSAGQNAL | YQFEEGERQV | DASLLEKASV | YHIADELMAY | HDIVGASYVI |
| msa118713.2{361_JM9130013} | GGKSAGQNAL | YQFEEGERQV | DASLLEKASV | YHIADELMAY | HDIVGASYVI |
| msa118713.2{361_M732} | GGKSAGQNAL | YQFEEGERQV | DASLLEKASV | YHIADELMAY | HDIVGASYVI |
| msa118713.2{GBS361_2603} | GGKSAGQNAL | YQFEEGERQV | DASLLEKASV | YHIADELMAY | HDIVGASYVI |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa118713.2{361_090} | STACSASNNA | VILGTQLLQD | GDCDLAICGG | CDELSDISLA | GFTSLGAINT |
| msa118713.2{361_1169NT} | STACSASNNA | VILGTQLLQD | GDCDLAICGG | CDELSDISLA | GFTSLGAINT |
| msa118713.2{361_CJB110} | STACSASNNA | VILGTQLLQD | GDCDLAICGG | CDELSDISLA | GFTSLGAINT |
| msa118713.2{361_M781} | STACSASNNA | VILGTQLLQD | GDCDLAICGG | CDELSDISLA | GFTSLGAINT |
| msa118713.2{361_18RS21} | STACSASNNA | VILGTQLLQD | GDCDLAICGG | CDELSDISLA | GFTSLGAINT |
| msa118713.2{361_A909} | STACSASNNA | VILGTQLLQD | GDCDLAICGG | CDELSDISLA | GFTSLGAINT |
| msa118713.2{361_COH1} | STACSASNNA | VILGTQLLQD | GDCDLAICGG | CDELSDISLA | GFTSLGAINT |
| msa118713.2{361_H36B} | STACSASNNA | VILGTQLLQD | GDCDLAICGG | CDELSDISLA | GFTSLGAINT |
| msa118713.2{361_JM9130013} | STACSASNNA | VILGTQLLQD | GDCDLAICGG | CDELSDISLA | GFTSLGAINT |
| msa118713.2{361_M732} | STACSASNNA | VILGTQLLQD | GDCDLAICGG | CDELSDISLA | GFTSLGAINT |
| msa118713.2{GBS361_2603} | STACSASNNA | VILGTQLLQD | GDCDLAICGG | CDELSDISLA | GFTSLGAINT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa118713.2{361_090} | EMACQPYSSG | KGINLGEAG | FVVLVKDQSL | AKYGKIIGGL | ITSDGYHITA |
| msa118713.2{361_1169NT} | EMACQPYSSG | KGINLGEAG | FVVLVKDQSL | AKYGKIIGGL | ITSDGYHITA |
| msa118713.2{361_CJB110} | EMACQPYSSG | KGINLGEAG | FVVLVKDQSL | AKYGKIIGGL | ITSDGYHITA |
| msa118713.2{361_M781} | EMACQPYSSG | KGINLGEAG | FVVLVKDQSL | AKYGKIIGGL | ITSDGYHITA |
| msa118713.2{361_18RS21} | EMACQPYSSG | KGINLGEAG | FVVLVKDQSL | AKYGKIIGGL | ITSDGYHITA |
| msa118713.2{361_A909} | EMACQPYSSG | KGINLGEAG | FVVLVKDQSL | AKYGKIIGGL | ITSDGYHITA |
| msa118713.2{361_COH1} | EMACQPYSSG | KGINLGEAG | FVVLVKDQSL | AKYGKIIGGL | ITSDGYHITA |
| msa118713.2{361_H36B} | EMACQPYSSG | KGINLGEAG | FVVLVKDQSL | AKYGKIIGGL | ITSDGYHITA |
| msa118713.2{361_JM9130013} | EMACQPYSSG | KGINLGEAG | FVVLVKDQSL | AKYGKIIGGL | ITSDGYHITA |
| msa118713.2{361_M732} | EMACQPYSSG | KGINLGEAG | FVVLVKDQSL | AKYGKIIGGL | ITSDGYHITA |
| msa118713.2{GBS361_2603} | EMACQPYSSG | KGINLGEAG | FVVLVKDQSL | AKYGKIIGGL | ITSDGYHITA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa118713.2{361_090} | PKPTGEGAAQ | IAKQLVTQAG | IDYSEIDYIN | GHGTGTQAND | KMEKNMYGKF |
| msa118713.2{361_1169NT} | PKPTGEGAAQ | IAKQLVTQAG | IDYSEIDYIN | GHGTGTQAND | KMEKNMYGKF |
| msa118713.2{361_CJB110} | PKPTGEGAAQ | IAKQLVTQAG | IDYSEIDYIN | GHGTGTQAND | KMEKNMYGKF |
| msa118713.2{361_M781} | PKPTGEGAAQ | IAKQLVTQAG | IDYSEIDYIN | GHGTGTQAND | KMEKNMYGKF |
| msa118713.2{361_18RS21} | PKPTGEGAAQ | IAKQLVTQAG | IDYSEIDYIN | GHGTGTQAND | KMEKNMYGKF |
| msa118713.2{361_A909} | PKPTGEGAAQ | IAKQLVTQAG | IDYSEIDYIN | GHGTGTQAND | KMEKNMYGKF |
| msa118713.2{361_COH1} | PKPTGEGAAQ | IAKQLVTQAG | IDYSEIDYIN | GHGTGTQAND | KMEKNMYGKF |
| msa118713.2{361_H36B} | PKPTGEGAAQ | IAKQLVTQAG | IDYSEIDYIN | GHGTGTQAND | KMEKNMYGKF |
| msa118713.2{361_JM9130013} | PKPTGEGAAQ | IAKQLVTQAG | IDYSEIDYIN | GHGTGTQAND | KMEKNMYGKF |
| msa118713.2{361_M732} | PKPTGEGAAQ | IAKQLVTQAG | IDYSEIDYIN | GHGTGTQAND | KMEKNMYGKF |
| msa118713.2{GBS361_2603} | PKPTGEGAAQ | IAKQLVTQAG | IDYSEIDYIN | GHGTGTQAND | KMEKNMYGKF |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa118713.2{361_090} | FPTTTLISST | KGQTGHTLGA | AGIIEINCL | AAIEBQTVPA | TKNEIGIEGF |
| msa118713.2{361_1169NT} | FPTTTLISST | KGQTGHTLGA | AGIIEINCL | AAIEBQTVPA | TKNEIGIEGF |
| msa118713.2{361_CJB110} | FPTTTLISST | KGQTGHTLGA | AGIIEINCL | AAIEBQTVPA | TKNEIGIEGF |
| msa118713.2{361_M781} | FPTTTLISST | KGQTGHTLGA | AGIIEINCL | AAIEBQTVPA | TKNEIGIEGF |
| msa118713.2{361_18RS21} | FPTTTLISST | KGQTGHTLGA | AGIIEINCL | AAIEBQTVPA | TKNEIGIEGF |
| msa118713.2{361_A909} | FPTTTLISST | KGQTGHTLGA | AGIIEINCL | AAIEBQTVPA | TKNEIGIEGF |
| msa118713.2{361_COH1} | FPTTTLISST | KGQTGHTLGA | AGIIEINCL | AAIEBQTVPA | TKNEIGIEGF |
| msa118713.2{361_H36B} | FPTTTLISST | KGQTGHTLGA | AGIIEINCL | AAIEBQTVPA | TKNEIGIEGF |
| msa118713.2{361_JM9130013} | FPTTTLISST | KGQTGHTLGA | AGIIEINCL | AAIEBQTVPA | TKNEIGIEGF |
| msa118713.2{361_M732} | FPTTTLISST | KGQTGHTLGA | AGIIEINCL | AAIEBQTVPA | TKNEIGIEGF |
| msa118713.2{GBS361_2603} | FPTTTLISST | KGQTGHTLGA | AGIIEINCL | AAIEBQTVPA | TKNEIGIEGF |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa118713.2{361_090} | PENFVYHQKR | EYPIRNALNF | SFAFGGNSG | ILLSSLDSP | ETLPARENLK |
| msa118713.2{361_1169NT} | PENFVYHQKR | EYPIRNALNF | SFAFGGNSG | ILLSSLDSP | ETLPARENLK |
| msa118713.2{361_CJB110} | PENFVYHQKR | EYPIRNALNF | SFAFGGNSG | ILLSSLDSP | ETLPARENLK |
| msa118713.2{361_M781} | PENFVYHQKR | EYPIRNALNF | SFAFGGNSG | ILLSSLDSP | ETLPARENLK |

Table 75: Comparative Sequences relating to SAG0671

| | | | | | | | |
|----------------------------|------------|-------------|-------------|-------------|-------------|-------------|-----|
| msa118713.2{361_18RS21} | PENFVYHQKR | EYPIRNALNF | SFAFGGNNSG | VLLSSLDSPL | ETLPARENLK | | |
| msa118713.2{361_A909} | PENFVYHQKR | EYPIRNALNF | SFAFGGNNSG | VLLSSLDSPL | ETLPARENLK | | |
| msa118713.2{361_COH1} | PENFVYHQKR | EYPIRNALNF | SFAFGGNNSG | VLLSSLDSPL | ETLPARENLK | | |
| msa118713.2{361_H36B} | PENFVYHQKR | EYPIRNALNF | SFAFGGNNSG | VLLSSLDSPL | ETLPARENLK | | |
| msa118713.2{361_JM9130013} | PENFVYHQKR | EYPIRNALNF | SFAFGGNNSG | VLLSSLDSPL | ETLPARENLK | | |
| msa118713.2{361_M732} | PENFVYHQKR | EYPIRNALNF | SFAFGGNNSG | VLLSSLDSPL | ETLPARENLK | | |
| msa118713.2{GBS361_2603} | PENFVYHQKR | EYPIRNALNF | SFAFGGNNSG | VLLSSLDSPL | ETLPARENLK | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | | | | | | |
| msa118713.2{361_090} | 401 | MAILSSVASI | SKNESLSITY | EKVASNFNDF | EALRFKGARP | PKTVNPAQFR | 450 |
| msa118713.2{361_1169NT} | MAILSSVASI | SKNESLSITY | EKVASNFNDF | EALRFKGARP | PKTVNPAQFR | | |
| msa118713.2{361_CJB110} | MAILSSVASI | SKNESLSITY | EKVASNFNDF | EALRFKGARP | PKTVNPAQFR | | |
| msa118713.2{361_M781} | MAILSSVASI | SKNESLSITY | EKVASNFNDF | EALRFKGARP | PKTVNPAQFR | | |
| msa118713.2{361_18RS21} | MAILSSVASI | SKNESLSITY | EKVASNFNDF | EALRFKGARP | PKTVNPAQFR | | |
| msa118713.2{361_A909} | MAILSSVASI | SKNESLSITY | EKVASNFNDF | EALRFKGARP | PKTVNPAQFR | | |
| msa118713.2{361_COH1} | MAILSSVASI | SKNESLSITY | EKVASNFNDF | EALRFKGARP | PKTVNPAQFR | | |
| msa118713.2{361_H36B} | MAILSSVASI | SKNESLSITY | EKVASNFNDF | EALRFKGARP | PKTVNPAQFR | | |
| msa118713.2{361_JM9130013} | MAILSSVASI | SKNESLSITY | EKVASNFNDF | EALRFKGARP | PKTVNPAQFR | | |
| msa118713.2{361_M732} | MAILSSVASI | SKNESLSITY | EKVASNFNDF | EALRFKGARP | PKTVNPAQFR | | |
| msa118713.2{GBS361_2603} | MAILSSVASI | SKNESLSITY | EKVASNFNDF | EALRFKGARP | PKTVNPAQFR | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | | | | | | |
| msa118713.2{361_090} | 451 | KMDDFSKMVA | VTTAQALIES | NINLKKQDTS | KVGIVFTTSL | GPVEVVEGIE | 500 |
| msa118713.2{361_1169NT} | KMDDFSKMVA | VTTAQALIES | NINLKKQDTS | KVGIVFTTSL | GPVEVVEGIE | | |
| msa118713.2{361_CJB110} | KMDDFSKMVA | VTTAQALIES | NINLKKQDTS | KVGIVFTTSL | GPVEVVEGIE | | |
| msa118713.2{361_M781} | KMDDFSKMVA | VTTAQALIES | NINLKKQDTS | KVGIVFTTSL | GPVEVVEGIE | | |
| msa118713.2{361_18RS21} | KMDDFSKMVA | VTTAQALIES | NINLKKQDTS | KVGIVFTTSL | GPVEVVEGIE | | |
| msa118713.2{361_A909} | KMDDFSKMVA | VTTAQALIES | NINLKKQDTS | KVGIVFTTSL | GPVEVVEGIE | | |
| msa118713.2{361_COH1} | KMDDFSKMVA | VTTAQALIES | NINLKKQDTS | KVGIVFTTSL | GPVEVVEGIE | | |
| msa118713.2{361_H36B} | KMDDFSKMVA | VTTAQALIES | NINLKKQDTS | KVGIVFTTSL | GPVEVVEGIE | | |
| msa118713.2{361_JM9130013} | KMDDFSKMVA | VTTAQALIES | NINLKKQDTS | KVGIVFTTSL | GPVEVVEGIE | | |
| msa118713.2{361_M732} | KMDDFSKMVA | VTTAQALIES | NINLKKQDTS | KVGIVFTTSL | GPVEVVEGIE | | |
| msa118713.2{GBS361_2603} | KMDDFSKMVA | VTTAQALIES | NINLKKQDTS | KVGIVFTTSL | GPVEVVEGIE | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | | | | | | |
| msa118713.2{361_090} | 501 | KQITTEGYAH | VSASRFPPFTV | MNAAAGMLSI | IFKITGPLSV | ISTNSGALDG | 550 |
| msa118713.2{361_1169NT} | KQITTEGYAH | VSASRFPPFTV | MNAAAGMLSI | IFKITGPLSV | ISTNSGALDG | | |
| msa118713.2{361_CJB110} | KQITTEGYAH | VSASRFPPFTV | MNAAAGMLSI | IFKITGPLSV | ISTNSGALDG | | |
| msa118713.2{361_M781} | KQITTEGYAH | VSASRFPPFTV | MNAAAGMLSI | IFKITGPLSV | ISTNSGALDG | | |
| msa118713.2{361_18RS21} | KQITTEGYAH | VSASRFPPFTV | MNAAAGMLSI | IFKITGPLSV | ISTNSGALDG | | |
| msa118713.2{361_A909} | KQITTEGYAH | VSASRFPPFTV | MNAAAGMLSI | IFKITGPLSV | ISTNSGALDG | | |
| msa118713.2{361_COH1} | KQITTEGYAH | VSASRFPPFTV | MNAAAGMLSI | IFKITGPLSV | ISTNSGALDG | | |
| msa118713.2{361_H36B} | KQITTEGYAH | VSASRFPPFTV | MNAAAGMLSI | IFKITGPLSV | ISTNSGALDG | | |
| msa118713.2{361_JM9130013} | KQITTEGYAH | VSASRFPPFTV | MNAAAGMLSI | IFKITGPLSV | ISTNSGALDG | | |
| msa118713.2{361_M732} | KQITTEGYAH | VSASRFPPFTV | MNAAAGMLSI | IFKITGPLSV | ISTNSGALDG | | |
| msa118713.2{GBS361_2603} | KQITTEGYAH | VSASRFPPFTV | MNAAAGMLSI | IFKITGPLSV | ISTNSGALDG | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | | | | | | |
| msa118713.2{361_090} | 551 | IYAKEMMRN | DNLDYVILVS | ANQWTDMSFM | WWQQLNYDSQ | MFVGS DYCSA | 600 |
| msa118713.2{361_1169NT} | IYAKEMMRN | DNLDYVILVS | ANQWTDMSFM | WWQQLNYDSQ | MFVGS DYCSA | | |
| msa118713.2{361_CJB110} | IYAKEMMRN | DNLDYVILVS | ANQWTDMSFM | WWQQLNYDSQ | MFVGS DYCSA | | |
| msa118713.2{361_M781} | IYAKEMMRN | DNLDYVILVS | ANQWTDMSFM | WWQQLNYDSQ | MFVGS DYCSA | | |
| msa118713.2{361_18RS21} | IYAKEMMRN | DNLDYVILVS | ANQWTDMSFM | WWQQLNYDSQ | MFVGS DYCSA | | |
| msa118713.2{361_A909} | IYAKEMMRN | DNLDYVILVS | ANQWTDMSFM | WWQQLNYDSQ | MFVGS DYCSA | | |
| msa118713.2{361_COH1} | IYAKEMMRN | DNLDYVILVS | ANQWTDMSFM | WWQQLNYDSQ | MFVGS DYCSA | | |
| msa118713.2{361_H36B} | IYAKEMMRN | DNLDYVILVS | ANQWTDMSFM | WWQQLNYDSQ | MFVGS DYCSA | | |
| msa118713.2{361_JM9130013} | IYAKEMMRN | DNLDYVILVS | ANQWTDMSFM | WWQQLNYDSQ | MFVGS DYCSA | | |
| msa118713.2{361_M732} | IYAKEMMRN | DNLDYVILVS | ANQWTDMSFM | WWQQLNYDSQ | MFVGS DYCSA | | |
| msa118713.2{GBS361_2603} | IYAKEMMRN | DNLDYVILVS | ANQWTDMSFM | WWQQLNYDSQ | MFVGS DYCSA | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | | | | | | |
| msa118713.2{361_090} | 601 | QVLSRQALDN | SPIILGSKQL | KYSHKTFITDV | MTIFDAALQN | LLSDLGLTIK | 650 |
| msa118713.2{361_1169NT} | QVLSRQALDN | SPIILGSKQL | KYSHKTFITDV | MTIFDAALQN | LLSDLGLTIK | | |
| msa118713.2{361_CJB110} | QVLSRQALDN | SPIILGSKQL | KYSHKTFITDV | MTIFDAALQN | LLSDLGLTIK | | |
| msa118713.2{361_M781} | QVLSRQALDN | SPIILGSKQL | KYSHKTFITDV | MTIFDAALQN | LLSDLGLTIK | | |
| msa118713.2{361_18RS21} | QVLSRQALDN | SPIILGSKQL | KYSHKTFITDV | MTIFDAALQN | LLSDLGLTIK | | |
| msa118713.2{361_A909} | QVLSRQALDN | SPIILGSKQL | KYSHKTFITDV | MTIFDAALQN | LLSDLGLTIK | | |
| msa118713.2{361_COH1} | QVLSRQALDN | SPIILGSKQL | KYSHKTFITDV | MTIFDAALQN | LLSDLGLTIK | | |
| msa118713.2{361_H36B} | QVLSRQALDN | SPIILGSKQL | KYSHKTFITDV | MTIFDAALQN | LLSDLGLTIK | | |
| msa118713.2{361_JM9130013} | QVLSRQALDN | SPIILGSKQL | KYSHKTFITDV | MTIFDAALQN | LLSDLGLTIK | | |
| msa118713.2{361_M732} | QVLSRQALDN | SPIILGSKQL | KYSHKTFITDV | MTIFDAALQN | LLSDLGLTIK | | |
| msa118713.2{GBS361_2603} | QVLSRQALDN | SPIILGSKQL | KYSHKTFITDV | MTIFDAALQN | LLSDLGLTIK | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| | | | | | | | |
| msa118713.2{361_090} | 651 | DIKGFVWNER | KKAVSSDYDF | LANLSEYNYM | PNLASGQFGF | SSNGAGEELD | 700 |
| msa118713.2{361_1169NT} | DIKGFVWNER | KKAVSSDYDF | LANLSEYNYM | PNLASGQFGF | SSNGAGEELD | | |
| msa118713.2{361_CJB110} | DIKGFVWNER | KKAVSSDYDF | LANLSEYNYM | PNLASGQFGF | SSNGAGEELD | | |

Table 75: Comparative Sequences relating to SAG0671

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| msa118713.2{361_M781} | DIKGFVWNER | KKAVSSDYDF | LANLSEYNYM | PNLASGQFGF | SSNGAGEELD |
| msa118713.2{361_18RS21} | DIKGFVWNER | KKAVSSDYDF | LANLSEYNYM | PNLASGQFGF | SSNGAGEELD |
| msa118713.2{361_A909} | DIKGFVWNER | KKAVSSDYDF | LANLSEYNYM | PNLASGQFGF | SSNGAGEELD |
| msa118713.2{361_COH1} | DIKGFVWNER | KKAVSSDYDF | LANLSEYNYM | PNLASGQFGF | SSNGAGEELD |
| msa118713.2{361_H36B} | DIKGFVWNER | KKAVSSDYDF | LANLSEYNYM | PNLASGQFGF | SSNGAGEELD |
| msa118713.2{361_JM9130013} | DIKGFVWNER | KKAVSSDYDF | LANLSEYNYM | PNLASGQFGF | SSNGAGEELD |
| msa118713.2{361_M732} | DIKGFVWNER | KKAVSSDYDF | LANLSEYNYM | PNLASGQFGF | SSNGAGEELD |
| msa118713.2{GBS361_2603} | DIKGFVWNER | KKAVSSDYDF | LANLSEYNYM | PNLASGQFGF | SSNGAGEELD |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 701 | | | 731 | |
| msa118713.2{361_090} | YTVNESIEKG | YYLVLSYSIF | GGISFAIEK | R | |
| msa118713.2{361_1169NT} | YTVNESIEKG | YYLVLSYSIF | GGISFAIEK | R | |
| msa118713.2{361_CJB110} | YTVNESIEKG | YYLVLSYSIF | GGISFAIEK | R | |
| msa118713.2{361_M781} | YTVNESIEKG | YYLVLSYSIF | GGISFAIEK | R | |
| msa118713.2{361_18RS21} | YTVNESIEKG | YYLVLSYSIF | GGISFAIEK | R | |
| msa118713.2{361_A909} | YTVNESIEKG | YYLVLSYSIF | GGISFAIEK | R | |
| msa118713.2{361_COH1} | YTVNESIEKG | YYLVLSYSIF | GGISFAIEK | R | |
| msa118713.2{361_H36B} | YTVNESIEKG | YYLVLSYSIF | GGISFAIEK | R | |
| msa118713.2{361_JM9130013} | YTVNESIEKG | YYLVLSYSIF | GGISFAIEK | R | |
| msa118713.2{361_M732} | YTVNESIEKG | YYLVLSYSIF | GGISFAIEK | R | |
| msa118713.2{GBS361_2603} | YTVNESIEKG | YYLVLSYSIF | GGISFAIEK | R | |
| Consensus | ***** | ***** | ***** | * | |

Table 76: Comparative Sequences relating to SAG0260

SEQ ID NO. 7601

STRAIN 2603

ATGAAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTAA
 AATAATATTAAATTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCTCTGGA
 GCAGGGAATCTACCTTGATTAAAACTATGCTTGGCATGAAAAAGCAGATAAGGGAACA
 GCTCTTGTCTTGATACCTCAAATGCCAGATCGTAATATTTTAAATCAAATGGCTATATG
 GCTCAATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTTGGA
 AAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACTCATATTTCTAAAGTA
 GTAGATCTAGAAAAACCACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAAAAA
 CGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTAACTCTAGATGAACCT
 ACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAG
 GATGAAGACATTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAATTAACAAGT
 AAGGTTGCACTACTATTACGTGGAACATTATTGCCTTTGATACTCCATTACATTTAAAA
 AAACAATTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7602

STRAIN 090

ATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACTGTTTTAAATAAT
 ATTAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCTC
 TGGAGCAGGGAATCTACCTTGATTAAAACTATGCTTGGCATGAAAAAG
 CAGATAAGGGAACAGCTCTTGTCTTGATACTCAAATGCCAGATCGTAAT
 ATTTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCTTATACGAATC
 TTTAACTGCCTTAGAAATTTATTATTCTTTGGAAAAATGAAAGGTATTCT
 AAAAACTGAATTAAAAACAGCAGATAACTCATATTTCTAAAGTAGTAGAT
 CTAGAAAAACCACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAA
 AAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTAA
 TCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATC
 TGGCAAGAGCTAATTAATATTAAAGGATGAAGGACGTTCTATCTTTATTAC
 AACCCACGTTATGGATGAAGCAGAAATTAACAAGTAAGGTTGCACTACTAT
 TACGTGGAACATTATTGCCTTTGATACTCCATTACATTTAAAAAAACAA
 TTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7603

STRAIN A909

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATGCCTCA
 GAAACCGTTTTAAATAATATTAAATTTGGAGGTGTTTAAAGGCGAAATAAT
 TGGATTAAATAGGACCCCTCTGGAGCAGGGAATCTACCTTGATTAAAACTA
 TGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTGATACT
 CAAATGCCAGATCATAATATTTTAAATCAAATTGGCTATATGGCTCAATC
 TGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTTG
 GAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACTCAT
 ATTTCTAAAGTAGTAGATCTAGAAAAACCACTTGATAAATTTGTCTCAGG
 TTAATCAGGAGGTATGAAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
 GAAACCCACAGTTTTAATCTAGATGAACCTACCGTTGGAATTGATCCA
 TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGAAGG
 ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAATTAACAA
 GTAAGGTTGCACTACTATTACGTGGAACATTATTGCCTTTGATACTCCA
 TTACATTTAAAAAAACAAATTTAATGTGAGTACTATTGAGGAAGTTTTCTT
 AAAAGCTGAAGGAGAA

SEQ ID NO. 7604

STRAIN H36B

AAAAAAGTCATTGATTAAAAAACTACAAAAAGCATATGCC
 TCAGAAACCGTTTTAAATAATATTAAATTTGGAGGTGTTTAAAGGCGAAAT
 AATTGGATTAAATAGGACCCCTCTGGAGCAGGGAATCTACCTTGATTAAAA
 CTATGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTGAT
 ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCA
 ATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCT
 TTGAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACT
 CATATTTCTAAAGTAGTAGATCTAGAAAAACCACTTGATAAATTTGTCTC
 AGGTTACTCAGGAGGTATGAAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
 TTGAAAAACCCACAGTTTTAATCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGA
 AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAATTA
 CAAGTAAGGTTGCACTACTATTACGTGGAACATTATTGCCTTTGATACT
 CCATTACATTTAAAAAAACAAATTTAATGTGAGTACTATTGAGGAAGTTTT
 CTTAAAGCTGAAGGAGAA

SEQ ID NO. 7605

STRAIN 18RS21

GATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTTAAATAA
 TATTAAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCT
 CTGGAGCAGGGAATCTACCTTGATTAAAACTATGCTTGGCATGAAAAA
 GCAGATAAGGGAACAGCTCTTGTCTTGATACTCAAATGCCAGATCGTAA
 TATTTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCTTATACGAGT
 CTTTAACTGGCTTAGAAAAATTTATTATTCTTTGAAAAATGAAAGGTATT
 CAAAAACCTGAATTAAAAACAGCAGATAACTCATATTTCTAAAGTAGTAGA
 TCTAGAAAAACCACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGA
 AAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTAA
 ATCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAAT
 CTGGCAAGAGCTAATTAATATTAAAGGATGAAGGACATTTCTATCTTTATTA
 CAACCCACGTTATGGATGAAGCAGAAATTAACAAGTAAGGTTGCACTACTA

Table 76: Comparative Sequences relating to SAG0260

TTACGTGGAACATTATTGCCCTTGATACTCCATTACATTAAAAAACA
ATTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7606

STRAIN M732

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATACGCCCTCA
GAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAAT
TGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAAAACTA
TGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACT
CAAATGCCAGATCGTAATTTTAAATCAAATGGCTATATGGCTCAATC
TGATGCCCTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTG
GAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACTCAT
ATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTCCTCAGG
TTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
GAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCA
TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGAAGG
ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAAACA
GTAAGGTGCACTACTATTACGTGGAACATTATTGCCCTTGATACTCCA
TTACATTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTCTT
AAAAGCTGAAGGAGAA

SEQ ID NO. 7607

STRAIN COH1

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATACGCCCTCAGAA
ACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAATGG
ATTAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAAAACTATGC
TTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACTCAA
ATGCCAGATCGTAATTTTAAATCAAATGGCTATATGGCTCAATCTGA
TGCTTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTGGA
AATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACTCATATT
TCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTCCTCAGGTTA
CTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTGGA
ACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCATCC
TTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGAAGGACG
TTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAAACAAGTA
AGGTTGCACTACTATTACGTGGAACATTATTGCCCTTGATACTCCATTA
CAITTAATAAACAATTTAATGTGAGTACTATTGAGGAAG

SEQ ID NO. 7608

STRAIN M781

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGA
AATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAA
AACTATGCTTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTTCTT
GATACTCAAATGCCAGATCGTAATTTTAAATCAAATGGCTATATGGC
TCAATCTGATGCCCTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTAT
TCTTTGGAATAAGTAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATA
ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCC
TACTTGGAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATT
GATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGA
TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
TAACAAGTAAGGTGCACTACTATTACGTGGAACATTATTGCCCTTGAT
ACTCCATTACATTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGT
TTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7609

STRAIN CJB110

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATG
CCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAA
ATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAA
AACTATGCTTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTTCTTG
ATACTCAAATGCCAGATCGTAATTTTAAATCAAATGGCTATATGGCT
CAATCTGATGCCCTTATACGAATCTTTAACTGCCCTAGAAAAATTTATTATT
CTTTGGAATAAGTAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAA
CTCATATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTC
TCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCT
ACTTGGAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTG
ATCATCTCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGAT
GAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
AACAAGTAAGGTGCACTACTATTACGTGGAACATTATTGCCCTTGATA
CTCCATTACATTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTT
TTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7610

STRAIN 1169NT

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGA
AATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAA
AACTATGCTTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTTCTT
GATACTCAAATGCCAGATCGTAATTTTAAATCAAATGGCTATATGGC
TCAATCTGATGCCCTTATACGAATCTTTAACTGCCCTAGAAAAATTTATTAT

Table 76: Comparative Sequences relating to SAG0260

TCCTTGGAAAAATGAAAGGTATTCAAAAACTGAATTAACAGCAGATA
 ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGT
 CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCC
 TACTTGGAAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATT
 GATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATTAAGGA
 TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
 TAACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGAT
 ACTCCATTACATTTAAAAAAACAATTAATGTGAGTACTATTGAGGAAGT
 TTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7611

STRAIN JM9130013

AAAAAAGTCATCGATTTAAAAAACTACAAAAGCATATGCC
 TCAGAAACCGTTTAAATAATTAATTTGGAGGTGTTTAAAGGCGAAAT
 AATTTGGATTAATAGGACCTCTGGAGCAGGGAATCTACCTTGATTAAAA
 CTATGCTTTGGCATGGAAGAACAGAGATAAGGGAACAGCTCTTGTTCCTGAT
 ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTTGGCTATATGGCTCA
 ATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCT
 TTGGAATAATGAAAGGTATTCAAAAACTGAATTAACAGCAGATAAAT
 CATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTC
 AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTAGCCATCGCCCTAC
 TTGGAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATTAATAGGATGA
 AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTA
 CAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACT
 CCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTT
 CTTAAAAAGCTGAAGGAGAA

PRETTY of: /biotmp/msa134270.2{*} April 10, 2003 02:14 ..

| | | | | | |
|----------------------------|--------------|-------------|------------|------------|------------|
| | 1 | | | | 50 |
| msa134270.2{391_COH1} | -----aaaaaag | tcacgcgATTT | AAAAAAACTA | CAAAAAGCAT | AcGCCTCAGA |
| msa134270.2{391_M732} | -----aaaaaag | tcacgcgATTT | AAAAAAACTA | CAAAAAGCAT | AcGCCTCAGA |
| msa134270.2{391_M781} | -----aaaaaag | tcacgcgATTT | AAAAAAACTA | CAAAAAGCAT | AcGCCTCAGA |
| msa134270.2{391_090} | ----- | -----ATTT | AAAAAAACTA | CAAAAAGCAT | AtGCCTCAGA |
| msa134270.2{391_CJB110} | -----aaaaaag | tcacgcgATTT | AAAAAAACTA | CAAAAAGCAT | AtGCCTCAGA |
| msa134270.2{391_1169NT} | -----aaaaaag | tcacgcgATTT | AAAAAAACTA | CAAAAAGCAT | AcGCCTCAGA |
| msa134270.2{391_18RS21} | ----- | -----gATTT | AAAAAAACTA | CAAAAAGCAT | AtGCCTCAGA |
| msa134270.2{391_2603} | atgaaaaaag | tcacgcgATTT | AAAAAAACTA | CAAAAAGCAT | AtGCCTCAGA |
| msa134270.2{391_A909} | -----aaaaaag | tcacgcgATTT | AAAAAAACTA | CAAAAAGCAT | AtGCCTCAGA |
| msa134270.2{391_JM9130013} | -----aaaaaag | tcacgcgATTT | AAAAAAACTA | CAAAAAGCAT | AtGCCTCAGA |
| msa134270.2{391_H36B} | -----aaaaaag | tcattgATTT | AAAAAAACTA | CAAAAAGCAT | AtGCCTCAGA |
| Consensus | ***----- | -----**** | ***** | ***** | *-***** |

| | | | | | |
|----------------------------|------------|------------|----------|------------|------------|
| | 51 | | | | 100 |
| msa134270.2{391_COH1} | AACtGTTTTA | AATAATATTA | ATTGAGGT | GTTTAAAGGa | GAAATAATTG |
| msa134270.2{391_M732} | AACtGTTTTA | AATAATATTA | ATTGAGGT | GTTTAAAGGa | GAAATAATTG |
| msa134270.2{391_M781} | AACtGTTTTA | AATAATATTA | ATTGAGGT | GTTTAAAGGa | GAAATAATTG |
| msa134270.2{391_090} | AACtGTTTTA | AATAATATTA | ATTGAGGT | GTTTAAAGGc | GAAATAATTG |
| msa134270.2{391_CJB110} | AACtGTTTTA | AATAATATTA | ATTGAGGT | GTTTAAAGGc | GAAATAATTG |
| msa134270.2{391_1169NT} | AACtGTTTTA | AATAATATTA | ATTGAGGT | GTTTAAAGGc | GAAATAATTG |
| msa134270.2{391_18RS21} | AACcGTTTTA | AATAATATTA | ATTGAGGT | GTTTAAAGGc | GAAATAATTG |
| msa134270.2{391_2603} | AACcGTTTTA | AATAATATTA | ATTGAGGT | GTTTAAAGGc | GAAATAATTG |
| msa134270.2{391_A909} | AACcGTTTTA | AATAATATTA | ATTGAGGT | GTTTAAAGGc | GAAATAATTG |
| msa134270.2{391_JM9130013} | AACcGTTTTA | AATAATATTA | ATTGAGGT | GTTTAAAGGc | GAAATAATTG |
| msa134270.2{391_H36B} | AACcGTTTTA | AATAATATTA | ATTGAGGT | GTTTAAAGGc | GAAATAATTG |
| Consensus | ***-***** | ***** | ***** | ***** | ***** |

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| | 101 | | | | 150 |
| msa134270.2{391_COH1} | GATTAATAGG | ACCCTCTGGA | GCAGGGAAAT | CTACCTTGAT | TAAAACTATG |
| msa134270.2{391_M732} | GATTAATAGG | ACCCTCTGGA | GCAGGGAAAT | CTACCTTGAT | TAAAACTATG |
| msa134270.2{391_M781} | GATTAATAGG | ACCCTCTGGA | GCAGGGAAAT | CTACCTTGAT | TAAAACTATG |
| msa134270.2{391_090} | GATTAATAGG | ACCCTCTGGA | GCAGGGAAAT | CTACCTTGAT | TAAAACTATG |
| msa134270.2{391_CJB110} | GATTAATAGG | ACCCTCTGGA | GCAGGGAAAT | CTACCTTGAT | TAAAACTATG |
| msa134270.2{391_1169NT} | GATTAATAGG | ACCCTCTGGA | GCAGGGAAAT | CTACCTTGAT | TAAAACTATG |
| msa134270.2{391_18RS21} | GATTAATAGG | ACCCTCTGGA | GCAGGGAAAT | CTACCTTGAT | TAAAACTATG |
| msa134270.2{391_2603} | GATTAATAGG | ACCCTCTGGA | GCAGGGAAAT | CTACCTTGAT | TAAAACTATG |
| msa134270.2{391_A909} | GATTAATAGG | ACCCTCTGGA | GCAGGGAAAT | CTACCTTGAT | TAAAACTATG |
| msa134270.2{391_JM9130013} | GATTAATAGG | ACCCTCTGGA | GCAGGGAAAT | CTACCTTGAT | TAAAACTATG |
| msa134270.2{391_H36B} | GATTAATAGG | ACCCTCTGGA | GCAGGGAAAT | CTACCTTGAT | TAAAACTATG |
| Consensus | ***** | ***** | ***** | ***** | ***** |

| | | | | | |
|-------------------------|------------|------------|------------|------------|------------|
| | 151 | | | | 200 |
| msa134270.2{391_COH1} | CTTGGCATGG | AAAAAGCAGA | TAAGGGAACA | GCTCTTGTTT | TTGATACTCA |
| msa134270.2{391_M732} | CTTGGCATGG | AAAAAGCAGA | TAAGGGAACA | GCTCTTGTTT | TTGATACTCA |
| msa134270.2{391_M781} | CTTGGCATGG | AAAAAGCAGA | TAAGGGAACA | GCTCTTGTTT | TTGATACTCA |
| msa134270.2{391_090} | CTTGGCATGG | AAAAAGCAGA | TAAGGGAACA | GCTCTTGTTT | TTGATACTCA |
| msa134270.2{391_CJB110} | CTTGGCATGG | AAAAAGCAGA | TAAGGGAACA | GCTCTTGTTT | TTGATACTCA |
| msa134270.2{391_1169NT} | CTTGGCATGG | AAAAAGCAGA | TAAGGGAACA | GCTCTTGTTT | TTGATACTCA |
| msa134270.2{391_18RS21} | CTTGGCATGG | AAAAAGCAGA | TAAGGGAACA | GCTCTTGTTT | TTGATACTCA |
| msa134270.2{391_2603} | CTTGGCATGG | AAAAAGCAGA | TAAGGGAACA | GCTCTTGTTT | TTGATACTCA |
| msa134270.2{391_A909} | CTTGGCATGG | AAAAAGCAGA | TAAGGGAACA | GCTCTTGTTT | TTGATACTCA |

Table 76: Comparative Sequences relating to SAG0260

| | | | | | |
|----------------------------|-------------|------------|-------------|------------|-------------|
| msa134270.2{391_JM9130013} | CTTGGCATGG | AAAAAGCAGA | TAAGGGAACA | GCTCTTGTTT | TTGATACTCA |
| msa134270.2{391_H36B} | CTTGGCATGG | AAAAAGCAGA | TAAGGGAACA | GCTCTTGTTT | TTGATACTCA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 201 | | | | 250 |
| msa134270.2{391_COH1} | AATGCCAGAT | CgTAATATTT | TAAATCAAAT | TGGCTATATG | GCTCAATCTG |
| msa134270.2{391_M732} | AATGCCAGAT | CgTAATATTT | TAAATCAAAT | TGGCTATATG | GCTCAATCTG |
| msa134270.2{391_M781} | AATGCCAGAT | CgTAATATTT | TAAATCAAAT | TGGCTATATG | GCTCAATCTG |
| msa134270.2{391_090} | AATGCCAGAT | CgTAATATTT | TAAATCAAAT | TGGCTATATG | GCTCAATCTG |
| msa134270.2{391_CJB110} | AATGCCAGAT | CgTAATATTT | TAAATCAAAT | TGGCTATATG | GCTCAATCTG |
| msa134270.2{391_1169NT} | AATGCCAGAT | CgTAATATTT | TAAATCAAAT | TGGCTATATG | GCTCAATCTG |
| msa134270.2{391_18RS21} | AATGCCAGAT | CgTAATATTT | TAAATCAAAT | TGGCTATATG | GCTCAATCTG |
| msa134270.2{391_2603} | AATGCCAGAT | CgTAATATTT | TAAATCAAAT | TGGCTATATG | GCTCAATCTG |
| msa134270.2{391_A909} | AATGCCAGAT | CgTAATATTT | TAAATCAAAT | TGGCTATATG | GCTCAATCTG |
| msa134270.2{391_JM9130013} | AATGCCAGAT | CgTAATATTT | TAAATCAAAT | TGGCTATATG | GCTCAATCTG |
| msa134270.2{391_H36B} | AATGCCAGAT | CgTAATATTT | TAAATCAAAT | TGGCTATATG | GCTCAATCTG |
| Consensus | ***** | *-***** | ***** | ***** | ***** |
| | 251 | | | | 300 |
| msa134270.2{391_COH1} | ATGCCCTTAcA | CGAgTCITTA | ACTGgCTTAG | AAAATTTATT | ATTCTTTGGA |
| msa134270.2{391_M732} | ATGCCCTTAcA | CGAgTCITTA | ACTGgCTTAG | AAAATTTATT | ATTCTTTGGA |
| msa134270.2{391_M781} | ATGCCCTTAcA | CGAgTCITTA | ACTGgCTTAG | AAAATTTATT | ATTCTTTGGA |
| msa134270.2{391_090} | ATGCCCTTAcA | CGAgTCITTA | ACTGgCTTAG | AAAATTTATT | ATTCTTTGGA |
| msa134270.2{391_CJB110} | ATGCCCTTAcA | CGAgTCITTA | ACTGgCTTAG | AAAATTTATT | ATTCTTTGGA |
| msa134270.2{391_1169NT} | ATGCCCTTAcA | CGAgTCITTA | ACTGgCTTAG | AAAATTTATT | ATTCTTTGGA |
| msa134270.2{391_18RS21} | ATGCCCTTAcA | CGAgTCITTA | ACTGgCTTAG | AAAATTTATT | ATTCTTTGGA |
| msa134270.2{391_2603} | ATGCCCTTAcA | CGAgTCITTA | ACTGgCTTAG | AAAATTTATT | ATTCTTTGGA |
| msa134270.2{391_A909} | ATGCCCTTAcA | CGAgTCITTA | ACTGgCTTAG | AAAATTTATT | ATTCTTTGGA |
| msa134270.2{391_JM9130013} | ATGCCCTTAcA | CGAgTCITTA | ACTGgCTTAG | AAAATTTATT | ATTCTTTGGA |
| msa134270.2{391_H36B} | ATGCCCTTAcA | CGAgTCITTA | ACTGgCTTAG | AAAATTTATT | ATTCTTTGGA |
| Consensus | *****-* | ***-***** | ****-***** | ***** | ***** |
| | 301 | | | | 350 |
| msa134270.2{391_COH1} | AAAATGAAAG | GTATTCAAAA | AACCTGAATTA | AAACAGCAGA | TAACCTCATAT |
| msa134270.2{391_M732} | AAAATGAAAG | GTATTCAAAA | AACCTGAATTA | AAACAGCAGA | TAACCTCATAT |
| msa134270.2{391_M781} | AAAATGAAAG | GTATTCAAAA | AACCTGAATTA | AAACAGCAGA | TAACCTCATAT |
| msa134270.2{391_090} | AAAATGAAAG | GTATTCAAAA | AACCTGAATTA | AAACAGCAGA | TAACCTCATAT |
| msa134270.2{391_CJB110} | AAAATGAAAG | GTATTCAAAA | AACCTGAATTA | AAACAGCAGA | TAACCTCATAT |
| msa134270.2{391_1169NT} | AAAATGAAAG | GTATTCAAAA | AACCTGAATTA | AAACAGCAGA | TAACCTCATAT |
| msa134270.2{391_18RS21} | AAAATGAAAG | GTATTCAAAA | AACCTGAATTA | AAACAGCAGA | TAACCTCATAT |
| msa134270.2{391_2603} | AAAATGAAAG | GTATTCAAAA | AACCTGAATTA | AAACAGCAGA | TAACCTCATAT |
| msa134270.2{391_A909} | AAAATGAAAG | GTATTCAAAA | AACCTGAATTA | AAACAGCAGA | TAACCTCATAT |
| msa134270.2{391_JM9130013} | AAAATGAAAG | GTATTCAAAA | AACCTGAATTA | AAACAGCAGA | TAACCTCATAT |
| msa134270.2{391_H36B} | AAAATGAAAG | GTATTCAAAA | AACCTGAATTA | AAACAGCAGA | TAACCTCATAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 351 | | | | 400 |
| msa134270.2{391_COH1} | TTCTAAAGTA | GTAGATCTAG | AAAACCAACT | TGATAAATTT | GTCTCAGGTT |
| msa134270.2{391_M732} | TTCTAAAGTA | GTAGATCTAG | AAAACCAACT | TGATAAATTT | GTCTCAGGTT |
| msa134270.2{391_M781} | TTCTAAAGTA | GTAGATCTAG | AAAACCAACT | TGATAAATTT | GTCTCAGGTT |
| msa134270.2{391_090} | TTCTAAAGTA | GTAGATCTAG | AAAACCAACT | TGATAAATTT | GTCTCAGGTT |
| msa134270.2{391_CJB110} | TTCTAAAGTA | GTAGATCTAG | AAAACCAACT | TGATAAATTT | GTCTCAGGTT |
| msa134270.2{391_1169NT} | TTCTAAAGTA | GTAGATCTAG | AAAACCAACT | TGATAAATTT | GTCTCAGGTT |
| msa134270.2{391_18RS21} | TTCTAAAGTA | GTAGATCTAG | AAAACCAACT | TGATAAATTT | GTCTCAGGTT |
| msa134270.2{391_2603} | TTCTAAAGTA | GTAGATCTAG | AAAACCAACT | TGATAAATTT | GTCTCAGGTT |
| msa134270.2{391_A909} | TTCTAAAGTA | GTAGATCTAG | AAAACCAACT | TGATAAATTT | GTCTCAGGTT |
| msa134270.2{391_JM9130013} | TTCTAAAGTA | GTAGATCTAG | AAAACCAACT | TGATAAATTT | GTCTCAGGTT |
| msa134270.2{391_H36B} | TTCTAAAGTA | GTAGATCTAG | AAAACCAACT | TGATAAATTT | GTCTCAGGTT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 401 | | | | 450 |
| msa134270.2{391_COH1} | ACTCAGGAGG | TATGAAAAGA | CGGCTTTCTC | TAGCCATCGC | CCTACTTGGA |
| msa134270.2{391_M732} | ACTCAGGAGG | TATGAAAAGA | CGGCTTTCTC | TAGCCATCGC | CCTACTTGGA |
| msa134270.2{391_M781} | ACTCAGGAGG | TATGAAAAGA | CGGCTTTCTC | TAGCCATCGC | CCTACTTGGA |
| msa134270.2{391_090} | ACTCAGGAGG | TATGAAAAGA | CGGCTTTCTC | TAGCCATCGC | CCTACTTGGA |
| msa134270.2{391_CJB110} | ACTCAGGAGG | TATGAAAAGA | CGGCTTTCTC | TAGCCATCGC | CCTACTTGGA |
| msa134270.2{391_1169NT} | ACTCAGGAGG | TATGAAAAGA | CGGCTTTCTC | TAGCCATCGC | CCTACTTGGA |
| msa134270.2{391_18RS21} | ACTCAGGAGG | TATGAAAAGA | CGGCTTTCTC | TAGCCATCGC | CCTACTTGGA |
| msa134270.2{391_2603} | ACTCAGGAGG | TATGAAAAGA | CGGCTTTCTC | TAGCCATCGC | CCTACTTGGA |
| msa134270.2{391_A909} | ACTCAGGAGG | TATGAAAAGA | CGGCTTTCTC | TAGCCATCGC | CCTACTTGGA |
| msa134270.2{391_JM9130013} | ACTCAGGAGG | TATGAAAAGA | CGGCTTTCTC | TAGCCATCGC | CCTACTTGGA |
| msa134270.2{391_H36B} | ACTCAGGAGG | TATGAAAAGA | CGGCTTTCTC | TAGCCATCGC | CCTACTTGGA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 451 | | | | 500 |
| msa134270.2{391_COH1} | AACCCACAG | TTTAAATCCT | AGATGAACCT | ACCGTTGGAA | TTGATCCATC |
| msa134270.2{391_M732} | AACCCACAG | TTTAAATCCT | AGATGAACCT | ACCGTTGGAA | TTGATCCATC |
| msa134270.2{391_M781} | AACCCACAG | TTTAAATCCT | AGATGAACCT | ACCGTTGGAA | TTGATCCATC |
| msa134270.2{391_090} | AACCCACAG | TTTAAATCCT | AGATGAACCT | ACCGTTGGAA | TTGATCCATC |
| msa134270.2{391_CJB110} | AACCCACAG | TTTAAATCCT | AGATGAACCT | ACCGTTGGAA | TTGATCCATC |
| msa134270.2{391_1169NT} | AACCCACAG | TTTAAATCCT | AGATGAACCT | ACCGTTGGAA | TTGATCCATC |
| msa134270.2{391_18RS21} | AACCCACAG | TTTAAATCCT | AGATGAACCT | ACCGTTGGAA | TTGATCCATC |
| msa134270.2{391_2603} | AACCCACAG | TTTAAATCCT | AGATGAACCT | ACCGTTGGAA | TTGATCCATC |

Table 76: Comparative Sequences relating to SAG0260

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| msa134270.2{391_A909} | AACCCACAG | TTTTAATCCT | AGATGAACCT | ACCGTTGGAA | TTGATCCATC |
| msa134270.2{391_JM9130013} | AACCCACAG | TTTTAATCCT | AGATGAACCT | ACCGTTGGAA | TTGATCCATC |
| msa134270.2{391_H36B} | AACCCACAG | TTTTAATCCT | AGATGAACCT | ACCGTTGGAA | TTGATCCATC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 501 | | | | | |
| msa134270.2{391_COH1} | CTTGAGGAGA | AAAATCTGGC | AAGAGCTAAT | TAATATTAAG | GATGAAGGAC |
| msa134270.2{391_M732} | CTTGAGGAGA | AAAATCTGGC | AAGAGCTAAT | TAATATTAAG | GATGAAGGAC |
| msa134270.2{391_M781} | CTTGAGGAGA | AAAATCTGGC | AAGAGCTAAT | TAATATTAAG | GATGAAGGAC |
| msa134270.2{391_090} | CTTGAGGAGA | AAAATCTGGC | AAGAGCTAAT | TAATATTAAG | GATGAAGGAC |
| msa134270.2{391_CJB110} | CTTGAGGAGA | AAAATCTGGC | AAGAGCTAAT | TAATATTAAG | GATGAAGGAC |
| msa134270.2{391_1169NT} | CTTGAGGAGA | AAAATCTGGC | AAGAGCTAAT | TAATATTAAG | GATGAAGGAC |
| msa134270.2{391_18RS21} | CTTGAGGAGA | AAAATCTGGC | AAGAGCTAAT | TAATATTAAG | GATGAAGGAC |
| msa134270.2{391_2603} | CTTGAGGAGA | AAAATCTGGC | AAGAGCTAAT | TAATATTAAG | GATGAAGGAC |
| msa134270.2{391_A909} | CTTGAGGAGA | AAAATCTGGC | AAGAGCTAAT | TAATATTAAG | GATGAAGGAC |
| msa134270.2{391_JM9130013} | CTTGAGGAGA | AAAATCTGGC | AAGAGCTAAT | TAATATTAAG | GATGAAGGAC |
| msa134270.2{391_H36B} | CTTGAGGAGA | AAAATCTGGC | AAGAGCTAAT | TAATATTAAG | GATGAAGGAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 551 | | | | | |
| msa134270.2{391_COH1} | gTTCTATCTT | TATTACAACC | CACGTTATGG | ATGAAGCAGA | ATTAACAAGT |
| msa134270.2{391_M732} | gTTCTATCTT | TATTACAACC | CACGTTATGG | ATGAAGCAGA | ATTAACAAGT |
| msa134270.2{391_M781} | gTTCTATCTT | TATTACAACC | CACGTTATGG | ATGAAGCAGA | ATTAACAAGT |
| msa134270.2{391_090} | gTTCTATCTT | TATTACAACC | CACGTTATGG | ATGAAGCAGA | ATTAACAAGT |
| msa134270.2{391_CJB110} | gTTCTATCTT | TATTACAACC | CACGTTATGG | ATGAAGCAGA | ATTAACAAGT |
| msa134270.2{391_1169NT} | gTTCTATCTT | TATTACAACC | CACGTTATGG | ATGAAGCAGA | ATTAACAAGT |
| msa134270.2{391_18RS21} | gTTCTATCTT | TATTACAACC | CACGTTATGG | ATGAAGCAGA | ATTAACAAGT |
| msa134270.2{391_2603} | gTTCTATCTT | TATTACAACC | CACGTTATGG | ATGAAGCAGA | ATTAACAAGT |
| msa134270.2{391_A909} | gTTCTATCTT | TATTACAACC | CACGTTATGG | ATGAAGCAGA | ATTAACAAGT |
| msa134270.2{391_JM9130013} | gTTCTATCTT | TATTACAACC | CACGTTATGG | ATGAAGCAGA | ATTAACAAGT |
| msa134270.2{391_H36B} | gTTCTATCTT | TATTACAACC | CACGTTATGG | ATGAAGCAGA | ATTAACAAGT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 601 | | | | | |
| msa134270.2{391_COH1} | AAGGTTGCAC | TACTATTACG | TGGAACATT | ATTGCCTTTG | ATACTCCATT |
| msa134270.2{391_M732} | AAGGTTGCAC | TACTATTACG | TGGAACATT | ATTGCCTTTG | ATACTCCATT |
| msa134270.2{391_M781} | AAGGTTGCAC | TACTATTACG | TGGAACATT | ATTGCCTTTG | ATACTCCATT |
| msa134270.2{391_090} | AAGGTTGCAC | TACTATTACG | TGGAACATT | ATTGCCTTTG | ATACTCCATT |
| msa134270.2{391_CJB110} | AAGGTTGCAC | TACTATTACG | TGGAACATT | ATTGCCTTTG | ATACTCCATT |
| msa134270.2{391_1169NT} | AAGGTTGCAC | TACTATTACG | TGGAACATT | ATTGCCTTTG | ATACTCCATT |
| msa134270.2{391_18RS21} | AAGGTTGCAC | TACTATTACG | TGGAACATT | ATTGCCTTTG | ATACTCCATT |
| msa134270.2{391_2603} | AAGGTTGCAC | TACTATTACG | TGGAACATT | ATTGCCTTTG | ATACTCCATT |
| msa134270.2{391_A909} | AAGGTTGCAC | TACTATTACG | TGGAACATT | ATTGCCTTTG | ATACTCCATT |
| msa134270.2{391_JM9130013} | AAGGTTGCAC | TACTATTACG | TGGAACATT | ATTGCCTTTG | ATACTCCATT |
| msa134270.2{391_H36B} | AAGGTTGCAC | TACTATTACG | TGGAACATT | ATTGCCTTTG | ATACTCCATT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 651 | | | | | |
| msa134270.2{391_COH1} | ACATTTAAAA | AAACAATTTA | ATGTGAGTAC | TATTGAGGAA | G----- |
| msa134270.2{391_M732} | ACATTTAAAA | AAACAATTTA | ATGTGAGTAC | TATTGAGGAA | GTTTCTTAA |
| msa134270.2{391_M781} | ACATTTAAAA | AAACAATTTA | ATGTGAGTAC | TATTGAGGAA | GTTTCTTAA |
| msa134270.2{391_090} | ACATTTAAAA | AAACAATTTA | ATGTGAGTAC | TATTGAGGAA | GTTTCTTAA |
| msa134270.2{391_CJB110} | ACATTTAAAA | AAACAATTTA | ATGTGAGTAC | TATTGAGGAA | GTTTCTTAA |
| msa134270.2{391_1169NT} | ACATTTAAAA | AAACAATTTA | ATGTGAGTAC | TATTGAGGAA | GTTTCTTAA |
| msa134270.2{391_18RS21} | ACATTTAAAA | AAACAATTTA | ATGTGAGTAC | TATTGAGGAA | GTTTCTTAA |
| msa134270.2{391_2603} | ACATTTAAAA | AAACAATTTA | ATGTGAGTAC | TATTGAGGAA | GTTTCTTAA |
| msa134270.2{391_A909} | ACATTTAAAA | AAACAATTTA | ATGTGAGTAC | TATTGAGGAA | GTTTCTTAA |
| msa134270.2{391_JM9130013} | ACATTTAAAA | AAACAATTTA | ATGTGAGTAC | TATTGAGGAA | GTTTCTTAA |
| msa134270.2{391_H36B} | ACATTTAAAA | AAACAATTTA | ATGTGAGTAC | TATTGAGGAA | GTTTCTTAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 701 | | | | | |
| msa134270.2{391_COH1} | ----- | 714 | | | |
| msa134270.2{391_M732} | AAGCTGAAGG | AGAA | | | |
| msa134270.2{391_M781} | AAGCTGAAGG | AGAA | | | |
| msa134270.2{391_090} | AAGCTGAAGG | AGAA | | | |
| msa134270.2{391_CJB110} | AAGCTGAAGG | AGAA | | | |
| msa134270.2{391_1169NT} | AAGCTGAAGG | AGAA | | | |
| msa134270.2{391_18RS21} | AAGCTGAAGG | AGAA | | | |
| msa134270.2{391_2603} | AAGCTGAAGG | AGAA | | | |
| msa134270.2{391_A909} | AAGCTGAAGG | AGAA | | | |
| msa134270.2{391_JM9130013} | AAGCTGAAGG | AGAA | | | |
| msa134270.2{391_H36B} | AAGCTGAAGG | AGAA | | | |
| Consensus | ***** | **** | | | |

SEQ ID NO. 7612

STRAIN 2603 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKMLGMEKADKGTALVLDTPMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKVVDLENQLDKFVSGYSGGKRRSLALALLGNPTVLILDEPTVGIDPSLRRIKWQELINKDEGHSIFITTHVDEAELTSKVALLLRGNI AFDTPLHLKKQFNV

SEQ ID NO. 7613

Table 76: Comparative Sequences relating to SAG0260

STRAIN 090 frame: 3
 LKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTALVLD
 QMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQIITHISKVVDLENQ
 LDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKDEGRSI
 FITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7614

STRAIN A909 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7615

STRAIN H36B frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7616

STRAIN 18RS21 frame: 1
 DLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTALVLD
 TQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKVVDLEN
 QLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKDEGHS
 IFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7617

STRAIN M732 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7618

STRAIN COH1 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7619

STRAIN M781 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7620

STRAIN CJB110 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7621

STRAIN 1169NT frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7622

STRAIN JM9130013 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

PRETTY of: /biotmp/msa134470.2{*} April 10, 2003 02:16 ..

| | 1 | 50 |
|----------------------------|---|----|
| msa134470.2{391_090} | -----LKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM | |
| msa134470.2{391_1169NT} | KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM | |
| msa134470.2{391_CJB110} | KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM | |
| msa134470.2{391_COH1} | KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM | |
| msa134470.2{391_M732} | KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM | |
| msa134470.2{391_M781} | KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM | |
| msa134470.2{391_18RS21} | -----DLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM | |
| msa134470.2{391_2603} | KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM | |
| msa134470.2{391_H36B} | KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM | |
| msa134470.2{391_JM9130013} | KKVIDLKKLQ KAYASETVLN NINLEVFKEI IGLIGPSGA GKSTLIKTM | |

Table 76: Comparative Sequences relating to SAG0260

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| msa134470.2{391_A909} | KKVIDLKKLQ | KAYASETVLN | NINLEVFKE | IIGLIGPSGA | GKSTLIKTML |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 51 | | | | 100 |
| msa134470.2{391_090} | GMEKADKGTA | LVLDTQMPDr | NILNQIGYMA | QSDALyESLT | aLENLLFFGK |
| msa134470.2{391_1169NT} | GMEKADKGTA | LVLDTQMPDr | NILNQIGYMA | QSDALyESLT | aLENLLFFGK |
| msa134470.2{391_CJB110} | GMEKADKGTA | LVLDTQMPDr | NILNQIGYMA | QSDALyESLT | aLENLLFFGK |
| msa134470.2{391_COH1} | GMEKADKGTA | LVLDTQMPDr | NILNQIGYMA | QSDALhESLT | gLENLLFFGK |
| msa134470.2{391_M732} | GMEKADKGTA | LVLDTQMPDr | NILNQIGYMA | QSDALhESLT | gLENLLFFGK |
| msa134470.2{391_M781} | GMEKADKGTA | LVLDTQMPDr | NILNQIGYMA | QSDALhESLT | gLENLLFFGK |
| msa134470.2{391_18RS21} | GMEKADKGTA | LVLDTQMPDr | NILNQIGYMA | QSDALyESLT | gLENLLFFGK |
| msa134470.2{391_2603} | GMEKADKGTA | LVLDTQMPDr | NILNQIGYMA | QSDALyESLT | gLENLLFFGK |
| msa134470.2{391_H36B} | GMEKADKGTA | LVLDTQMPDr | NILNQIGYMA | QSDALyESLT | gLENLLFFGK |
| msa134470.2{391_JM9130013} | GMEKADKGTA | LVLDTQMPDr | NILNQIGYMA | QSDALyESLT | gLENLLFFGK |
| msa134470.2{391_A909} | GMEKADKGTA | LVLDTQMPDh | NILNQIGYMA | QSDALyESLT | gLENLLFFGK |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 101 | | | | 150 |
| msa134470.2{391_090} | MKGIOKTELK | QQITHISKVV | DLENQLDKFV | SGYSGGMKRR | LSLAIALLGN |
| msa134470.2{391_1169NT} | MKGIOKTELK | QQITHISKVV | DLENQLDKFV | SGYSGGMKRR | LSLAIALLGN |
| msa134470.2{391_CJB110} | MKGIOKTELK | QQITHISKVV | DLENQLDKFV | SGYSGGMKRR | LSLAIALLGN |
| msa134470.2{391_COH1} | MKGIOKTELK | QQITHISKVV | DLENQLDKFV | SGYSGGMKRR | LSLAIALLGN |
| msa134470.2{391_M732} | MKGIOKTELK | QQITHISKVV | DLENQLDKFV | SGYSGGMKRR | LSLAIALLGN |
| msa134470.2{391_M781} | MKGIOKTELK | QQITHISKVV | DLENQLDKFV | SGYSGGMKRR | LSLAIALLGN |
| msa134470.2{391_18RS21} | MKGIOKTELK | QQITHISKVV | DLENQLDKFV | SGYSGGMKRR | LSLAIALLGN |
| msa134470.2{391_2603} | MKGIOKTELK | QQITHISKVV | DLENQLDKFV | SGYSGGMKRR | LSLAIALLGN |
| msa134470.2{391_H36B} | MKGIOKTELK | QQITHISKVV | DLENQLDKFV | SGYSGGMKRR | LSLAIALLGN |
| msa134470.2{391_JM9130013} | MKGIOKTELK | QQITHISKVV | DLENQLDKFV | SGYSGGMKRR | LSLAIALLGN |
| msa134470.2{391_A909} | MKGIOKTELK | QQITHISKVV | DLENQLDKFV | SGYSGGMKRR | LSLAIALLGN |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 151 | | | | 200 |
| msa134470.2{391_090} | PTVLILDEPT | VGIDPSLRK | IWQELINIKD | EGrSIFITTH | VMDEAELTSK |
| msa134470.2{391_1169NT} | PTVLILDEPT | VGIDPSLRK | IWQELINIKD | EGrSIFITTH | VMDEAELTSK |
| msa134470.2{391_CJB110} | PTVLILDEPT | VGIDPSLRK | IWQELINIKD | EGrSIFITTH | VMDEAELTSK |
| msa134470.2{391_COH1} | PTVLILDEPT | VGIDPSLRK | IWQELINIKD | EGrSIFITTH | VMDEAELTSK |
| msa134470.2{391_M732} | PTVLILDEPT | VGIDPSLRK | IWQELINIKD | EGrSIFITTH | VMDEAELTSK |
| msa134470.2{391_M781} | PTVLILDEPT | VGIDPSLRK | IWQELINIKD | EGrSIFITTH | VMDEAELTSK |
| msa134470.2{391_18RS21} | PTVLILDEPT | VGIDPSLRK | IWQELINIKD | EGhSIFITTH | VMDEAELTSK |
| msa134470.2{391_2603} | PTVLILDEPT | VGIDPSLRK | IWQELINIKD | EGhSIFITTH | VMDEAELTSK |
| msa134470.2{391_H36B} | PTVLILDEPT | VGIDPSLRK | IWQELINIKD | EGrSIFITTH | VMDEAELTSK |
| msa134470.2{391_JM9130013} | PTVLILDEPT | VGIDPSLRK | IWQELINIKD | EGrSIFITTH | VMDEAELTSK |
| msa134470.2{391_A909} | PTVLILDEPT | VGIDPSLRK | IWQELINIKD | EGrSIFITTH | VMDEAELTSK |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 201 | | 224 | | |
| msa134470.2{391_090} | VALLLRGNII | AFDTPHLKK | QFNV | | |
| msa134470.2{391_1169NT} | VALLLRGNII | AFDTPHLKK | QFNV | | |
| msa134470.2{391_CJB110} | VALLLRGNII | AFDTPHLKK | QFNV | | |
| msa134470.2{391_COH1} | VALLLRGNII | AFDTPHLKK | QFNV | | |
| msa134470.2{391_M732} | VALLLRGNII | AFDTPHLKK | QFNV | | |
| msa134470.2{391_M781} | VALLLRGNII | AFDTPHLKK | QFNV | | |
| msa134470.2{391_18RS21} | VALLLRGNII | AFDTPHLKK | QFNV | | |
| msa134470.2{391_2603} | VALLLRGNII | AFDTPHLKK | QFNV | | |
| msa134470.2{391_H36B} | VALLLRGNII | AFDTPHLKK | QFNV | | |
| msa134470.2{391_JM9130013} | VALLLRGNII | AFDTPHLKK | QFNV | | |
| msa134470.2{391_A909} | VALLLRGNII | AFDTPHLKK | QFNV | | |
| Consensus | ***** | ***** | **** | | |

Table 77: Comparative Sequences relating to SAG2059

SEQ ID NO. 7701

STRAIN 2603

TTGCCTATGTTGCTGTTGGTTTAGTTTTAGAGGGTGGCGGAATGAGAGGTCTTTATACT
GCTGGAGTTTTAGATGCTTTTCTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTC
TCTGCTGCTGCTGCTGTTTGGTGGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
TACAATAAAAAAGTATTTATCCCACCTAAATATATGAGTCTAAGGTCATGGTTTCGAACA
GGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTATGAAATGGATGTATTT
GACGATGAAGCATTTAAAAAATCAAGTATGATTTTTACGTAGTTGCTACAGAGATGACA
TCTGGTAAACCTGAATATTTTAAATTTGATAGTGTTTTGAACAAATGGAATTTTACGT
GCTAGTTGAGCATTACAGTAGTCTCAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGATTGACAAG
TTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTCAAGTGGACGATTG
TATAAACTCTGTATAGGAAATATCCTAATTTTGTAAAGACAGCCTCGAATCGGTACCAA
CAGTATAATAATAGTCTTGAAAAGGTCTAGAGCCTTGAAAAAACAGGCGATCTATTTGCA
ATTAGACCGAGTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAATAGTTAT
CTAATGAAA

SEQ ID NO. 7702

STRAIN 090

CCTATGTTGTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTATAGTGTCTTT
CTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGCTCTGCTGGTGC
ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAAGTATTTATCCCACCTAAATATATGAGTCTAAGGTCATGG
TTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
AAAATTGATAGTGTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGC
ATTACAGTAGTCTCAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
GCCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAA
AAGGTCTAGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCGAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7703

STRAIN A909

CCTATGTTGTCTGTTGGTTTAGTTTTAGAG
GGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTATAGTGTCTTTCT
AGATGCAGGAATAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGCAT
TGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
AATAAAAAAGTATTTATCCCACCTAAATATATGAGTCTAAGGTCATGGCT
TCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTA
TGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGAT
TTTTACGAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
AATTGATAGTGTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGCAT
TACCAGTAGTCTCAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
GGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGAT
TGACAAGTTGATTTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
CTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
GTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAAA
GGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
TAGTTATCTAATGAAA

SEQ ID NO. 7704

STRAIN H36B

CCTATGTTGTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTATAGTGTCTTT
CTAGATGCAGGAATAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGC
ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAAGTATTTATCCCACCTAAATATATGAGTCTAAGGTCATGG
CTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTA
TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTACGAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTT
AAAATTGATAGTGTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGC
ATTACAGTAGTCTCAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
GCCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
TTGTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAA
AAGGTCTAGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCAAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7705

Table 77: Comparative Sequences relating to SAG2059

STRAIN 18RS21

CCTATGTTGTCGTGGTTTGTAGTTTGTAGAGG
 GTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTGTAGATGCTTTTCTA
 GATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTGCATT
 GTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACA
 ATAAAAAGTATTTATCCCAACCCTAAATATATGAGTCTAAGGTCATGGTTT
 CGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTAT
 GAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGATT
 TTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAA
 ATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAAGCATT
 ACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATG
 GTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGATTT
 GACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCC
 TTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTG
 TAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAAAG
 GTCATGAGCCTTGAAAAACAGCGCATCTATTGCAATTAGACCGAGTAA
 GAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGTA
 TTTATCAGCTTGGTATGAAAAGATGCTAAAAGTGTGATGCCTGAGCTGAAT
 AGTTATCTAATGAAA

SEQ ID NO. 7706

STRAIN M732

CCTATGTTGTCGTGGTTTGTAGTTTGTAGA
 GGGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTGTAGATGCTTTTC
 TAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCA
 TTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATA
 CAATAAAAAGTATTTATCCCAACCCTGAATATATGAGTCTAAGATCATGGC
 TTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCT
 ATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGA
 TTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTA
 AAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAAGCA
 TTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGA
 TGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGAT
 TTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAG
 CCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTT
 TGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAA
 AGGTCATGAGCCTTGAAAAACAGCGCATCTATTGCAATTAGACCGAGT
 AAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAG
 TATTATCAGCTTGGTATGAAAATATGCTAAAAGTGTGATGCCTGAGCTGA
 ATAGTTATCTAATGAAA

SEQ ID NO. 7707

STRAIN COH1

CCTATGTTGTCGTGGTTTGTAGTTTGA
 GAGGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTGTAGATGCTTT
 TCTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTG
 CATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
 TACAATAAAAAGTATTTATCCCAACCCTGAATATATGAGTCTAAGATCATG
 GCTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
 CTATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATT
 GATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
 TAAATTTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAAG
 CATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
 GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGG
 ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
 AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
 TTTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAAGTTCATGAGCCTTGAAAAACAGCGCATCTATTGCAATTAGACCGA
 GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 AGTATTTATCAGCTTGGTATGAAAATATGCTAAAAGTGTGATGCCTGAGCT
 GAATAGTTATCTAATGAAA

SEQ ID NO. 7708

STRAIN M781

CCTATGTTGTCGTGGTTTGTAGTTTGTAG
 AGGGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTGTAGATGCTTTT
 CTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGC
 ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
 ACAATAAAAAGTATTTATCCCAACCCTGAATATATGAGTCTAAGATCATGG
 CTTTGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
 TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
 ATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
 AAAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAAGC
 ATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
 ATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGA
 TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
 GCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
 TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAGGTCATGAGCCTTGAAAAACAGCGCATCTATTGCAATTAGACCGAG
 TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
 GTATTTATCAGCTTGGTATGAAAATATGCTAAAAGTGTGATGCCTGAGCTG
 AATAGTTATCTAATGAAA

Table 77: Comparative Sequences relating to SAG2059

SEQ ID NO. 7709

STRAIN CJB110

CCTATGTTGTCGTTGGTTTGTAGTTTAA
 GAGGGTGGCGGAATGAGAGGTCCTTATACCTGCTGGAGTTTGTAGATGCTTT
 TCTAGATGCAGGAATAAAATAGATGGTATCGTATCTGTCTCTGCTGGTG
 CATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTGC
 TACAATAAAAGATATTATCCCACCCTAAATATATGAGTCTAAGGTCATG
 GTTTCGAACAGGAATTTTGTAAATAAGATTTCACCTATTATGAAGTTC
 CTATGAAATTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATT
 GATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
 TAAATTTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCA
 CATACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
 GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTAGG
 ATTTGACAAGTTGATTGTTGTGATGACTAGGCCCTCAATTATCAGAAAA
 AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
 TTTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAGGTCATGAGCCTTGAAAAACAGGCGATCTATTGCAATTAGACCGA
 GTAAGAGCTTGGTTATGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 AGTATTTATCAGCTTGGTATGAAAGATGCTAAAGTGTGATGCCTGAGCT
 GAATAGTTATCTAATGAAA

SEQ ID NO. 7710

STRAIN 1169NT

CCTATGTTGTCGTTGGTTTGTAGTTTGTAGGGTG
 GCGGAATGAGAGGTCCTTATACCTGCTGGAGTTTGTAGATGCTTTTCTAGAT
 GCAGGAATAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCATTGTT
 TGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTCGATACAATA
 AAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGATCATGGCTTCGA
 ACAGGGAATTTTGTAAATAAGATTTCACCTATTATGAAGTTCTCTATGAA
 ATTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATTGATTTT
 ACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAAT
 GATAGTGTCTTGAACAAATGGAAATTTTACGTGCTAGTTTCAAGTATACC
 AGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATGGTG
 GTTTATCTGATAGTATCCCGTTGATTTTGCCCGTGGTTTAGGATTGAC
 AAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTTC
 AAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTGTAA
 AGACAGCCTCGAATCGGTACCAACAGTATAATAATAGCCTTGAAAGGTC
 ATGAGCCTTGAAAAACAGGCGATCTATTGCAATTAGGCCGAGTAAAAAG
 CTTGGTTATTGTCGCTTAGAGAAGAATCCGGATAAACTTGATAGTATTT
 ATCAGCTTGGTATGAAAGATGCTAAAGTGTGATGCCTGAGCTGAATAGT
 TATCTAATGAAA

SEQ ID NO. 7711

STRAIN JM9130013

CCTATGTTGTCGTTGGTTTGTAGTTTGTAGAG
 GGTGGCGGAATGAGAGGTCCTTATACCTGCTGGAGTTTGTAGATGCTTTTCT
 AGATGCAGGAATAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGCA
 TGTGTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTCGATAC
 AATAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCTAGGCT
 TCGAACAGGGAATTTTGTAAATAAGATTTCACCTATTATGAAGTTCTCTA
 TGAAATTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATTGAT
 TTTTACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
 AATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAAGCAT
 TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
 GGTGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGATT
 TGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
 CTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
 GTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAAA
 GGTCTAGAGCCTTGAAAAACAGGCGATCTATTGCAATTAGACCAAGTA
 AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
 ATTTATCAGCTTGGTATGAAAGATGCTAAAGTGGGATGCCTGAGCTGAA
 TAGTTATCTAATGAAA

PRETTY of: /biotmp/msa47199.2{*} February 19, 2003 05:51 ..

| | | | |
|---------------------------|-------------|-------------|------------|
| | 1 | | 50 |
| msa47199.2{394_A909} | ----CCTATGT | TGTCGTGTTGG | TTTAGTTTTA |
| msa47199.2{394_H36B} | ----CCTATGT | TGTCGTGTTGG | TTTAGTTTTA |
| msa47199.2{394_JM9130013} | ----CCTATGT | TGTCGTGTTGG | TTTAGTTTTA |
| msa47199.2{394_090} | ----CCTATGT | TGTCGTGTTGG | TTTAGTTTTA |
| msa47199.2{394_18RS21} | ----CCTATGT | TGTCGTGTTGG | TTTAGTTTTA |
| msa47199.2{394_2603} | ttgCCTATGT | TGTCGTGTTGG | TTTAGTTTTA |
| msa47199.2{394_CJB110} | ----CCTATGT | TGTCGTGTTGG | TTTAGTTTTA |
| msa47199.2{394_COH1} | ----CCTATGT | TGTCGTGTTGG | TTTAGTTTTA |
| msa47199.2{394_M732} | ----CCTATGT | TGTCGTGTTGG | TTTAGTTTTA |
| msa47199.2{394_M781} | ----CCTATGT | TGTCGTGTTGG | TTTAGTTTTA |
| msa47199.2{394_1169NT} | ----CCTATGT | TGTCGTGTTGG | TTTAGTTTTA |
| Consensus | ***** | ***** | ***** |
| | 51 | | 100 |
| msa47199.2{394_A909} | TCCTTATACT | GCTGGAGTTT | TAGATGCTTT |
| msa47199.2{394_H36B} | TCCTTATACT | GCTGGAGTTT | TAGATGCTTT |
| msa47199.2{394_JM9130013} | TCCTTATACT | GCTGGAGTTT | TAGATGCTTT |

Table 77: Comparative Sequences relating toSAG2059

| | | | | | |
|---------------------------|------------|------------|-------------|------------|-------------|
| msa47199.2{394_090} | TCTTTATACT | GCTGGAGTTT | TAGATGCTTT | TCTAGATGCA | GGAATAAAAA |
| msa47199.2{394_18RS21} | TCTTTATACT | GCTGGAGTTT | TAGATGCTTT | TCTAGATGCA | GGAATAAAAA |
| msa47199.2{394_2603} | TCTTTATACT | GCTGGAGTTT | TAGATGCTTT | TCTAGATGCA | GGAATAAAAA |
| msa47199.2{394_CJB110} | TCTTTATACT | GCTGGAGTTT | TAGATGCTTT | TCTAGATGCA | GGAATAAAAA |
| msa47199.2{394_COH1} | TCTTTATACT | GCTGGAGTTT | TAGATGCTTT | TCTAGATGCA | GGAATAAAAA |
| msa47199.2{394_M732} | TCTTTATACT | GCTGGAGTTT | TAGATGCTTT | TCTAGATGCA | GGAATAAAAA |
| msa47199.2{394_M781} | TCTTTATACT | GCTGGAGTTT | TAGATGCTTT | TCTAGATGCA | GGAATAAAAA |
| msa47199.2{394_1169NT} | TCTTTATACT | GCTGGAGTTT | TAGATGCTTT | TCTAGATGCA | GGAATAAAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa47199.2{394_A909} | TAGATGGTAT | CaTATCTGTC | TCTGCTGGTG | CATTGTTTGG | TGTTAAATTTT |
| msa47199.2{394_H36B} | TAGATGGTAT | CaTATCTGTC | TCTGCTGGTG | CATTGTTTGG | TGTTAAATTTT |
| msa47199.2{394_JM9130013} | TAGATGGTAT | CaTATCTGTC | TCTGCTGGTG | CATTGTTTGG | TGTTAAATTTT |
| msa47199.2{394_090} | TAGATGGTAT | CgTATCTGTC | TCTGCTGGTG | CATTGTTTGG | TGTTAAATTTT |
| msa47199.2{394_18RS21} | TAGATGGTAT | CgTATCTGTC | TCTGCTGGTG | CATTGTTTGG | TGTTAAATTTT |
| msa47199.2{394_2603} | TAGATGGTAT | CgTATCTGTC | TCTGCTGGTG | CATTGTTTGG | TGTTAAATTTT |
| msa47199.2{394_CJB110} | TAGATGGTAT | CgTATCTGTC | TCTGCTGGTG | CATTGTTTGG | TGTTAAATTTT |
| msa47199.2{394_COH1} | TAGATGGTAT | CgTATCTGTC | TCTGCTGGTG | CATTGTTTGG | TGTTAAATTTT |
| msa47199.2{394_M732} | TAGATGGTAT | CgTATCTGTC | TCTGCTGGTG | CATTGTTTGG | TGTTAAATTTT |
| msa47199.2{394_M781} | TAGATGGTAT | CgTATCTGTC | TCTGCTGGTG | CATTGTTTGG | TGTTAAATTTT |
| msa47199.2{394_1169NT} | TAGATGGTAT | CgTATCTGTC | TCTGCTGGTG | CATTGTTTGG | TGTTAAATTTT |
| Consensus | ***** | *-***** | *****-**** | ***** | ***** |
| msa47199.2{394_A909} | GTATCTAGAC | AACGAGAGAG | GGCTTTGCGA | TACAATAAAA | AGTATTTTATC |
| msa47199.2{394_H36B} | GTATCTAGAC | AACGAGAGAG | GGCTTTGCGA | TACAATAAAA | AGTATTTTATC |
| msa47199.2{394_JM9130013} | GTATCTAGAC | AACGAGAGAG | GGCTTTGCGA | TACAATAAAA | AGTATTTTATC |
| msa47199.2{394_090} | GTATCTAGAC | AACGAGAGAG | GGCTTTGCGA | TACAATAAAA | AGTATTTTATC |
| msa47199.2{394_18RS21} | GTATCTAGAC | AACGAGAGAG | GGCTTTGCGA | TACAATAAAA | AGTATTTTATC |
| msa47199.2{394_2603} | GTATCTAGAC | AACGAGAGAG | GGCTTTGCGA | TACAATAAAA | AGTATTTTATC |
| msa47199.2{394_CJB110} | GTATCTAGAC | AACGAGAGAG | GGCTTTGCGA | TACAATAAAA | AGTATTTTATC |
| msa47199.2{394_COH1} | GTATCTAGAC | AACGAGAGAG | GGCTTTGCGA | TACAATAAAA | AGTATTTTATC |
| msa47199.2{394_M732} | GTATCTAGAC | AACGAGAGAG | GGCTTTGCGA | TACAATAAAA | AGTATTTTATC |
| msa47199.2{394_M781} | GTATCTAGAC | AACGAGAGAG | GGCTTTGCGA | TACAATAAAA | AGTATTTTATC |
| msa47199.2{394_1169NT} | GTATCTAGAC | AACGAGAGAG | GGCTTTGCGA | TACAATAAAA | AGTATTTTATC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa47199.2{394_A909} | CCACCCTaAA | TATATGAGTC | TAAGgTCATG | GcTTcGAACA | GGGAATTTTG |
| msa47199.2{394_H36B} | CCACCCTaAA | TATATGAGTC | TAAGgTCATG | GcTTcGAACA | GGGAATTTTG |
| msa47199.2{394_JM9130013} | CCACCCTaAA | TATATGAGTC | TAAGgTCATG | GcTTcGAACA | GGGAATTTTG |
| msa47199.2{394_090} | CCACCCTaAA | TATATGAGTC | TAAGgTCATG | GcTTcGAACA | GGGAATTTTG |
| msa47199.2{394_18RS21} | CCACCCTaAA | TATATGAGTC | TAAGgTCATG | GcTTcGAACA | GGGAATTTTG |
| msa47199.2{394_2603} | CCACCCTaAA | TATATGAGTC | TAAGgTCATG | GcTTcGAACA | GGGAATTTTG |
| msa47199.2{394_CJB110} | CCACCCTaAA | TATATGAGTC | TAAGgTCATG | GcTTcGAACA | GGGAATTTTG |
| msa47199.2{394_COH1} | CCACCCTgAA | TATATGAGTC | TAAGaTCATG | GcTTcGAACA | GGGAATTTTG |
| msa47199.2{394_M732} | CCACCCTgAA | TATATGAGTC | TAAGaTCATG | GcTTcGAACA | GGGAATTTTG |
| msa47199.2{394_M781} | CCACCCTgAA | TATATGAGTC | TAAGaTCATG | GcTTcGAACA | GGGAATTTTG |
| msa47199.2{394_1169NT} | CCACCCTaAA | TATATGAGTC | TAAGaTCATG | GcTTcGAACA | GGGAATTTTG |
| Consensus | *****-** | ***** | *****-***** | *-***** | ***** |
| msa47199.2{394_A909} | TTAATAAAGA | TTTCACCTAT | TATGAAGTTC | CTATGAAATT | GGATGTATTT |
| msa47199.2{394_H36B} | TTAATAAAGA | TTTCACCTAT | TATGAAGTTC | CTATGAAATT | GGATGTATTT |
| msa47199.2{394_JM9130013} | TTAATAAAGA | TTTCACCTAT | TATGAAGTTC | CTATGAAATT | GGATGTATTT |
| msa47199.2{394_090} | TTAATAAAGA | TTTCACCTAT | TATGAAGTTC | CTATGAAATT | GGATGTATTT |
| msa47199.2{394_18RS21} | TTAATAAAGA | TTTCACCTAT | TATGAAGTTC | CTATGAAATT | GGATGTATTT |
| msa47199.2{394_2603} | TTAATAAAGA | TTTCACCTAT | TATGAAGTTC | CTATGAAATT | GGATGTATTT |
| msa47199.2{394_CJB110} | TTAATAAAGA | TTTCACCTAT | TATGAAGTTC | CTATGAAATT | GGATGTATTT |
| msa47199.2{394_COH1} | TTAATAAAGA | TTTCACCTAT | TATGAAGTTC | CTATGAAATT | GGATGTATTT |
| msa47199.2{394_M732} | TTAATAAAGA | TTTCACCTAT | TATGAAGTTC | CTATGAAATT | GGATGTATTT |
| msa47199.2{394_M781} | TTAATAAAGA | TTTCACCTAT | TATGAAGTTC | CTATGAAATT | GGATGTATTT |
| msa47199.2{394_1169NT} | TTAATAAAGA | TTTCACCTAT | TATGAAGTTC | CTATGAAATT | GGATGTATTT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa47199.2{394_A909} | GACGATGAAG | CATTTAAAAA | ATCAAGTATT | GATTTTTACG | cAGTTGCTAC |
| msa47199.2{394_H36B} | GACGATGAAG | CATTTAAAAA | ATCAAGTATT | GATTTTTACG | cAGTTGCTAC |
| msa47199.2{394_JM9130013} | GACGATGAAG | CATTTAAAAA | ATCAAGTATT | GATTTTTACG | cAGTTGCTAC |
| msa47199.2{394_090} | GACGATGAAG | CATTTAAAAA | ATCAAGTATT | GATTTTTACG | cAGTTGCTAC |
| msa47199.2{394_18RS21} | GACGATGAAG | CATTTAAAAA | ATCAAGTATT | GATTTTTACG | cAGTTGCTAC |
| msa47199.2{394_2603} | GACGATGAAG | CATTTAAAAA | ATCAAGTATT | GATTTTTACG | cAGTTGCTAC |
| msa47199.2{394_CJB110} | GACGATGAAG | CATTTAAAAA | ATCAAGTATT | GATTTTTACG | cAGTTGCTAC |
| msa47199.2{394_COH1} | GACGATGAAG | CATTTAAAAA | ATCAAGTATT | GATTTTTACG | cAGTTGCTAC |
| msa47199.2{394_M732} | GACGATGAAG | CATTTAAAAA | ATCAAGTATT | GATTTTTACG | cAGTTGCTAC |
| msa47199.2{394_M781} | GACGATGAAG | CATTTAAAAA | ATCAAGTATT | GATTTTTACG | cAGTTGCTAC |
| msa47199.2{394_1169NT} | GACGATGAAG | CATTTAAAAA | ATCAAGTATT | GATTTTTACG | cAGTTGCTAC |
| Consensus | ***** | ***** | ***** | ***** | -***** |
| msa47199.2{394_A909} | AGAGATGACA | TCTGGTAAAC | CTGAgTATTT | TAAAATTGAT | AGTGTtTTTG |
| msa47199.2{394_H36B} | AGAGATGACA | TCTGGTAAAC | CTGAgTATTT | TAAAATTGAT | AGTGTtTTTG |

Table 77: Comparative Sequences relating toSAG2059

| | | | | | |
|---------------------------|-------------|------------|------------|------------|------------|
| msa47199.2{394_JM9130013} | AGAGATGACA | TCTGGTAAAC | CTGAgTATTT | TAAAATTGAT | AGTGTtTTTG |
| msa47199.2{394_090} | AGAGATGACA | TCTGGTAAAC | CTGAaTATTT | TAAAATTGAT | AGTGTtTTTG |
| msa47199.2{394_18RS21} | AGAGATGACA | TCTGGTAAAC | CTGAaTATTT | TAAAATTGAT | AGTGTtTTTG |
| msa47199.2{394_2603} | AGAGATGACA | TCTGGTAAAC | CTGAaTATTT | TAAAATTGAT | AGTGTtTTTG |
| msa47199.2{394_CJB110} | AGAGATGACA | TCTGGTAAAC | CTGAaTATTT | TAAAATTGAT | AGTGTtTTTG |
| msa47199.2{394_COH1} | AGAGATGACA | TCTGGTAAAC | CTGAaTATTT | TAAAATTGAT | AGTGTtTTTG |
| msa47199.2{394_M732} | AGAGATGACA | TCTGGTAAAC | CTGAaTATTT | TAAAATTGAT | AGTGTtTTTG |
| msa47199.2{394_M781} | AGAGATGACA | TCTGGTAAAC | CTGAaTATTT | TAAAATTGAT | AGTGTtTTTG |
| msa47199.2{394_1169NT} | AGAGATGACA | TCTGGTAAAC | CTGAaTATTT | TAAAATTGAT | AGTGTtTTTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa47199.2{394_A909} | AACAAATGGA | AATTTTACGT | GCTAGTTCAG | CATTACCAGT | AGTCTCAAAG |
| msa47199.2{394_H36B} | AACAAATGGA | AATTTTACGT | GCTAGTTCAG | CATTACCAGT | AGTCTCAAAG |
| msa47199.2{394_JM9130013} | AACAAATGGA | AATTTTACGT | GCTAGTTCAG | CATTACCAGT | AGTCTCAAAG |
| msa47199.2{394_090} | AACAAATGGA | AATTTTACGT | GCTAGTTCAG | CATTACCAGT | AGTCTCAAAG |
| msa47199.2{394_18RS21} | AACAAATGGA | AATTTTACGT | GCTAGTTCAG | CATTACCAGT | AGTCTCAAAG |
| msa47199.2{394_2603} | AACAAATGGA | AATTTTACGT | GCTAGTTCAG | CATTACCAGT | AGTCTCAAAG |
| msa47199.2{394_CJB110} | AACAAATGGA | AATTTTACGT | GCTAGTTCAG | CATTACCAGT | AGTCTCAAAG |
| msa47199.2{394_COH1} | AACAAATGGA | AATTTTACGT | GCTAGTTCAG | CATTACCAGT | AGTCTCAAAG |
| msa47199.2{394_M732} | AACAAATGGA | AATTTTACGT | GCTAGTTCAG | CATTACCAGT | AGTCTCAAAG |
| msa47199.2{394_M781} | AACAAATGGA | AATTTTACGT | GCTAGTTCAG | CATTACCAGT | AGTCTCAAAG |
| msa47199.2{394_1169NT} | AACAAATGGA | AATTTTACGT | GCTAGTTCAG | CATTACCAGT | AGTCTCAAAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa47199.2{394_A909} | ATGGTTGtTT | GGCAGGGGAA | AAAGTACTTA | GATGGTGGTT | TATCTGATAG |
| msa47199.2{394_H36B} | ATGGTTGtTT | GGCAGGGGAA | AAAGTACTTA | GATGGTGGTT | TATCTGATAG |
| msa47199.2{394_JM9130013} | ATGGTTGtTT | GGCAGGGGAA | AAAGTACTTA | GATGGTGGTT | TATCTGATAG |
| msa47199.2{394_090} | ATGGTTGtTT | GGCAGGGGAA | AAAGTACTTA | GATGGTGGTT | TATCTGATAG |
| msa47199.2{394_18RS21} | ATGGTTGtTT | GGCAGGGGAA | AAAGTACTTA | GATGGTGGTT | TATCTGATAG |
| msa47199.2{394_2603} | ATGGTTGtTT | GGCAGGGGAA | AAAGTACTTA | GATGGTGGTT | TATCTGATAG |
| msa47199.2{394_CJB110} | ATGGTTGtTT | GGCAGGGGAA | AAAGTACTTA | GATGGTGGTT | TATCTGATAG |
| msa47199.2{394_COH1} | ATGGTTGtTT | GGCAGGGGAA | AAAGTACTTA | GATGGTGGTT | TATCTGATAG |
| msa47199.2{394_M732} | ATGGTTGtTT | GGCAGGGGAA | AAAGTACTTA | GATGGTGGTT | TATCTGATAG |
| msa47199.2{394_M781} | ATGGTTGtTT | GGCAGGGGAA | AAAGTACTTA | GATGGTGGTT | TATCTGATAG |
| msa47199.2{394_1169NT} | ATGGTTGtTT | GGCAGGGGAA | AAAGTACTTA | GATGGTGGTT | TATCTGATAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa47199.2{394_A909} | TATtCCCCGTT | GATTTTGCCC | GTGGTTTAGG | ATTGACAAG | TTGATTGTTG |
| msa47199.2{394_H36B} | TATtCCCCGTT | GATTTTGCCC | GTGGTTTAGG | ATTGACAAG | TTGATTGTTG |
| msa47199.2{394_JM9130013} | TATtCCCCGTT | GATTTTGCCC | GTGGTTTAGG | ATTGACAAG | TTGATTGTTG |
| msa47199.2{394_090} | TATtCCCCGTT | GATTTTGCCC | GTGGTTTAGG | ATTGACAAG | TTGATTGTTG |
| msa47199.2{394_18RS21} | TATtCCCCGTT | GATTTTGCCC | GTGGTTTAGG | ATTGACAAG | TTGATTGTTG |
| msa47199.2{394_2603} | TATtCCCCGTT | GATTTTGCCC | GTGGTTTAGG | ATTGACAAG | TTGATTGTTG |
| msa47199.2{394_CJB110} | TATtCCCCGTT | GATTTTGCCC | GTGGTTTAGG | ATTGACAAG | TTGATTGTTG |
| msa47199.2{394_COH1} | TATtCCCCGTT | GATTTTGCCC | GTGGTTTAGG | ATTGACAAG | TTGATTGTTG |
| msa47199.2{394_M732} | TATtCCCCGTT | GATTTTGCCC | GTGGTTTAGG | ATTGACAAG | TTGATTGTTG |
| msa47199.2{394_M781} | TATtCCCCGTT | GATTTTGCCC | GTGGTTTAGG | ATTGACAAG | TTGATTGTTG |
| msa47199.2{394_1169NT} | TATtCCCCGTT | GATTTTGCCC | GTGGTTTAGG | ATTGACAAG | TTGATTGTTG |
| Consensus | ***-***** | ***** | ***** | ***** | ***** |
| msa47199.2{394_A909} | TGATGACTAG | GCCGCTCAAT | TATCAGAAAA | AGCCTTCAAG | TGGACGATTG |
| msa47199.2{394_H36B} | TGATGACTAG | GCCGCTCAAT | TATCAGAAAA | AGCCTTCAAG | TGGACGATTG |
| msa47199.2{394_JM9130013} | TGATGACTAG | GCCGCTCAAT | TATCAGAAAA | AGCCTTCAAG | TGGACGATTG |
| msa47199.2{394_090} | TGATGACTAG | GCCGCTCAAT | TATCAGAAAA | AGCCTTCAAG | TGGACGATTG |
| msa47199.2{394_18RS21} | TGATGACTAG | GCCGCTCAAT | TATCAGAAAA | AGCCTTCAAG | TGGACGATTG |
| msa47199.2{394_2603} | TGATGACTAG | GCCGCTCAAT | TATCAGAAAA | AGCCTTCAAG | TGGACGATTG |
| msa47199.2{394_CJB110} | TGATGACTAG | GCCGCTCAAT | TATCAGAAAA | AGCCTTCAAG | TGGACGATTG |
| msa47199.2{394_COH1} | TGATGACTAG | GCCGCTCAAT | TATCAGAAAA | AGCCTTCAAG | TGGACGATTG |
| msa47199.2{394_M732} | TGATGACTAG | GCCGCTCAAT | TATCAGAAAA | AGCCTTCAAG | TGGACGATTG |
| msa47199.2{394_M781} | TGATGACTAG | GCCGCTCAAT | TATCAGAAAA | AGCCTTCAAG | TGGACGATTG |
| msa47199.2{394_1169NT} | TGATGACTAG | GCCGCTCAAT | TATCAGAAAA | AGCCTTCAAG | TGGACGATTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa47199.2{394_A909} | TATAAAACTC | TGTATAGGAA | ATATCCTAAT | TTTGTAAGA | CAGCCTCGAA |
| msa47199.2{394_H36B} | TATAAAACTC | TGTATAGGAA | ATATCCTAAT | TTTGTAAGA | CAGCCTCGAA |
| msa47199.2{394_JM9130013} | TATAAAACTC | TGTATAGGAA | ATATCCTAAT | TTTGTAAGA | CAGCCTCGAA |
| msa47199.2{394_090} | TATAAAACTC | TGTATAGGAA | ATATCCTAAT | TTTGTAAGA | CAGCCTCGAA |
| msa47199.2{394_18RS21} | TATAAAACTC | TGTATAGGAA | ATATCCTAAT | TTTGTAAGA | CAGCCTCGAA |
| msa47199.2{394_2603} | TATAAAACTC | TGTATAGGAA | ATATCCTAAT | TTTGTAAGA | CAGCCTCGAA |
| msa47199.2{394_CJB110} | TATAAAACTC | TGTATAGGAA | ATATCCTAAT | TTTGTAAGA | CAGCCTCGAA |
| msa47199.2{394_COH1} | TATAAAACTC | TGTATAGGAA | ATATCCTAAT | TTTGTAAGA | CAGCCTCGAA |
| msa47199.2{394_M732} | TATAAAACTC | TGTATAGGAA | ATATCCTAAT | TTTGTAAGA | CAGCCTCGAA |
| msa47199.2{394_M781} | TATAAAACTC | TGTATAGGAA | ATATCCTAAT | TTTGTAAGA | CAGCCTCGAA |
| msa47199.2{394_1169NT} | TATAAAACTC | TGTATAGGAA | ATATCCTAAT | TTTGTAAGA | CAGCCTCGAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa47199.2{394_A909} | cCGGTACCAA | CAGTATAATA | ATAGcCTTGA | AAAGGTCATG | AGCCTTGAAA |
| | | | | | |

Table 77: Comparative Sequences relating to SAG2059

| | | | | | |
|---------------------------|------------|------------|------------|------------|------------|
| msa47199.2{394_H36B} | cCGGTACCAA | CAGTATAATA | ATAGcCTTGA | AAAGGTCATG | AGCCTTGAAA |
| msa47199.2{394_JM9130013} | cCGGTACCAA | CAGTATAATA | ATAGcCTTGA | AAAGGTCATG | AGCCTTGAAA |
| msa47199.2{394_090} | tCGGTACCAA | CAGTATAATA | ATAGtCTTGA | AAAGGTCATG | AGCCTTGAAA |
| msa47199.2{394_18RS21} | tCGGTACCAA | CAGTATAATA | ATAGtCTTGA | AAAGGTCATG | AGCCTTGAAA |
| msa47199.2{394_2603} | tCGGTACCAA | CAGTATAATA | ATAGtCTTGA | AAAGGTCATG | AGCCTTGAAA |
| msa47199.2{394_CJB110} | tCGGTACCAA | CAGTATAATA | ATAGtCTTGA | AAAGGTCATG | AGCCTTGAAA |
| msa47199.2{394_COH1} | tCGGTACCAA | CAGTATAATA | ATAGtCTTGA | AAAGGTCATG | AGCCTTGAAA |
| msa47199.2{394_M732} | tCGGTACCAA | CAGTATAATA | ATAGtCTTGA | AAAGGTCATG | AGCCTTGAAA |
| msa47199.2{394_M781} | tCGGTACCAA | CAGTATAATA | ATAGtCTTGA | AAAGGTCATG | AGCCTTGAAA |
| msa47199.2{394_1169NT} | tCGGTACCAA | CAGTATAATA | ATAGcCTTGA | AAAGGTCATG | AGCCTTGAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa47199.2{394_A909} | AAACAGGCGA | TCTATTTGCA | ATTAGaCCaA | GTAAGAGCTT | GGTTATTGgC |
| msa47199.2{394_H36B} | AAACAGGCGA | TCTATTTGCA | ATTAGaCCaA | GTAAGAGCTT | GGTTATTGgC |
| msa47199.2{394_JM9130013} | AAACAGGCGA | TCTATTTGCA | ATTAGaCCaA | GTAAGAGCTT | GGTTATTGgC |
| msa47199.2{394_090} | AAACAGGCGA | TCTATTTGCA | ATTAGaCCgA | GTAAGAGCTT | GGTTATTGgC |
| msa47199.2{394_18RS21} | AAACAGGCGA | TCTATTTGCA | ATTAGaCCgA | GTAAGAGCTT | GGTTATTGgC |
| msa47199.2{394_2603} | AAACAGGCGA | TCTATTTGCA | ATTAGaCCgA | GTAAGAGCTT | GGTTATTGgC |
| msa47199.2{394_CJB110} | AAACAGGCGA | TCTATTTGCA | ATTAGaCCgA | GTAAGAGCTT | GGTTATTGgC |
| msa47199.2{394_COH1} | AAACAGGCGA | TCTATTTGCA | ATTAGaCCgA | GTAAGAGCTT | GGTTATTGgC |
| msa47199.2{394_M732} | AAACAGGCGA | TCTATTTGCA | ATTAGaCCgA | GTAAGAGCTT | GGTTATTGgC |
| msa47199.2{394_M781} | AAACAGGCGA | TCTATTTGCA | ATTAGaCCgA | GTAAGAGCTT | GGTTATTGgC |
| msa47199.2{394_1169NT} | AAACAGGCGA | TCTATTTGCA | ATTAGgCCgA | GTAAaAGCTT | GGTTATTGtC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa47199.2{394_A909} | CGCTTAGAGA | AGAATCCGGA | TAAACTTGAT | AGTATTTATC | AGCTTGGTAT |
| msa47199.2{394_H36B} | CGCTTAGAGA | AGAATCCGGA | TAAACTTGAT | AGTATTTATC | AGCTTGGTAT |
| msa47199.2{394_JM9130013} | CGCTTAGAGA | AGAATCCGGA | TAAACTTGAT | AGTATTTATC | AGCTTGGTAT |
| msa47199.2{394_090} | CGCTTAGAGA | AGAATCCGGA | TAAACTTGAT | AGTATTTATC | AGCTTGGTAT |
| msa47199.2{394_18RS21} | CGCTTAGAGA | AGAATCCGGA | TAAACTTGAT | AGTATTTATC | AGCTTGGTAT |
| msa47199.2{394_2603} | CGCTTAGAGA | AGAATCCGGA | TAAACTTGAT | AGTATTTATC | AGCTTGGTAT |
| msa47199.2{394_CJB110} | CGCTTAGAGA | AGAATCCGGA | TAAACTTGAT | AGTATTTATC | AGCTTGGTAT |
| msa47199.2{394_COH1} | CGCTTAGAGA | AGAATCCGGA | TAAACTTGAT | AGTATTTATC | AGCTTGGTAT |
| msa47199.2{394_M732} | CGCTTAGAGA | AGAATCCGGA | TAAACTTGAT | AGTATTTATC | AGCTTGGTAT |
| msa47199.2{394_M781} | CGCTTAGAGA | AGAATCCGGA | TAAACTTGAT | AGTATTTATC | AGCTTGGTAT |
| msa47199.2{394_1169NT} | CGCTTAGAGA | AGAATCCGGA | TAAACTTGAT | AGTATTTATC | AGCTTGGTAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa47199.2{394_A909} | GAAAgATGCT | AAAAGTGgGA | TGCCTGAGCT | GAATAGTTAT | CTAATGAAA |
| msa47199.2{394_H36B} | GAAAgATGCT | AAAAGTGgGA | TGCCTGAGCT | GAATAGTTAT | CTAATGAAA |
| msa47199.2{394_JM9130013} | GAAAgATGCT | AAAAGTGgGA | TGCCTGAGCT | GAATAGTTAT | CTAATGAAA |
| msa47199.2{394_090} | GAAAgATGCT | AAAAGTGtGA | TGCCTGAGCT | GAATAGTTAT | CTAATGAAA |
| msa47199.2{394_18RS21} | GAAAgATGCT | AAAAGTGtGA | TGCCTGAGCT | GAATAGTTAT | CTAATGAAA |
| msa47199.2{394_2603} | GAAAgATGCT | AAAAGTGtGA | TGCCTGAGCT | GAATAGTTAT | CTAATGAAA |
| msa47199.2{394_CJB110} | GAAAgATGCT | AAAAGTGtGA | TGCCTGAGCT | GAATAGTTAT | CTAATGAAA |
| msa47199.2{394_COH1} | GAAAtATGCT | AAAAGTGtGA | TGCCTGAGCT | GAATAGTTAT | CTAATGAAA |
| msa47199.2{394_M732} | GAAAtATGCT | AAAAGTGtGA | TGCCTGAGCT | GAATAGTTAT | CTAATGAAA |
| msa47199.2{394_M781} | GAAAtATGCT | AAAAGTGtGA | TGCCTGAGCT | GAATAGTTAT | CTAATGAAA |
| msa47199.2{394_1169NT} | GAAAgATGCT | AAAAGTGtGA | TGCCTGAGCT | GAATAGTTAT | CTAATGAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |

SEQ ID NO. 7712

STRAIN 2603 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKYLKSHPKYMSLRSLRWTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IIVMTRPLNYQKKPSSGRLYKTYLRKYPNFVKTASNRYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSMPELNSYLMK

SEQ ID NO. 7713

STRAIN 090 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKYLKSHPKYMSLRSLRWTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IIVMTRPLNYQKKPSSGRLYKTYLRKYPNFVKTASNRYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSMPELNSYLMK

SEQ ID NO. 7714

STRAIN A909 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIIISVSAGALFGVNFVSRQRERLRY
 NKYLKSHPKYMSLRSLRWTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYAVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IIVMTRPLNYQKKPSSGRLYKTYLRKYPNFVKTASNRYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSMPELNSYLMK

SEQ ID NO. 7715

STRAIN H36B frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIIISVSAGALFGVNFVSRQRERLRY
 NKYLKSHPKYMSLRSLRWTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYAVATEMTS

Table 77: Comparative Sequences relating to SAG2059

GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7716

STRAIN 18RS21 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7717

STRAIN M732 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7718

STRAIN COH1 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7719

STRAIN M781 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7720

STRAIN CJB110 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7721

STRAIN JM9130013 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIISVSAGALFGVNFVSRQRERALRY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7722

STRAIN 1169NT frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKCYLSHPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVVAEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

| | | | | | |
|---------------------------|------------|------------|-------------|-------------|------------|
| | 1 | | | | 50 |
| msa47322.2{394_A909} | PMLSVGLVLE | GGGMRGLYTA | GVLDAPFLDAG | IKVDGIISVS | AGALFGVNFV |
| msa47322.2{394_H36B} | PMLSVGLVLE | GGGMRGLYTA | GVLDAPFLDAG | IKVDGIISVS | AGALFGVNFV |
| msa47322.2{394_JM9130013} | PMLSVGLVLE | GGGMRGLYTA | GVLDAPFLDAG | IKVDGIISVS | AGALFGVNFV |
| msa47322.2{394_090} | PMLSVGLVLE | GGGMRGLYTA | GVLDAPFLDAG | IKIDGIISVS | AGALFGVNFV |
| msa47322.2{394_1169NT} | PMLSVGLVLE | GGGMRGLYTA | GVLDAPFLDAG | IKIDGIISVS | AGALFGVNFV |
| msa47322.2{394_18RS21} | PMLSVGLVLE | GGGMRGLYTA | GVLDAPFLDAG | IKIDGIISVS | AGALFGVNFV |
| msa47322.2{394_2603} | PMLSVGLVLE | GGGMRGLYTA | GVLDAPFLDAG | IKIDGIISVS | AGALFGVNFV |
| msa47322.2{394_CJB110} | PMLSVGLVLE | GGGMRGLYTA | GVLDAPFLDAG | IKIDGIISVS | AGALFGVNFV |
| msa47322.2{394_COH1} | PMLSVGLVLE | GGGMRGLYTA | GVLDAPFLDAG | IKIDGIISVS | AGALFGVNFV |
| msa47322.2{394_M732} | PMLSVGLVLE | GGGMRGLYTA | GVLDAPFLDAG | IKIDGIISVS | AGALFGVNFV |
| msa47322.2{394_M781} | PMLSVGLVLE | GGGMRGLYTA | GVLDAPFLDAG | IKIDGIISVS | AGALFGVNFV |
| Consensus | ***** | ***** | ***** | **--***--** | ***** |
| | 51 | | | | 100 |
| msa47322.2{394_A909} | SRQRERALRY | NKKYLSHPkY | MSLRSLwRTG | NFVNKDFTYY | EVPMKLDVFD |
| msa47322.2{394_H36B} | SRQRERALRY | NKKYLSHPkY | MSLRSLwRTG | NFVNKDFTYY | EVPMKLDVFD |
| msa47322.2{394_JM9130013} | SRQRERALRY | NKKYLSHPkY | MSLRSLwRTG | NFVNKDFTYY | EVPMKLDVFD |
| msa47322.2{394_090} | SRQRERALRY | NKKYLSHPkY | MSLRSLwRTG | NFVNKDFTYY | EVPMKLDVFD |
| msa47322.2{394_1169NT} | SRQRERALRY | NKKYLSHPkY | MSLRSLwRTG | NFVNKDFTYY | EVPMKLDVFD |
| msa47322.2{394_18RS21} | SRQRERALRY | NKKYLSHPkY | MSLRSLwRTG | NFVNKDFTYY | EVPMKLDVFD |

Table 77: Comparative Sequences relating toSAG2059

| | | | | | |
|---------------------------|-------------|------------|------------|------------|------------|
| msa47322.2{394_2603} | SRQRERALRY | NKKYLSHPkY | MSLRSWfRTG | NFVNKDFTYY | EVPMKLDVFD |
| msa47322.2{394_CJB110} | SRQRERALRY | NKKYLSHPkY | MSLRSWfRTG | NFVNKDFTYY | EVPMKLDVFD |
| msa47322.2{394_COH1} | SRQRERALRY | NKKYLSHPeY | MSLRSWlRTG | NFVNKDFTYY | EVPMKLDVFD |
| msa47322.2{394_M732} | SRQRERALRY | NKKYLSHPeY | MSLRSWlRTG | NFVNKDFTYY | EVPMKLDVFD |
| msa47322.2{394_M781} | SRQRERALRY | NKKYLSHPeY | MSLRSWlRTG | NFVNKDFTYY | EVPMKLDVFD |
| Consensus | ***** | *****-* | *****-*** | ***** | ***** |
| msa47322.2{394_A909} | DEAFKKSSID | FYaVATEMTS | GKPEYFKIDS | VFEQMEILRA | SSALPVVSKM |
| msa47322.2{394_H36B} | DEAFKKSSID | FYaVATEMTS | GKPEYFKIDS | VFEQMEILRA | SSALPVVSKM |
| msa47322.2{394_JM9130013} | DEAFKKSSID | FYaVATEMTS | GKPEYFKIDS | VFEQMEILRA | SSALPVVSKM |
| msa47322.2{394_090} | DEAFKKSSID | FYaVATEMTS | GKPEYFKIDS | VFEQMEILRA | SSALPVVSKM |
| msa47322.2{394_1169NT} | DEAFKKSSID | FYaVATEMTS | GKPEYFKIDS | VFEQMEILRA | SSALPVVSKM |
| msa47322.2{394_18RS21} | DEAFKKSSID | FYaVATEMTS | GKPEYFKIDS | VFEQMEILRA | SSALPVVSKM |
| msa47322.2{394_2603} | DEAFKKSSID | FYaVATEMTS | GKPEYFKIDS | VFEQMEILRA | SSALPVVSKM |
| msa47322.2{394_CJB110} | DEAFKKSSID | FYaVATEMTS | GKPEYFKIDS | VFEQMEILRA | SSALPVVSKM |
| msa47322.2{394_COH1} | DEAFKKSSID | FYaVATEMTS | GKPEYFKIDS | VFEQMEILRA | SSALPVVSKM |
| msa47322.2{394_M732} | DEAFKKSSID | FYaVATEMTS | GKPEYFKIDS | VFEQMEILRA | SSALPVVSKM |
| msa47322.2{394_M781} | DEAFKKSSID | FYaVATEMTS | GKPEYFKIDS | VFEQMEILRA | SSALPVVSKM |
| Consensus | ***** | **_***** | ***** | ***** | ***** |
| msa47322.2{394_A909} | VvWQGGKKYLD | GGLSDSIPVD | FARGLGFDKL | IVVMTRPLNY | QKKPSSGRLY |
| msa47322.2{394_H36B} | VvWQGGKKYLD | GGLSDSIPVD | FARGLGFDKL | IVVMTRPLNY | QKKPSSGRLY |
| msa47322.2{394_JM9130013} | VvWQGGKKYLD | GGLSDSIPVD | FARGLGFDKL | IVVMTRPLNY | QKKPSSGRLY |
| msa47322.2{394_090} | VdWQGGKKYLD | GGLSDSIPVD | FARGLGFDKL | IVVMTRPLNY | QKKPSSGRLY |
| msa47322.2{394_1169NT} | VdWQGGKKYLD | GGLSDSIPVD | FARGLGFDKL | IVVMTRPLNY | QKKPSSGRLY |
| msa47322.2{394_18RS21} | VdWQGGKKYLD | GGLSDSIPVD | FARGLGFDKL | IVVMTRPLNY | QKKPSSGRLY |
| msa47322.2{394_2603} | VdWQGGKKYLD | GGLSDSIPVD | FARGLGFDKL | IVVMTRPLNY | QKKPSSGRLY |
| msa47322.2{394_CJB110} | VdWQGGKKYLD | GGLSDSIPVD | FARGLGFDKL | IVVMTRPLNY | QKKPSSGRLY |
| msa47322.2{394_COH1} | VdWQGGKKYLD | GGLSDSIPVD | FARGLGFDKL | IVVMTRPLNY | QKKPSSGRLY |
| msa47322.2{394_M732} | VdWQGGKKYLD | GGLSDSIPVD | FARGLGFDKL | IVVMTRPLNY | QKKPSSGRLY |
| msa47322.2{394_M781} | VdWQGGKKYLD | GGLSDSIPVD | FARGLGFDKL | IVVMTRPLNY | QKKPSSGRLY |
| Consensus | *_****** | ***** | ***** | ***** | ***** |
| msa47322.2{394_A909} | KTLYRKYPNF | VKTASNRYQQ | YNNLEKVMS | LEKTGDLFAI | RPSKSLVIGR |
| msa47322.2{394_H36B} | KTLYRKYPNF | VKTASNRYQQ | YNNLEKVMS | LEKTGDLFAI | RPSKSLVIGR |
| msa47322.2{394_JM9130013} | KTLYRKYPNF | VKTASNRYQQ | YNNLEKVMS | LEKTGDLFAI | RPSKSLVIGR |
| msa47322.2{394_090} | KTLYRKYPNF | VKTASNRYQQ | YNNLEKVMS | LEKTGDLFAI | RPSKSLVIGR |
| msa47322.2{394_1169NT} | KTLYRKYPNF | VKTASNRYQQ | YNNLEKVMS | LEKTGDLFAI | RPSKSLVIGR |
| msa47322.2{394_18RS21} | KTLYRKYPNF | VKTASNRYQQ | YNNLEKVMS | LEKTGDLFAI | RPSKSLVIGR |
| msa47322.2{394_2603} | KTLYRKYPNF | VKTASNRYQQ | YNNLEKVMS | LEKTGDLFAI | RPSKSLVIGR |
| msa47322.2{394_CJB110} | KTLYRKYPNF | VKTASNRYQQ | YNNLEKVMS | LEKTGDLFAI | RPSKSLVIGR |
| msa47322.2{394_COH1} | KTLYRKYPNF | VKTASNRYQQ | YNNLEKVMS | LEKTGDLFAI | RPSKSLVIGR |
| msa47322.2{394_M732} | KTLYRKYPNF | VKTASNRYQQ | YNNLEKVMS | LEKTGDLFAI | RPSKSLVIGR |
| msa47322.2{394_M781} | KTLYRKYPNF | VKTASNRYQQ | YNNLEKVMS | LEKTGDLFAI | RPSKSLVIGR |
| Consensus | ***** | ***** | ***** | ***** | *****_* |
| msa47322.2{394_A909} | LEKNPDKLDS | IYQLGMKdAK | SgMPELNSYL | MK | |
| msa47322.2{394_H36B} | LEKNPDKLDS | IYQLGMKdAK | SgMPELNSYL | MK | |
| msa47322.2{394_JM9130013} | LEKNPDKLDS | IYQLGMKdAK | SgMPELNSYL | MK | |
| msa47322.2{394_090} | LEKNPDKLDS | IYQLGMKdAK | SvMPELNSYL | MK | |
| msa47322.2{394_1169NT} | LEKNPDKLDS | IYQLGMKdAK | SvMPELNSYL | MK | |
| msa47322.2{394_18RS21} | LEKNPDKLDS | IYQLGMKdAK | SvMPELNSYL | MK | |
| msa47322.2{394_2603} | LEKNPDKLDS | IYQLGMKdAK | SvMPELNSYL | MK | |
| msa47322.2{394_CJB110} | LEKNPDKLDS | IYQLGMKdAK | SvMPELNSYL | MK | |
| msa47322.2{394_COH1} | LEKNPDKLDS | IYQLGMKyAK | SvMPELNSYL | MK | |
| msa47322.2{394_M732} | LEKNPDKLDS | IYQLGMKyAK | SvMPELNSYL | MK | |
| msa47322.2{394_M781} | LEKNPDKLDS | IYQLGMKyAK | SvMPELNSYL | MK | |
| Consensus | ***** | *****_* | *_****** | ** | |

Table 78: Comparative Sequences relating to SAG1016

SEQ ID NO. 7801

STRAIN 2603

ATGAAAGTTTGTAGTGTGATGATGAACCAAGTTGCACGTAACGAATTAATTTACCTTCTT
 AATAAGATGATTTCTAACCTCGTTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCT
 ATTTTACTTAGAGAACTTTTGTAGTAGCACTGTTAGATATCCATCTCAGAGATGATTCT
 GGGTTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTTGCG
 ACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGATTATTTGTTA
 AAACCCCTATGATTTTGTAGGCTAAAGCAAGCTATGGATAGAGTAAAGGAGCGCTAAGT
 ACATCTACAATTTATAGAGAGCGTAACCTCCGGTCTCTCTTCAAGCAACAGTATCCATG
 ACAGTAGAAGATCGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATG
 CAAGGAAAACTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAA
 CAATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTACATCGCTCTTACATTGTG
 AACATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCAACACTTCAGTTACACCTT
 TGTATAAAATAACAGTTCCTGTTAGCAGAGCAATGTAAACCCCTAAACAAATGTTA
 GGCATATCTACC

SEQ ID NO. 7802

STRAIN 090

AAAGTTTGTAGTGTGATGATGAACCAAGTTGCACGTAA
 CGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
 AGGCGCATGATATGGCTACTGCACTAGCTATTTTACTTAGAGAACTTTT
 GATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATT
 AGCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTTGCGA
 CTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGAT
 TATTTGTAAACCCCTATGATTTTGTAGGCTAAAGCAAGCTATGGATAG
 AGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCG
 GTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTAT
 CTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACT
 GATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAAC
 AATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTACATCGCTCT
 TACATTGTGAACATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCA
 AACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAG
 CAAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7803

STRAIN A909

AAAGTTTGTAGTGTGATGATGAACCAAGTTGCACGTAA
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
 GCGCATGATATGGCTACTGCACTAGCTATTTTACTTAGAGAACTTTT
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTCGCGAC
 TGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAACCCCTATGAGTTTGTAGGCTAAAGCAAGCTATGGATAGA
 GTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCG
 CCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG
 ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAACA
 ATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTGACCGCTCTT
 ACATTGTGAATATTAAATGCTATTAAACGATTGAACCTTGGTTTAAACCA
 ACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAG
 AAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7804

STRAIN H36B

AAAGTTTGTAGTGTGATGATGAACCAAGTTGCACGT
 AACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGC
 AGAGGCGCATGATATGGCTACTGCACTAGCTATTTTACTTAGAGAACTT
 TTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAA
 TTAGCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTCGC
 GACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTG
 ATTATTTGTTAAACCCCTATGAGTTTGTAGGCTAAAGCAAGCTATGGAT
 AGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTC
 CGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCT
 ATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAA
 CTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACA
 ACAATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTGACCGCT
 CTTACATTGTGAATATTAAATGCTATTAAACGATTGAACCTTGGTTTAAAC
 CAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAG
 AGCAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7805

STRAIN 18RS21

AAAGTTTGTAGTGTGATGATGAACCAAGTTGCACGTAA
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
 GCGCATGATATGGCTACTGCACTAGCTATTTTACTTAGAGAACTTTT
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTTGCGAC
 TGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAACCCCTATGATTTTGTAGGCTAAAGCAAGCTATGGATAGA
 GTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG

Table 78: Comparative Sequences relating to SAG1016

ATTATACAAACACCTGATAAAATTTATGAAATTTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
 ACATTTGTGAACATTAAATGCTATTAAAAACGATTGAACCTTGGTTTAAACCA
 ACATTTGAGTTACACCTTTGTAATAAAATAACAGTTCTCTGTTAGCAGAGC
 AAATGTAAACCCCTAAACCAAATGTTAGGCATATCTACC

SEQ ID NO. 7806

STRAIN M732

AAAGTTTTAGTAGTTGATGATGAACCAAGTT
 GCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGT
 TATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAG
 AAATTTTGTAGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGG
 TTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCAACCAATTATTGAT
 ATTCGCGACTGCTTATGATCAATATGCTATTCAAGGCTTTTGAGCAGGATG
 CGCGTGATTATTTGTTAAACCCCTATGAGTTTGTAGGTTAAAGCAAGCT
 ATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGT
 AGCTTCCGGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATC
 GAATCTATCTGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCAA
 GGAAAACTGATTATACAAACACCTGATAAAAAATTATGAAATTTGATGGCTC
 TCTACAACCAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTAC
 ATCGCTCTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGG
 TTTAACCAACACCTTCAAGTTACACCTTTGTAATAAAATAACAGTTCTCTG
 TAGCAGAGCAATGTAAACCCCTAAACCAAATGTTAGGCATATCTACC

SEQ ID NO. 7807

STRAIN COH1

AAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTA
 ACCAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCA
 GAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAACTTT
 TGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAAT
 TAGCAGAGTATATCAATAAAATGCCAAACCAACCAATTATTGATATTCGCG
 ACTGCTTATGATCAATATGCTATTCAAGGCTTTTGAGCAGGATGCGCGTGA
 TTTATTTGTTAAACCCCTATGAGTTTGTAGGTTAAAGCAAGCTATGGATA
 GAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCC
 GGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTA
 TCTGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCAAGGAAAC
 TGATTATACAAACACCTGATAAAAAATTATGAAATTTGATGGCTCTCTACA
 CAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTC
 TTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGGTTTAAAC
 AAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCTCTGTTAGCAGA
 GCAATGTAAACCCCTAAACCAAATGTTAGGCATATCTACC

SEQ ID NO. 7808

STRAIN M781

AAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTAAC
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAACTTTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCAACCAATTATTGATATTCGCGAC
 TGCTTATGATCAATATGCTATTCAAGGCTTTTGAGCAGGATGCGCGTGATT
 ATTTGTTAAAAACCCCTATGAGTTTGTAGGTTAAAGCAAGCTATGGATAGA
 GTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCCGG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCAAGGAAACCTG
 ATTATACAAACACCTGATAAAAAATTATGAAATTTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
 ACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCA
 ACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCTCTGTTAGCAGAGC
 AAATGTAAACCCCTAAACCAAATGTTAGGCATATCTACC

SEQ ID NO. 7809

STRAIN CJB110

CTTAATAAGTATGATTCTAACCTCGTTATAGCAGAGGCGCATGATATGGC
 TACTGCATTAGCTATTTTACTTAGAGAACTTTTGATGTAGCACTGTTAG
 ATATCCATCTCAGAGATGATTCTGGGTTGCAATTAGCAGAGTATATCAAT
 AAAATGCCAAACCAACCAATTATTGATATTCGCGACTGCTTATGATCAATA
 TGCTATTCAAGCTTTTGAGCATGATGCGCGTGATTATTTGTTAAACCCCT
 ATGAGTTTGTAGGCTAAAGCAAGTATGATAGAGTAAAGGAGCGCTA
 AGTACATCTACAATTATAGAGAGCGTAACCTTCGGCCCTCTCTTCAAGCA
 ACAGTATCCATTGACAGTAGAAGATnGAATCTATCTGGTGTGCGCGGATG
 ATATCCTTTTGATTGAAGCTATGCAAGGAAACCTGATTATACAAACACCT
 GATAAAAAATTATGAAATTTGATGGCTCTCTACAACAATGGCAAGATAAACT
 ACCATCATCTCAATTTGTACGGGTGCAACCGCTCTTACATTGTGAATATTA
 ATGCTATTAACGAGATTGAACCTTGGTTTAAACCAACACTTCAGTTACAC
 CTTTGTAAATAAAATAACAGTTCTCTGTTAGCAGAGCAATGTAAACCCCT
 AAAACAAATGTTAGG

SEQ ID NO. 7810

STRAIN 1169NT

AAAGTTTTAGTAGTTGATGATGAACCAAG
 TTGCACGTAACGAATTAATTTATCTTCTTAATAAGTATGATTCTAACCTC
 GTTATAGCAGAGGCGCATGATATAGCTACTGCATTAGCTATTTTACTTAG

Table 78: Comparative Sequences relating to SAG1016

AGAAACCTTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTG
GGTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACTATTATG
ATATTCCGCACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGA
TGCCTGTGATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAG
CTATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGC
GTAACCTTCCGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGA
TCGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGC
AAGGAAAACGTATTATACAAACACCTGATAAAAATTATGAAATTGATGGC
TCTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGT
GCACCGCTCTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTT
GGTTTAAACCAACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCTC
GTTAGCAGAGCAAATGTAAACCCCTAAACAAATGTTAGGCATATCTAC
C

SEQ ID NO. 7811

STRAIN JM9130013

AAAGTTTGTAGTGTGATGATGAACCACT

TGCACGTAAACGAATTAATTACCTTCTTAATAAGTATGATTCTAACCTCG
TTATAGCAGAGGCGCATGATATGGCTACTGCAATTAGCTATTTTACTTAGA
GAAACTTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGG
GTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACTATTATG
TATTCCGCACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGAT
GCGCGTGATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAGC
TATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCG
TAACCTTCCGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGAT
CGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCA
AGGAAAACCTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCT
CTCTACACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTG
CACCGCTCTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTG
GTTTAAACCAACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCTC
TTAGCAGAGCAAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa141507.2{ *} April 10, 2003 06:36 ..

| | | | |
|----------------------------|-------------|------------|----------------------------------|
| | 1 | | 50 |
| msa141507.2{399_A909} | ----aaagttt | tagtagttga | tgatgaacca gttgcacgta acgaattaat |
| msa141507.2{399_CJB110} | ----- | ----- | ----- |
| msa141507.2{399_H36B} | ----aaagttt | tagtagttga | tgatgaacca gttgcacgta acgaattaat |
| msa141507.2{399_JM9130013} | ----aaagttt | tagtagttga | tgatgaacca gttgcacgta acgaattaat |
| msa141507.2{399_1169NT} | ----aaagttt | tagtagttga | tgatgaacca gttgcacgta acgaattaat |
| msa141507.2{399_090} | ----aaagttt | tagtagttga | tgatgaacca gttgcacgta acgaattaat |
| msa141507.2{399_18RS21} | ----aaagttt | tagtagttga | tgatgaacca gttgcacgta acgaattaat |
| msa141507.2{399_2603} | atgaaagttt | tagtagttga | tgatgaacca gttgcacgta acgaattaat |
| msa141507.2{399_COH1} | ----aaagttt | tagtagttga | tgatgaacca gttgcacgta acgaattaat |
| msa141507.2{399_M732} | ----aaagttt | tagtagttga | tgatgaacca gttgcacgta acgaattaat |
| msa141507.2{399_M781} | ----aaagttt | tagtagttga | tgatgaacca gttgcacgta acgaattaat |
| Consensus | ***** | ----- | ----- |
| | 51 | | 100 |
| msa141507.2{399_A909} | ttaccttCTT | AATAAGTATG | ATTCTAACCT CGTTATAGCA GAGGCGCATG |
| msa141507.2{399_CJB110} | -----CTT | AATAAGTATG | ATTCTAACCT CGTTATAGCA GAGGCGCATG |
| msa141507.2{399_H36B} | ttaccttCTT | AATAAGTATG | ATTCTAACCT CGTTATAGCA GAGGCGCATG |
| msa141507.2{399_JM9130013} | ttaccttCTT | AATAAGTATG | ATTCTAACCT CGTTATAGCA GAGGCGCATG |
| msa141507.2{399_1169NT} | ttatcttCTT | AATAAGTATG | ATTCTAACCT CGTTATAGCA GAGGCGCATG |
| msa141507.2{399_090} | ttaccttCTT | AATAAGTATG | ATTCTAACCT CGTTATAGCA GAGGCGCATG |
| msa141507.2{399_18RS21} | ttaccttCTT | AATAAGTATG | ATTCTAACCT CGTTATAGCA GAGGCGCATG |
| msa141507.2{399_2603} | ttaccttCTT | AATAAGTATG | ATTCTAACCT CGTTATAGCA GAGGCGCATG |
| msa141507.2{399_COH1} | ttaccttCTT | AATAAGTATG | ATTCTAACCT CGTTATAGCA GAGGCGCATG |
| msa141507.2{399_M732} | ttaccttCTT | AATAAGTATG | ATTCTAACCT CGTTATAGCA GAGGCGCATG |
| msa141507.2{399_M781} | ttaccttCTT | AATAAGTATG | ATTCTAACCT CGTTATAGCA GAGGCGCATG |
| Consensus | ----- | ***** | ***** |
| | 101 | | 150 |
| msa141507.2{399_A909} | ATATgGCTAC | TGCATTAGCT | ATTTTACTTA GAGAACTTT TGATGTAGCA |
| msa141507.2{399_CJB110} | ATATgGCTAC | TGCATTAGCT | ATTTTACTTA GAGAACTTT TGATGTAGCA |
| msa141507.2{399_H36B} | ATATgGCTAC | TGCATTAGCT | ATTTTACTTA GAGAACTTT TGATGTAGCA |
| msa141507.2{399_JM9130013} | ATATgGCTAC | TGCATTAGCT | ATTTTACTTA GAGAACTTT TGATGTAGCA |
| msa141507.2{399_1169NT} | ATATgGCTAC | TGCATTAGCT | ATTTTACTTA GAGAACTTT TGATGTAGCA |
| msa141507.2{399_090} | ATATgGCTAC | TGCATTAGCT | ATTTTACTTA GAGAACTTT TGATGTAGCA |
| msa141507.2{399_18RS21} | ATATgGCTAC | TGCATTAGCT | ATTTTACTTA GAGAACTTT TGATGTAGCA |
| msa141507.2{399_2603} | ATATgGCTAC | TGCATTAGCT | ATTTTACTTA GAGAACTTT TGATGTAGCA |
| msa141507.2{399_COH1} | ATATgGCTAC | TGCATTAGCT | ATTTTACTTA GAGAACTTT TGATGTAGCA |
| msa141507.2{399_M732} | ATATgGCTAC | TGCATTAGCT | ATTTTACTTA GAGAACTTT TGATGTAGCA |
| msa141507.2{399_M781} | ATATgGCTAC | TGCATTAGCT | ATTTTACTTA GAGAACTTT TGATGTAGCA |
| Consensus | ***** | ***** | ***** |
| | 151 | | 200 |
| msa141507.2{399_A909} | CTGTTAGATA | TCCATCTCAG | AGATGATTCT GGGTTGCAAT TAGCAGAGTA |
| msa141507.2{399_CJB110} | CTGTTAGATA | TCCATCTCAG | AGATGATTCT GGGTTGCAAT TAGCAGAGTA |
| msa141507.2{399_H36B} | CTGTTAGATA | TCCATCTCAG | AGATGATTCT GGGTTGCAAT TAGCAGAGTA |
| msa141507.2{399_JM9130013} | CTGTTAGATA | TCCATCTCAG | AGATGATTCT GGGTTGCAAT TAGCAGAGTA |
| msa141507.2{399_1169NT} | CTGTTAGATA | TCCATCTCAG | AGATGATTCT GGGTTGCAAT TAGCAGAGTA |

Table 78: Comparative Sequences relating to SAG1016

| | | | | | |
|----------------------------|-------------|------------|------------|------------|-------------|
| msa141507.2{399_090} | CTGTTAGATA | TCCATCTCAG | AGATGATTCT | GGGTTGCAAT | TAGCAGAGTA |
| msa141507.2{399_18RS21} | CTGTTAGATA | TCCATCTCAG | AGATGATTCT | GGGTTGCAAT | TAGCAGAGTA |
| msa141507.2{399_2603} | CTGTTAGATA | TCCATCTCAG | AGATGATTCT | GGGTTGCAAT | TAGCAGAGTA |
| msa141507.2{399_COH1} | CTGTTAGATA | TCCATCTCAG | AGATGATTCT | GGGTTGCAAT | TAGCAGAGTA |
| msa141507.2{399_M732} | CTGTTAGATA | TCCATCTCAG | AGATGATTCT | GGGTTGCAAT | TAGCAGAGTA |
| msa141507.2{399_M781} | CTGTTAGATA | TCCATCTCAG | AGATGATTCT | GGGTTGCAAT | TAGCAGAGTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa141507.2{399_A909} | TATCAATAAA | ATGCCCAAAC | CACCATTATT | GATATTcGCG | ACTGCTTATG |
| msa141507.2{399_CJB110} | TATCAATAAA | ATGCCCAAAC | CACCATTATT | GATATTcGCG | ACTGCTTATG |
| msa141507.2{399_H36B} | TATCAATAAA | ATGCCCAAAC | CACCATTATT | GATATTcGCG | ACTGCTTATG |
| msa141507.2{399_JM9130013} | TATCAATAAA | ATGCCCAAAC | CACCATTATT | GATATTcGCG | ACTGCTTATG |
| msa141507.2{399_1169NT} | TATCAATAAA | ATGCCCAAAC | CACCATTATT | GATATTcGCG | ACTGCTTATG |
| msa141507.2{399_090} | TATCAATAAA | ATGCCCAAAC | CACCATTATT | GATATTcGCG | ACTGCTTATG |
| msa141507.2{399_18RS21} | TATCAATAAA | ATGCCCAAAC | CACCATTATT | GATATTcGCG | ACTGCTTATG |
| msa141507.2{399_2603} | TATCAATAAA | ATGCCCAAAC | CACCATTATT | GATATTcGCG | ACTGCTTATG |
| msa141507.2{399_COH1} | TATCAATAAA | ATGCCCAAAC | CACCATTATT | GATATTcGCG | ACTGCTTATG |
| msa141507.2{399_M732} | TATCAATAAA | ATGCCCAAAC | CACCATTATT | GATATTcGCG | ACTGCTTATG |
| msa141507.2{399_M781} | TATCAATAAA | ATGCCCAAAC | CACCATTATT | GATATTcGCG | ACTGCTTATG |
| Consensus | ***** | ***** | ***** | *****-*** | ***** |
| msa141507.2{399_A909} | ATCAATATGC | TATTCAaGCT | TTTGAGCAtG | ATGCGCGTGA | TTATTTGTGA |
| msa141507.2{399_CJB110} | ATCAATATGC | TATTCAaGCT | TTTGAGCAtG | ATGCGCGTGA | TTATTTGTGA |
| msa141507.2{399_H36B} | ATCAATATGC | TATTCAaGCT | TTTGAGCAtG | ATGCGCGTGA | TTATTTGTGA |
| msa141507.2{399_JM9130013} | ATCAATATGC | TATTCAaGCT | TTTGAGCAtG | ATGCGCGTGA | TTATTTGTGA |
| msa141507.2{399_1169NT} | ATCAATATGC | TATTCAaGCT | TTTGAGCAtG | ATGCGCGTGA | TTATTTGTGA |
| msa141507.2{399_090} | ATCAATATGC | TATTCAaGCT | TTTGAGCAtG | ATGCGCGTGA | TTATTTGTGA |
| msa141507.2{399_18RS21} | ATCAATATGC | TATTCAaGCT | TTTGAGCAtG | ATGCGCGTGA | TTATTTGTGA |
| msa141507.2{399_2603} | ATCAATATGC | TATTCAaGCT | TTTGAGCAtG | ATGCGCGTGA | TTATTTGTGA |
| msa141507.2{399_COH1} | ATCAATATGC | TATTCAaGCT | TTTGAGCAtG | ATGCGCGTGA | TTATTTGTGA |
| msa141507.2{399_M732} | ATCAATATGC | TATTCAaGCT | TTTGAGCAtG | ATGCGCGTGA | TTATTTGTGA |
| msa141507.2{399_M781} | ATCAATATGC | TATTCAaGCT | TTTGAGCAtG | ATGCGCGTGA | TTATTTGTGA |
| Consensus | ***** | *****-*** | *****-* | ***** | ***** |
| msa141507.2{399_A909} | AAACCCCTATG | AgTTTGATAG | GcTAAAGCAA | GcTATGGATA | GAGTAAAAGG |
| msa141507.2{399_CJB110} | AAACCCCTATG | AgTTTGATAG | GcTAAAGCAA | GnTATGGATA | GAGTAAAAGG |
| msa141507.2{399_H36B} | AAACCCCTATG | AgTTTGATAG | GcTAAAGCAA | GcTATGGATA | GAGTAAAAGG |
| msa141507.2{399_JM9130013} | AAACCCCTATG | AgTTTGATAG | GcTAAAGCAA | GcTATGGATA | GAGTAAAAGG |
| msa141507.2{399_1169NT} | AAACCCCTATG | AgTTTGATAG | GcTAAAGCAA | GcTATGGATA | GAGTAAAAGG |
| msa141507.2{399_090} | AAACCCCTATG | AtTTTGATAG | GcTAAAGCAA | GcTATGGATA | GAGTAAAAGG |
| msa141507.2{399_18RS21} | AAACCCCTATG | AtTTTGATAG | GcTAAAGCAA | GcTATGGATA | GAGTAAAAGG |
| msa141507.2{399_2603} | AAACCCCTATG | AtTTTGATAG | GcTAAAGCAA | GcTATGGATA | GAGTAAAAGG |
| msa141507.2{399_COH1} | AAACCCCTATG | AgTTTGATAG | GtTAAAGCAA | GcTATGGATA | GAGTAAAAGG |
| msa141507.2{399_M732} | AAACCCCTATG | AgTTTGATAG | GtTAAAGCAA | GcTATGGATA | GAGTAAAAGG |
| msa141507.2{399_M781} | AAACCCCTATG | AgTTTGATAG | GtTAAAGCAA | GcTATGGATA | GAGTAAAAGG |
| Consensus | ***** | *-***** | *-***** | *-***** | ***** |
| msa141507.2{399_A909} | AGCGCTAAGT | ACATCTACAA | TTATAGAGAG | CGTAaCTTCC | GGcCCTCTCT |
| msa141507.2{399_CJB110} | AGCGCTAAGT | ACATCTACAA | TTATAGAGAG | CGTAaCTTCC | GGcCCTCTCT |
| msa141507.2{399_H36B} | AGCGCTAAGT | ACATCTACAA | TTATAGAGAG | CGTAaCTTCC | GGcCCTCTCT |
| msa141507.2{399_JM9130013} | AGCGCTAAGT | ACATCTACAA | TTATAGAGAG | CGTAaCTTCC | GGcCCTCTCT |
| msa141507.2{399_1169NT} | AGCGCTAAGT | ACATCTACAA | TTATAGAGAG | CGTAaCTTCC | GGcCCTCTCT |
| msa141507.2{399_090} | AGCGCTAAGT | ACATCTACAA | TTATAGAGAG | CGTAaCTTCC | GGcCCTCTCT |
| msa141507.2{399_18RS21} | AGCGCTAAGT | ACATCTACAA | TTATAGAGAG | CGTAaCTTCC | GGcCCTCTCT |
| msa141507.2{399_2603} | AGCGCTAAGT | ACATCTACAA | TTATAGAGAG | CGTAaCTTCC | GGcCCTCTCT |
| msa141507.2{399_COH1} | AGCGCTAAGT | ACATCTACAA | TTATAGAGAG | CGTAaCTTCC | GGcCCTCTCT |
| msa141507.2{399_M732} | AGCGCTAAGT | ACATCTACAA | TTATAGAGAG | CGTAaCTTCC | GGcCCTCTCT |
| msa141507.2{399_M781} | AGCGCTAAGT | ACATCTACAA | TTATAGAGAG | CGTAaCTTCC | GGcCCTCTCT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa141507.2{399_A909} | TCAAGCAACA | GTATCCATTG | ACAGTAGAAG | ATcGAATCTA | TCTGGTGTCTG |
| msa141507.2{399_CJB110} | TCAAGCAACA | GTATCCATTG | ACAGTAGAAG | ATnGAATCTA | TCTGGTGTCTG |
| msa141507.2{399_H36B} | TCAAGCAACA | GTATCCATTG | ACAGTAGAAG | ATcGAATCTA | TCTGGTGTCTG |
| msa141507.2{399_JM9130013} | TCAAGCAACA | GTATCCATTG | ACAGTAGAAG | ATcGAATCTA | TCTGGTGTCTG |
| msa141507.2{399_1169NT} | TCAAGCAACA | GTATCCATTG | ACAGTAGAAG | ATcGAATCTA | TCTGGTGTCTG |
| msa141507.2{399_090} | TCAAGCAACA | GTATCCATTG | ACAGTAGAAG | ATcGAATCTA | TCTGGTGTCTG |
| msa141507.2{399_18RS21} | TCAAGCAACA | GTATCCATTG | ACAGTAGAAG | ATcGAATCTA | TCTGGTGTCTG |
| msa141507.2{399_2603} | TCAAGCAACA | GTATCCATTG | ACAGTAGAAG | ATcGAATCTA | TCTGGTGTCTG |
| msa141507.2{399_COH1} | TCAAGCAACA | GTATCCATTG | ACAGTAGAAG | ATcGAATCTA | TCTGGTGTCTG |
| msa141507.2{399_M732} | TCAAGCAACA | GTATCCATTG | ACAGTAGAAG | ATcGAATCTA | TCTGGTGTCTG |
| msa141507.2{399_M781} | TCAAGCAACA | GTATCCATTG | ACAGTAGAAG | ATcGAATCTA | TCTGGTGTCTG |
| Consensus | ***** | ***** | ***** | **-***** | ***** |
| msa141507.2{399_A909} | GCGGATGATA | TCCTTTTGAT | TGAAGCTATG | CAAGGAAAAC | TGATTATACA |
| msa141507.2{399_CJB110} | GCGGATGATA | TCCTTTTGAT | TGAAGCTATG | CAAGGAAAAC | TGATTATACA |
| msa141507.2{399_H36B} | GCGGATGATA | TCCTTTTGAT | TGAAGCTATG | CAAGGAAAAC | TGATTATACA |
| msa141507.2{399_JM9130013} | GCGGATGATA | TCCTTTTGAT | TGAAGCTATG | CAAGGAAAAC | TGATTATACA |

Table 78: Comparative Sequences relating to SAG1016

| | | | | | |
|----------------------------|-----------------|------------|------------|-----------------|------------|
| msa141507.2{399_1169NT} | GCGGATGATA | TCCTTTTGAT | TGAAGCTATG | CAAGGAAAAC | TGATTATACA |
| msa141507.2{399_090} | GCGGATGATA | TCCTTTTGAT | TGAAGCTATG | CAAGGAAAAC | TGATTATACA |
| msa141507.2{399_18RS21} | GCGGATGATA | TCCTTTTGAT | TGAAGCTATG | CAAGGAAAAC | TGATTATACA |
| msa141507.2{399_2603} | GCGGATGATA | TCCTTTTGAT | TGAAGCTATG | CAAGGAAAAC | TGATTATACA |
| msa141507.2{399_COH1} | GCGGATGATA | TCCTTTTGAT | TGAAGCTATG | CAAGGAAAAC | TGATTATACA |
| msa141507.2{399_M732} | GCGGATGATA | TCCTTTTGAT | TGAAGCTATG | CAAGGAAAAC | TGATTATACA |
| msa141507.2{399_M781} | GCGGATGATA | TCCTTTTGAT | TGAAGCTATG | CAAGGAAAAC | TGATTATACA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa141507.2{399_A909} | AACACCTGAT | AAAAATTATG | AAATTGATGG | CTCTCTACAA | CAATGGCAAG |
| msa141507.2{399_CJB110} | AACACCTGAT | AAAAATTATG | AAATTGATGG | CTCTCTACAA | CAATGGCAAG |
| msa141507.2{399_H36B} | AACACCTGAT | AAAAATTATG | AAATTGATGG | CTCTCTACAA | CAATGGCAAG |
| msa141507.2{399_JM9130013} | AACACCTGAT | AAAAATTATG | AAATTGATGG | CTCTCTACAA | CAATGGCAAG |
| msa141507.2{399_1169NT} | AACACCTGAT | AAAAATTATG | AAATTGATGG | CTCTCTACAA | CAATGGCAAG |
| msa141507.2{399_090} | AACACCTGAT | AAAAATTATG | AAATTGATGG | CTCTCTACAA | CAATGGCAAG |
| msa141507.2{399_18RS21} | AACACCTGAT | AAAAATTATG | AAATTGATGG | CTCTCTACAA | CAATGGCAAG |
| msa141507.2{399_2603} | AACACCTGAT | AAAAATTATG | AAATTGATGG | CTCTCTACAA | CAATGGCAAG |
| msa141507.2{399_COH1} | AACACCTGAT | AAAAATTATG | AAATTGATGG | CTCTCTACAA | CAATGGCAAG |
| msa141507.2{399_M732} | AACACCTGAT | AAAAATTATG | AAATTGATGG | CTCTCTACAA | CAATGGCAAG |
| msa141507.2{399_M781} | AACACCTGAT | AAAAATTATG | AAATTGATGG | CTCTCTACAA | CAATGGCAAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa141507.2{399_A909} | ATAAACTACC | ATCATCTCAA | TTTGTACGGG | TgCAcCGCTC | TTACATTGTG |
| msa141507.2{399_CJB110} | ATAAACTACC | ATCATCTCAA | TTTGTACGGG | TgCAcCGCTC | TTACATTGTG |
| msa141507.2{399_H36B} | ATAAACTACC | ATCATCTCAA | TTTGTACGGG | TgCAcCGCTC | TTACATTGTG |
| msa141507.2{399_JM9130013} | ATAAACTACC | ATCATCTCAA | TTTGTACGGG | TgCAcCGCTC | TTACATTGTG |
| msa141507.2{399_1169NT} | ATAAACTACC | ATCATCTCAA | TTTGTACGGG | TgCAcCGCTC | TTACATTGTG |
| msa141507.2{399_090} | ATAAACTACC | ATCATCTCAA | TTTGTACGGG | TaCatCGCTC | TTACATTGTG |
| msa141507.2{399_18RS21} | ATAAACTACC | ATCATCTCAA | TTTGTACGGG | TaCatCGCTC | TTACATTGTG |
| msa141507.2{399_2603} | ATAAACTACC | ATCATCTCAA | TTTGTACGGG | TaCatCGCTC | TTACATTGTG |
| msa141507.2{399_COH1} | ATAAACTACC | ATCATCTCAA | TTTGTACGGG | TaCatCGCTC | TTACATTGTG |
| msa141507.2{399_M732} | ATAAACTACC | ATCATCTCAA | TTTGTACGGG | TaCatCGCTC | TTACATTGTG |
| msa141507.2{399_M781} | ATAAACTACC | ATCATCTCAA | TTTGTACGGG | TaCatCGCTC | TTACATTGTG |
| Consensus | ***** | ***** | ***** | *_*_*_*_*_*_*_* | ***** |
| msa141507.2{399_A909} | AAtATTAATG | CTATTAAAC | GATTGAACCT | TGGTTTAACC | AAACACTTCA |
| msa141507.2{399_CJB110} | AAtATTAATG | CTATTAAAC | GATTGAACCT | TGGTTTAACC | AAACACTTCA |
| msa141507.2{399_H36B} | AAtATTAATG | CTATTAAAC | GATTGAACCT | TGGTTTAACC | AAACACTTCA |
| msa141507.2{399_JM9130013} | AAtATTAATG | CTATTAAAC | GATTGAACCT | TGGTTTAACC | AAACACTTCA |
| msa141507.2{399_1169NT} | AAtATTAATG | CTATTAAAC | GATTGAACCT | TGGTTTAACC | AAACACTTCA |
| msa141507.2{399_090} | AAtATTAATG | CTATTAAAC | GATTGAACCT | TGGTTTAACC | AAACACTTCA |
| msa141507.2{399_18RS21} | AAtATTAATG | CTATTAAAC | GATTGAACCT | TGGTTTAACC | AAACACTTCA |
| msa141507.2{399_2603} | AAtATTAATG | CTATTAAAC | GATTGAACCT | TGGTTTAACC | AAACACTTCA |
| msa141507.2{399_COH1} | AAtATTAATG | CTATTAAAC | GATTGAACCT | TGGTTTAACC | AAACACTTCA |
| msa141507.2{399_M732} | AAtATTAATG | CTATTAAAC | GATTGAACCT | TGGTTTAACC | AAACACTTCA |
| msa141507.2{399_M781} | AAtATTAATG | CTATTAAAC | GATTGAACCT | TGGTTTAACC | AAACACTTCA |
| Consensus | *_*_*_*_*_*_*_* | ***** | ***** | ***** | ***** |
| msa141507.2{399_A909} | GTTACACCTT | TGTAATAAAA | TAACAGTTCC | TGTTAGCAGA | GCAAATGTAA |
| msa141507.2{399_CJB110} | GTTACACCTT | TGTAATAAAA | TAACAGTTCC | TGTTAGCAGA | GCAAATGTAA |
| msa141507.2{399_H36B} | GTTACACCTT | TGTAATAAAA | TAACAGTTCC | TGTTAGCAGA | GCAAATGTAA |
| msa141507.2{399_JM9130013} | GTTACACCTT | TGTAATAAAA | TAACAGTTCC | TGTTAGCAGA | GCAAATGTAA |
| msa141507.2{399_1169NT} | GTTACACCTT | TGTAATAAAA | TAACAGTTCC | TGTTAGCAGA | GCAAATGTAA |
| msa141507.2{399_090} | GTTACACCTT | TGTAATAAAA | TAACAGTTCC | TGTTAGCAGA | GCAAATGTAA |
| msa141507.2{399_18RS21} | GTTACACCTT | TGTAATAAAA | TAACAGTTCC | TGTTAGCAGA | GCAAATGTAA |
| msa141507.2{399_2603} | GTTACACCTT | TGTAATAAAA | TAACAGTTCC | TGTTAGCAGA | GCAAATGTAA |
| msa141507.2{399_COH1} | GTTACACCTT | TGTAATAAAA | TAACAGTTCC | TGTTAGCAGA | GCAAATGTAA |
| msa141507.2{399_M732} | GTTACACCTT | TGTAATAAAA | TAACAGTTCC | TGTTAGCAGA | GCAAATGTAA |
| msa141507.2{399_M781} | GTTACACCTT | TGTAATAAAA | TAACAGTTCC | TGTTAGCAGA | GCAAATGTAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa141507.2{399_A909} | AACCCCTAAA | ACAAATGTTA | GGcatatcta | cc | |
| msa141507.2{399_CJB110} | AACCCCTAAA | ACAAATGTTA | GG----- | -- | |
| msa141507.2{399_H36B} | AACCCCTAAA | ACAAATGTTA | GGcatatcta | cc | |
| msa141507.2{399_JM9130013} | AACCCCTAAA | ACAAATGTTA | GGcatatcta | cc | |
| msa141507.2{399_1169NT} | AACCCCTAAA | ACAAATGTTA | GGcatatcta | cc | |
| msa141507.2{399_090} | AACCCCTAAA | ACAAATGTTA | GGcatatcta | cc | |
| msa141507.2{399_18RS21} | AACCCCTAAA | ACAAATGTTA | GGcatatcta | cc | |
| msa141507.2{399_2603} | AACCCCTAAA | ACAAATGTTA | GGcatatcta | cc | |
| msa141507.2{399_COH1} | AACCCCTAAA | ACAAATGTTA | GGcatatcta | cc | |
| msa141507.2{399_M732} | AACCCCTAAA | ACAAATGTTA | GGcatatcta | cc | |
| msa141507.2{399_M781} | AACCCCTAAA | ACAAATGTTA | GGcatatcta | cc | |
| Consensus | ***** | ***** | ***** | ***** | --- |

SEQ ID NO. 7812

STRAIN 2603 frame: 1

KVLVVDDEBPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPLLIIFATAYDQYAIQAFEHDDARDYLLKPYDFDRLKQAMDRVKGALST

Table 78: Comparative Sequences relating to SAG1016

STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7813

STRAIN 090 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7814

STRAIN A909 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7815

STRAIN H36B frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7816

STRAIN 18RS21 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7817

STRAIN M732 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7818

STRAIN COH1 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7819

STRAIN M781 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7820

STRAIN CJB110 frame: 1

LNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG LQLAEYINKMPKPPLLI F
ATAYDQYAI QAFEHDARDYLLKPYEFDRLKQXMDRVKGALSTSTIIESVTSGLPLFKQQYP
LTVEDXIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQWQDKLPSSQFVRVHRSYI
VNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQML

SEQ ID NO. 7821

STRAIN 1169NT frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDIATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7822

STRAIN JM9130013 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGLPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

Table 78: Comparative Sequences relating to SAG1016

PRETTY of: /biotmp/msa141801.2{*} April 10, 2003 06:38 ..

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| | 1 | | | | 50 |
| msa141801.2{399_COH1} | kvlvvddp | arneliy1LN | KYDSNLVIAE | AHDmATALAI | LLRETFDVAL |
| msa141801.2{399_M732} | kvlvvddp | arneliy1LN | KYDSNLVIAE | AHDmATALAI | LLRETFDVAL |
| msa141801.2{399_M781} | kvlvvddp | arneliy1LN | KYDSNLVIAE | AHDmATALAI | LLRETFDVAL |
| msa141801.2{399_090} | kvlvvddp | arneliy1LN | KYDSNLVIAE | AHDmATALAI | LLRETFDVAL |
| msa141801.2{399_18RS21} | kvlvvddp | arneliy1LN | KYDSNLVIAE | AHDmATALAI | LLRETFDVAL |
| msa141801.2{399_2603} | kvlvvddp | arneliy1LN | KYDSNLVIAE | AHDmATALAI | LLRETFDVAL |
| msa141801.2{399_A909} | kvlvvddp | arneliy1LN | KYDSNLVIAE | AHDmATALAI | LLRETFDVAL |
| msa141801.2{399_H36B} | kvlvvddp | arneliy1LN | KYDSNLVIAE | AHDmATALAI | LLRETFDVAL |
| msa141801.2{399_JM9130013} | kvlvvddp | arneliy1LN | KYDSNLVIAE | AHDmATALAI | LLRETFDVAL |
| msa141801.2{399_1169NT} | kvlvvddp | arneliy1LN | KYDSNLVIAE | AHDmATALAI | LLRETFDVAL |
| msa141801.2{399_CJB110} | -----LN | KYDSNLVIAE | AHDmATALAI | LLRETFDVAL | |
| Consensus | ----- | ***** | ***** | ***** | ***** |
| | 51 | | | | 100 |
| msa141801.2{399_COH1} | LDIHLRDDSG | LQLAEYINKM | PKPPLLIFAT | AYDQYAIQAF | EqDARDYLLK |
| msa141801.2{399_M732} | LDIHLRDDSG | LQLAEYINKM | PKPPLLIFAT | AYDQYAIQAF | EqDARDYLLK |
| msa141801.2{399_M781} | LDIHLRDDSG | LQLAEYINKM | PKPPLLIFAT | AYDQYAIQAF | EqDARDYLLK |
| msa141801.2{399_090} | LDIHLRDDSG | LQLAEYINKM | PKPPLLIFAT | AYDQYAIQAF | EhDARDYLLK |
| msa141801.2{399_18RS21} | LDIHLRDDSG | LQLAEYINKM | PKPPLLIFAT | AYDQYAIQAF | EhDARDYLLK |
| msa141801.2{399_2603} | LDIHLRDDSG | LQLAEYINKM | PKPPLLIFAT | AYDQYAIQAF | EhDARDYLLK |
| msa141801.2{399_A909} | LDIHLRDDSG | LQLAEYINKM | PKPPLLIFAT | AYDQYAIQAF | EhDARDYLLK |
| msa141801.2{399_H36B} | LDIHLRDDSG | LQLAEYINKM | PKPPLLIFAT | AYDQYAIQAF | EhDARDYLLK |
| msa141801.2{399_JM9130013} | LDIHLRDDSG | LQLAEYINKM | PKPPLLIFAT | AYDQYAIQAF | EhDARDYLLK |
| msa141801.2{399_1169NT} | LDIHLRDDSG | LQLAEYINKM | PKPPLLIFAT | AYDQYAIQAF | EhDARDYLLK |
| msa141801.2{399_CJB110} | LDIHLRDDSG | LQLAEYINKM | PKPPLLIFAT | AYDQYAIQAF | EhDARDYLLK |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 101 | | | | 150 |
| msa141801.2{399_COH1} | PYeFDRLKQa | MDRVKGALST | STIIESVaSG | PLFKQQYPLT | VEDrIYLVSA |
| msa141801.2{399_M732} | PYeFDRLKQa | MDRVKGALST | STIIESVaSG | PLFKQQYPLT | VEDrIYLVSA |
| msa141801.2{399_M781} | PYeFDRLKQa | MDRVKGALST | STIIESVaSG | PLFKQQYPLT | VEDrIYLVSA |
| msa141801.2{399_090} | PYdFDRLKQa | MDRVKGALST | STIIESVtSG | PLFKQQYPLT | VEDrIYLVSA |
| msa141801.2{399_18RS21} | PYdFDRLKQa | MDRVKGALST | STIIESVtSG | PLFKQQYPLT | VEDrIYLVSA |
| msa141801.2{399_2603} | PYdFDRLKQa | MDRVKGALST | STIIESVtSG | PLFKQQYPLT | VEDrIYLVSA |
| msa141801.2{399_A909} | PYeFDRLKQa | MDRVKGALST | STIIESVtSG | PLFKQQYPLT | VEDrIYLVSA |
| msa141801.2{399_H36B} | PYeFDRLKQa | MDRVKGALST | STIIESVtSG | PLFKQQYPLT | VEDrIYLVSA |
| msa141801.2{399_JM9130013} | PYeFDRLKQa | MDRVKGALST | STIIESVtSG | PLFKQQYPLT | VEDrIYLVSA |
| msa141801.2{399_1169NT} | PYeFDRLKQa | MDRVKGALST | STIIESVtSG | PLFKQQYPLT | VEDrIYLVSA |
| msa141801.2{399_CJB110} | PYeFDRLKQx | MDRVKGALST | STIIESVtSG | PLFKQQYPLT | VEDxIYLVSA |
| Consensus | **----- | ***** | ***** | ***** | ***** |
| | 151 | | | | 200 |
| msa141801.2{399_COH1} | DDILLIEAMQ | GKLIITPDK | NYEIDGSLQQ | WQDKLPSSQF | VRVHRSYIVN |
| msa141801.2{399_M732} | DDILLIEAMQ | GKLIITPDK | NYEIDGSLQQ | WQDKLPSSQF | VRVHRSYIVN |
| msa141801.2{399_M781} | DDILLIEAMQ | GKLIITPDK | NYEIDGSLQQ | WQDKLPSSQF | VRVHRSYIVN |
| msa141801.2{399_090} | DDILLIEAMQ | GKLIITPDK | NYEIDGSLQQ | WQDKLPSSQF | VRVHRSYIVN |
| msa141801.2{399_18RS21} | DDILLIEAMQ | GKLIITPDK | NYEIDGSLQQ | WQDKLPSSQF | VRVHRSYIVN |
| msa141801.2{399_2603} | DDILLIEAMQ | GKLIITPDK | NYEIDGSLQQ | WQDKLPSSQF | VRVHRSYIVN |
| msa141801.2{399_A909} | DDILLIEAMQ | GKLIITPDK | NYEIDGSLQQ | WQDKLPSSQF | VRVHRSYIVN |
| msa141801.2{399_H36B} | DDILLIEAMQ | GKLIITPDK | NYEIDGSLQQ | WQDKLPSSQF | VRVHRSYIVN |
| msa141801.2{399_JM9130013} | DDILLIEAMQ | GKLIITPDK | NYEIDGSLQQ | WQDKLPSSQF | VRVHRSYIVN |
| msa141801.2{399_1169NT} | DDILLIEAMQ | GKLIITPDK | NYEIDGSLQQ | WQDKLPSSQF | VRVHRSYIVN |
| msa141801.2{399_CJB110} | DDILLIEAMQ | GKLIITPDK | NYEIDGSLQQ | WQDKLPSSQF | VRVHRSYIVN |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 201 | | | | 243 |
| msa141801.2{399_COH1} | INAIKTIEPW | FNQTLQLHLC | NKITVPVSRA | NVKPLKQMLg | ist |
| msa141801.2{399_M732} | INAIKTIEPW | FNQTLQLHLC | NKITVPVSRA | NVKPLKQMLg | ist |
| msa141801.2{399_M781} | INAIKTIEPW | FNQTLQLHLC | NKITVPVSRA | NVKPLKQMLg | ist |
| msa141801.2{399_090} | INAIKTIEPW | FNQTLQLHLC | NKITVPVSRA | NVKPLKQMLg | ist |
| msa141801.2{399_18RS21} | INAIKTIEPW | FNQTLQLHLC | NKITVPVSRA | NVKPLKQMLg | ist |
| msa141801.2{399_2603} | INAIKTIEPW | FNQTLQLHLC | NKITVPVSRA | NVKPLKQMLg | ist |
| msa141801.2{399_A909} | INAIKTIEPW | FNQTLQLHLC | NKITVPVSRA | NVKPLKQMLg | ist |
| msa141801.2{399_H36B} | INAIKTIEPW | FNQTLQLHLC | NKITVPVSRA | NVKPLKQMLg | ist |
| msa141801.2{399_JM9130013} | INAIKTIEPW | FNQTLQLHLC | NKITVPVSRA | NVKPLKQMLg | ist |
| msa141801.2{399_1169NT} | INAIKTIEPW | FNQTLQLHLC | NKITVPVSRA | NVKPLKQMLg | ist |
| msa141801.2{399_CJB110} | INAIKTIEPW | FNQTLQLHLC | NKITVPVSRA | NVKPLKQML- | --- |
| Consensus | ***** | ***** | ***** | ***** | --- |

Table 79: Comparative Sequences relating to SAG2150

SEQ ID NO. 7901

STRAIN 2603

ATGGGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCCGGCACTCCTTTTGAAGGG
 CGTGCCCTTTTGGACGTCAATCTGAAAATGAAGATGCTTCTATACCGCGTTTCATTGGG
 CACACAGGTTCTGAAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACA
 AAAGGTGAGGTAATTTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATC
 AAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTCAGCTTTTGA
 GAGACAGTTTAAAGGATGTTGCTTTTGGACCAAAAATTTTGGTATTTCTCAGATTGAA
 GCTGAAAGGCTGGCTGAAGAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGAT
 AAAAAATCCATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTA
 GCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGA
 AGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTATCGTCTTA
 GTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTATGTGTATGTTTGAAGCA
 GGGAAAGTAACCTTATCAGGACAACCAAAACAGATTTTCAAGAAGTAGAAGCTTTTAGAA
 AGTAACAATTAGGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGA
 TTAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7902

STRAIN 090

GGAAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
 GGCACCTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAATTTGA
 AGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCTGGAAAATCAA
 CTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAAAGGTGAGGTA
 ATTGTGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
 ATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTCAGC
 TTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACCAAAAATTTT
 GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAGGTT
 AGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTTGAACCTTTCTG
 GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
 AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGGAAG
 AAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTA
 TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
 GTGTATGTTTGAAGCAGGGGAAAGTAACCTTATCAGGACAACCAAAACA
 GATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAAACAATTAGGAGTTCCCA
 AAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
 AGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7903

STRAIN A909

GGAAATTGAATTTAAAAATGTAAGTTATACCTATCAA
 GCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAAT
 TGAAGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCTGGAAAAT
 CAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAAAGGTGAG
 GTAATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAAT
 CAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTC
 AGCTTTTGAAGAGACAGTTTAAAGATGTTGCTTTTGGACCAAAAAT
 TTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAG
 GTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTTGAACCTTT
 CTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGA
 CCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATCCTAAGGG
 AAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGA
 CTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGAC
 TATGTGTATGTTTGAAGCAGGGGAAAGTAACCTTATCAGGACAACCAAA
 GCAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAAACAATTAGGAGTTT
 CCAAAATCACCAGTTTGTCTCAAAGGCTATCTCATAAGGGATTAAATTTA
 CCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGG
 A

SEQ ID NO. 7904

STRAIN H36B

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
 TGAAAATTTGAAGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
 AGGTGAGGTAATTTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTT
 GAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGGAAAGTAACCTTATCAGGAC
 AACCAAGCAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAAACAATTA
 GGAGTTCCCAAAATCACCAGTTTGTCTCAAAGGCTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7905

STRAIN 18RS21

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
 AGGTGAGGTAATGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGTTAGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATTT
 GAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7906

STRAIN M732

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
 TGAAAATTGAAGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
 AGGTGAGGTAATGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGTTAGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATTT
 GAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7907

STRAIN COH1

GGAAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
 GGCATCCTCTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAATTGA
 AGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAATCAA
 CTATTATGCAACTTTTGAATGGTTTACATATTCTACAAAAGGTGAGGTA
 ATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
 ATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTCAGC
 TTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
 GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAGGTT
 AGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATTTGAACCTTTCTG
 GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
 AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGAAG
 AAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTA
 TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
 GTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAAACA
 GATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTAGGAGTTCCCA
 AAATCACCAGTTTGCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
 AGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7908

STRAIN M781

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
 TGAAAATTGAAGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
 AGGTGAGGTAATGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGTTAGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATTT
 GAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7909

STRAIN CJB110

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATGAAGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCT
 GGAATTAACATATTATGCACTTTTGAATGGTTTACATATTCTTACAAA
 AGGTGAGGTAATGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAAC
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTCAATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGTGACTATGTGTATGTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7910

STRAIN 1169NT

GGAATGAATTTAAAAATGTAA

GTATACCTATCAAGCCGGCACTCTTTTGAAGGGCGTGCCCTTTTGGAC
 GTCAATCTGAAAATGAAGATGCTTCTATACCGCGTTTCATTGGGCACAC
 AGGTTCTGGAATAATCAACTATTATGCAACTTTTGAATGGTTTACATATT
 CTACAAAAGGTGAGGTAATTTGTGCGATGATTTTCTATTAAAGCAGGGGAC
 AAGAACAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTTCA
 ATTTCCAGAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTT
 TTGGACACACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCT
 GAAGAAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAA
 TCCATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTA
 TTTTAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGA
 CTTGATCTTAAGGGAAGAAAAGAAATTAATGACTCTTTTAAAAATCTTCA
 TAAAAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAG
 CGGATTATGCTGACTATGTGTATGTTTAGAAGCAGGGAAAGTAACCTTA
 TCAGGACCAACCAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAAAGTAA
 ACAATTAGGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATA
 AGGGATTAAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAG
 GCTATTAAAGCATGGA

SEQ ID NO. 7911

STRAIN JM9130013

GGAATGAATTTAAAAATGTAAAGTT

ATACCTATCAAGCCGGCACTCTTTTGAAGGGCGTGCCCTTTTGGACGTT
 AATCTGAAAATGAAGATGCTTCTATACCGCATTTCATTGGGCACACAGG
 TTCTGGAATAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTTA
 CAAAAGGTGAGGTAATTTGTGCGATGATTTTCTATTAAAGCAGGGGACAAG
 AACAAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTTCAAT
 TCCAGAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTG
 GACCACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAA
 GAAAAATTAAGGTTAGTTGGTATTAGTGAGGATTTATTCGATAAAAATCC
 ATTGAAGCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTT
 TAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTT
 GATCTTAAGGGAAGAAAAGAAATTAATGACTCTTTTAAAAATCTTCATAA
 AAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGG
 ATTATGCTGACTATGTGTATGTTTAGAAGCAGGGAAAGTAACCTTATCA
 GGACAACCAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAAAGTAAACA
 ATTAGGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGG
 GATTAAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCT
 ATTAAGCATGGA

PRETTY of: /biotmp/msa238454.2{*} May 14, 2003 06:55 ..

| | | | |
|----------------------------|-----------------------|-----------------------|------------|
| | 1 | | 50 |
| msa238454.2{401_A909} | ---GGAATTG AATTTAAAAA | TGTAAGTTAT ACCTATCAAG | CCGGCACTCC |
| msa238454.2{401_H36B} | ---GGAATTG AATTTAAAAA | TGTAAGTTAT ACCTATCAAG | CCGGCACTCC |
| msa238454.2{401_090} | ---GGAATTG AATTTAAAAA | TGTAAGTTAT ACCTATCAAG | CCGGCACTCC |
| msa238454.2{401_1169NT} | ---GGAATTG AATTTAAAAA | TGTAAGTTAT ACCTATCAAG | CCGGCACTCC |
| msa238454.2{401_18RS21} | ---GGAATTG AATTTAAAAA | TGTAAGTTAT ACCTATCAAG | CCGGCACTCC |
| msa238454.2{401_2603} | atgGGAATTG AATTTAAAAA | TGTAAGTTAT ACCTATCAAG | CCGGCACTCC |
| msa238454.2{401_CJB110} | ---GGAATTG AATTTAAAAA | TGTAAGTTAT ACCTATCAAG | CCGGCACTCC |
| msa238454.2{401_COH1} | ---GGAATTG AATTTAAAAA | TGTAAGTTAT ACCTATCAAG | CCGGCACTCC |
| msa238454.2{401_M732} | ---GGAATTG AATTTAAAAA | TGTAAGTTAT ACCTATCAAG | CCGGCACTCC |
| msa238454.2{401_M781} | ---GGAATTG AATTTAAAAA | TGTAAGTTAT ACCTATCAAG | CCGGCACTCC |
| msa238454.2{401_JM9130013} | ---GGAATTG AATTTAAAAA | TGTAAGTTAT ACCTATCAAG | CCGGCACTCC |
| Consensus | ***** | ***** | ***** |

| | | | |
|-------------------------|-----------------------|-----------------------|------------|
| | 51 | | 100 |
| msa238454.2{401_A909} | TTTTGAAGGG CGTGCCCTTT | TTGACGTcAA TCTGAAAATT | GAAGATGcTT |
| msa238454.2{401_H36B} | TTTTGAAGGG CGTGCCCTTT | TTGACGTcAA TCTGAAAATT | GAAGATGcTT |
| msa238454.2{401_090} | TTTTGAAGGG CGTGCCCTTT | TTGACGTcAA TCTGAAAATT | GAAGATGcTT |
| msa238454.2{401_1169NT} | TTTTGAAGGG CGTGCCCTTT | TTGACGTcAA TCTGAAAATT | GAAGATGcTT |
| msa238454.2{401_18RS21} | TTTTGAAGGG CGTGCCCTTT | TTGACGTcAA TCTGAAAATT | GAAGATGcTT |
| msa238454.2{401_2603} | TTTTGAAGGG CGTGCCCTTT | TTGACGTcAA TCTGAAAATT | GAAGATGcTT |
| msa238454.2{401_CJB110} | TTTTGAAGGG CGTGCCCTTT | TTGACGTcAA TCTGAAAATT | GAAGATGcTT |

Table 79: Comparative Sequences relating to SAG2150

| | | | | | |
|----------------------------|------------|------------|------------|-------------|-------------|
| msa238454.2{401_COH1} | TTTTGAAGGG | CGTGCCCTTT | TTGACGTcAA | TCTGAAAAAT | GAAGATGtTT |
| msa238454.2{401_M732} | TTTTGAAGGG | CGTGCCCTTT | TTGACGTcAA | TCTGAAAAAT | GAAGATGtTT |
| msa238454.2{401_M781} | TTTTGAAGGG | CGTGCCCTTT | TTGACGTcAA | TCTGAAAAAT | GAAGATGtTT |
| msa238454.2{401_JM9130013} | TTTTGAAGGG | CGTGCCCTTT | TTGACGTcAA | TCTGAAAAAT | GAAGATGcTT |
| Consensus | ***** | ***** | *****_* | ***** | *****_* |
| msa238454.2{401_A909} | CCTATACCGC | gTTCATTGGG | CACACAGGTT | CTGGAAAAATC | AACTATTATG |
| msa238454.2{401_H36B} | CCTATACCGC | gTTCATTGGG | CACACAGGTT | CTGGAAAAATC | AACTATTATG |
| msa238454.2{401_090} | CCTATACCGC | gTTCATTGGG | CACACAGGTT | CTGGAAAAATC | AACTATTATG |
| msa238454.2{401_1169NT} | CCTATACCGC | gTTCATTGGG | CACACAGGTT | CTGGAAAAATC | AACTATTATG |
| msa238454.2{401_18RS21} | CCTATACCGC | gTTCATTGGG | CACACAGGTT | CTGGAAAAATC | AACTATTATG |
| msa238454.2{401_2603} | CCTATACCGC | gTTCATTGGG | CACACAGGTT | CTGGAAAAATC | AACTATTATG |
| msa238454.2{401_CJB110} | CCTATACCGC | gTTCATTGGG | CACACAGGTT | CTGGAAAAATC | AACTATTATG |
| msa238454.2{401_COH1} | CCTATACCGC | gTTCATTGGG | CACACAGGTT | CTGGAAAAATC | AACTATTATG |
| msa238454.2{401_M732} | CCTATACCGC | gTTCATTGGG | CACACAGGTT | CTGGAAAAATC | AACTATTATG |
| msa238454.2{401_M781} | CCTATACCGC | gTTCATTGGG | CACACAGGTT | CTGGAAAAATC | AACTATTATG |
| msa238454.2{401_JM9130013} | CCTATACCGC | gTTCATTGGG | CACACAGGTT | CTGGAAAAATC | AACTATTATG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa238454.2{401_A909} | CAACTTTTGA | ATGGTTTACA | TATTCCTACA | AAAGGTGAGG | TAATTGTCTGA |
| msa238454.2{401_H36B} | CAACTTTTGA | ATGGTTTACA | TATTCCTACA | AAAGGTGAGG | TAATTGTCTGA |
| msa238454.2{401_090} | CAACTTTTGA | ATGGTTTACA | TATTCCTACA | AAAGGTGAGG | TAATTGTCTGA |
| msa238454.2{401_1169NT} | CAACTTTTGA | ATGGTTTACA | TATTCCTACA | AAAGGTGAGG | TAATTGTCTGA |
| msa238454.2{401_18RS21} | CAACTTTTGA | ATGGTTTACA | TATTCCTACA | AAAGGTGAGG | TAATTGTCTGA |
| msa238454.2{401_2603} | CAACTTTTGA | ATGGTTTACA | TATTCCTACA | AAAGGTGAGG | TAATTGTCTGA |
| msa238454.2{401_CJB110} | CAACTTTTGA | ATGGTTTACA | TATTCCTACA | AAAGGTGAGG | TAATTGTCTGA |
| msa238454.2{401_COH1} | CAACTTTTGA | ATGGTTTACA | TATTCCTACA | AAAGGTGAGG | TAATTGTCTGA |
| msa238454.2{401_M732} | CAACTTTTGA | ATGGTTTACA | TATTCCTACA | AAAGGTGAGG | TAATTGTCTGA |
| msa238454.2{401_M781} | CAACTTTTGA | ATGGTTTACA | TATTCCTACA | AAAGGTGAGG | TAATTGTCTGA |
| msa238454.2{401_JM9130013} | CAACTTTTGA | ATGGTTTACA | TATTCCTACA | AAAGGTGAGG | TAATTGTCTGA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa238454.2{401_A909} | TGATTTTTCT | ATTAAAGCAG | GGGACAAGAA | CAAAGAAATC | AAATTTATAA |
| msa238454.2{401_H36B} | TGATTTTTCT | ATTAAAGCAG | GGGACAAGAA | CAAAGAAATC | AAATTTATAA |
| msa238454.2{401_090} | TGATTTTTCT | ATTAAAGCAG | GGGACAAGAA | CAAAGAAATC | AAATTTATAA |
| msa238454.2{401_1169NT} | TGATTTTTCT | ATTAAAGCAG | GGGACAAGAA | CAAAGAAATC | AAATTTATAA |
| msa238454.2{401_18RS21} | TGATTTTTCT | ATTAAAGCAG | GGGACAAGAA | CAAAGAAATC | AAATTTATAA |
| msa238454.2{401_2603} | TGATTTTTCT | ATTAAAGCAG | GGGACAAGAA | CAAAGAAATC | AAATTTATAA |
| msa238454.2{401_CJB110} | TGATTTTTCT | ATTAAAGCAG | GGGACAAGAA | CAAAGAAATC | AAATTTATAA |
| msa238454.2{401_COH1} | TGATTTTTCT | ATTAAAGCAG | GGGACAAGAA | CAAAGAAATC | AAATTTATAA |
| msa238454.2{401_M732} | TGATTTTTCT | ATTAAAGCAG | GGGACAAGAA | CAAAGAAATC | AAATTTATAA |
| msa238454.2{401_M781} | TGATTTTTCT | ATTAAAGCAG | GGGACAAGAA | CAAAGAAATC | AAATTTATAA |
| msa238454.2{401_JM9130013} | TGATTTTTCT | ATTAAAGCAG | GGGACAAGAA | CAAAGAAATC | AAATTTATAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa238454.2{401_A909} | GGCAAAAAGT | TGGTTTAGTT | TTTCAATTTC | CAGAAAGTCA | GCTTTTGTAA |
| msa238454.2{401_H36B} | GGCAAAAAGT | TGGTTTAGTT | TTTCAATTTC | CAGAAAGTCA | GCTTTTGTAA |
| msa238454.2{401_090} | GGCAAAAAGT | TGGTTTAGTT | TTTCAATTTC | CAGAAAGTCA | GCTTTTGTAA |
| msa238454.2{401_1169NT} | GGCAAAAAGT | TGGTTTAGTT | TTTCAATTTC | CAGAAAGTCA | GCTTTTGTAA |
| msa238454.2{401_18RS21} | GGCAAAAAGT | TGGTTTAGTT | TTTCAATTTC | CAGAAAGTCA | GCTTTTGTAA |
| msa238454.2{401_2603} | GGCAAAAAGT | TGGTTTAGTT | TTTCAATTTC | CAGAAAGTCA | GCTTTTGTAA |
| msa238454.2{401_CJB110} | GGCAAAAAGT | TGGTTTAGTT | TTTCAATTTC | CAGAAAGTCA | GCTTTTGTAA |
| msa238454.2{401_COH1} | GGCAAAAAGT | TGGTTTAGTT | TTTCAATTTC | CAGAAAGTCA | GCTTTTGTAA |
| msa238454.2{401_M732} | GGCAAAAAGT | TGGTTTAGTT | TTTCAATTTC | CAGAAAGTCA | GCTTTTGTAA |
| msa238454.2{401_M781} | GGCAAAAAGT | TGGTTTAGTT | TTTCAATTTC | CAGAAAGTCA | GCTTTTGTAA |
| msa238454.2{401_JM9130013} | GGCAAAAAGT | TGGTTTAGTT | TTTCAATTTC | CAGAAAGTCA | GCTTTTGTAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa238454.2{401_A909} | GAGACAGTTT | TAAAgGATGT | TGCTTTTGA | CCACAAAATT | TTGGTATTTC |
| msa238454.2{401_H36B} | GAGACAGTTT | TAAAgGATGT | TGCTTTTGA | CCACAAAATT | TTGGTATTTC |
| msa238454.2{401_090} | GAGACAGTTT | TAAAgGATGT | TGCTTTTGA | CCACAAAATT | TTGGTATTTC |
| msa238454.2{401_1169NT} | GAGACAGTTT | TAAAgGATGT | TGCTTTTGA | CCACAAAATT | TTGGTATTTC |
| msa238454.2{401_18RS21} | GAGACAGTTT | TAAAgGATGT | TGCTTTTGA | CCACAAAATT | TTGGTATTTC |
| msa238454.2{401_2603} | GAGACAGTTT | TAAAgGATGT | TGCTTTTGA | CCACAAAATT | TTGGTATTTC |
| msa238454.2{401_CJB110} | GAGACAGTTT | TAAAgGATGT | TGCTTTTGA | CCACAAAATT | TTGGTATTTC |
| msa238454.2{401_COH1} | GAGACAGTTT | TAAAgGATGT | TGCTTTTGA | CCACAAAATT | TTGGTATTTC |
| msa238454.2{401_M732} | GAGACAGTTT | TAAAgGATGT | TGCTTTTGA | CCACAAAATT | TTGGTATTTC |
| msa238454.2{401_M781} | GAGACAGTTT | TAAAgGATGT | TGCTTTTGA | CCACAAAATT | TTGGTATTTC |
| msa238454.2{401_JM9130013} | GAGACAGTTT | TAAAgGATGT | TGCTTTTGA | CCACAAAATT | TTGGTATTTC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa238454.2{401_A909} | TCAGATTGAA | GCTGAAAGGC | TGGCTGAAGA | AAAATTAAAG | TTAGTTGGTA |
| msa238454.2{401_H36B} | TCAGATTGAA | GCTGAAAGGC | TGGCTGAAGA | AAAATTAAAG | TTAGTTGGTA |
| msa238454.2{401_090} | TCAGATTGAA | GCTGAAAGGC | TGGCTGAAGA | AAAATTAAAG | TTAGTTGGTA |
| msa238454.2{401_1169NT} | TCAGATTGAA | GCTGAAAGGC | TGGCTGAAGA | AAAATTAAAG | TTAGTTGGTA |
| msa238454.2{401_18RS21} | TCAGATTGAA | GCTGAAAGGC | TGGCTGAAGA | AAAATTAAAG | TTAGTTGGTA |
| msa238454.2{401_2603} | TCAGATTGAA | GCTGAAAGGC | TGGCTGAAGA | AAAATTAAAG | TTAGTTGGTA |

Table 79: Comparative Sequences relating to SAG2150

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| msa238454.2{401_CJB110} | TCAGATTGAA | GCTGAAAGGC | TGGCTGAAGA | AAAATTAAGG | TTAGTTGGTA |
| msa238454.2{401_COH1} | TCAGATTGAA | GCTGAAAGGC | TGGCTGAAGA | AAAATTAAGG | TTAGTTGGTA |
| msa238454.2{401_M732} | TCAGATTGAA | GCTGAAAGGC | TGGCTGAAGA | AAAATTAAGG | TTAGTTGGTA |
| msa238454.2{401_M781} | TCAGATTGAA | GCTGAAAGGC | TGGCTGAAGA | AAAATTAAGG | TTAGTTGGTA |
| msa238454.2{401_JM9130013} | TCAGATTGAA | GCTGAAAGGC | TGGCTGAAGA | AAAATTAAGG | TTAGTTGGTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa238454.2{401_A909} | TcAGTGAGGA | TTTATTCGAT | AAAAATCCAT | TTGAACCTTC | TGGAGGGCAG |
| msa238454.2{401_H36B} | TcAGTGAGGA | TTTATTCGAT | AAAAATCCAT | TTGAACCTTC | TGGAGGGCAG |
| msa238454.2{401_090} | TcAGTGAGGA | TTTATTCGAT | AAAAATCCAT | TTGAACCTTC | TGGAGGGCAG |
| msa238454.2{401_1169NT} | TcAGTGAGGA | TTTATTCGAT | AAAAATCCAT | TTGAACCTTC | TGGAGGGCAG |
| msa238454.2{401_18RS21} | TcAGTGAGGA | TTTATTCGAT | AAAAATCCAT | TTGAACCTTC | TGGAGGGCAG |
| msa238454.2{401_2603} | TcAGTGAGGA | TTTATTCGAT | AAAAATCCAT | TTGAACCTTC | TGGAGGGCAG |
| msa238454.2{401_CJB110} | TcAGTGAGGA | TTTATTCGAT | AAAAATCCAT | TTGAACCTTC | TGGAGGGCAG |
| msa238454.2{401_COH1} | TcAGTGAGGA | TTTATTCGAT | AAAAATCCAT | TTGAACCTTC | TGGAGGGCAG |
| msa238454.2{401_M732} | TcAGTGAGGA | TTTATTCGAT | AAAAATCCAT | TTGAACCTTC | TGGAGGGCAG |
| msa238454.2{401_M781} | TcAGTGAGGA | TTTATTCGAT | AAAAATCCAT | TTGAACCTTC | TGGAGGGCAG |
| msa238454.2{401_JM9130013} | TcAGTGAGGA | TTTATTCGAT | AAAAATCCAT | TTGAACCTTC | TGGAGGGCAG |
| Consensus | *-***** | ***** | ***** | ***** | ***** |
| msa238454.2{401_A909} | ATGAGGCGGG | TTGCTATAGC | TGGTATTTTA | GCGATGGAAC | CCAAAGTACT |
| msa238454.2{401_H36B} | ATGAGGCGGG | TTGCTATAGC | TGGTATTTTA | GCGATGGAAC | CCAAAGTACT |
| msa238454.2{401_090} | ATGAGGCGGG | TTGCTATAGC | TGGTATTTTA | GCGATGGAAC | CCAAAGTACT |
| msa238454.2{401_1169NT} | ATGAGGCGGG | TTGCTATAGC | TGGTATTTTA | GCGATGGAAC | CCAAAGTACT |
| msa238454.2{401_18RS21} | ATGAGGCGGG | TTGCTATAGC | TGGTATTTTA | GCGATGGAAC | CCAAAGTACT |
| msa238454.2{401_2603} | ATGAGGCGGG | TTGCTATAGC | TGGTATTTTA | GCGATGGAAC | CCAAAGTACT |
| msa238454.2{401_CJB110} | ATGAGGCGGG | TTGCTATAGC | TGGTATTTTA | GCGATGGAAC | CCAAAGTACT |
| msa238454.2{401_COH1} | ATGAGGCGGG | TTGCTATAGC | TGGTATTTTA | GCGATGGAAC | CCAAAGTACT |
| msa238454.2{401_M732} | ATGAGGCGGG | TTGCTATAGC | TGGTATTTTA | GCGATGGAAC | CCAAAGTACT |
| msa238454.2{401_M781} | ATGAGGCGGG | TTGCTATAGC | TGGTATTTTA | GCGATGGAAC | CCAAAGTACT |
| msa238454.2{401_JM9130013} | ATGAGGCGGG | TTGCTATAGC | TGGTATTTTA | GCGATGGAAC | CCAAAGTACT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa238454.2{401_A909} | AGTACTaGAT | GAGCCAACAG | CTGGACTTGA | TCCTAAGGGA | AGAAAAGAAT |
| msa238454.2{401_H36B} | AGTACTaGAT | GAGCCAACAG | CTGGACTTGA | TCCTAAGGGA | AGAAAAGAAT |
| msa238454.2{401_090} | AGTACTgGAT | GAGCCAACAG | CTGGACTTGA | TCCTAAGGGA | AGAAAAGAAT |
| msa238454.2{401_1169NT} | AGTACTgGAT | GAGCCAACAG | CTGGACTTGA | TCCTAAGGGA | AGAAAAGAAT |
| msa238454.2{401_18RS21} | AGTACTgGAT | GAGCCAACAG | CTGGACTTGA | TCCTAAGGGA | AGAAAAGAAT |
| msa238454.2{401_2603} | AGTACTgGAT | GAGCCAACAG | CTGGACTTGA | TCCTAAGGGA | AGAAAAGAAT |
| msa238454.2{401_CJB110} | AGTACTgGAT | GAGCCAACAG | CTGGACTTGA | TCCTAAGGGA | AGAAAAGAAT |
| msa238454.2{401_COH1} | AGTACTgGAT | GAGCCAACAG | CTGGACTTGA | TCCTAAGGGA | AGAAAAGAAT |
| msa238454.2{401_M732} | AGTACTgGAT | GAGCCAACAG | CTGGACTTGA | TCCTAAGGGA | AGAAAAGAAT |
| msa238454.2{401_M781} | AGTACTgGAT | GAGCCAACAG | CTGGACTTGA | TCCTAAGGGA | AGAAAAGAAT |
| msa238454.2{401_JM9130013} | AGTACTgGAT | GAGCCAACAG | CTGGACTTGA | TCCTAAGGGA | AGAAAAGAAT |
| Consensus | *****-*** | ***** | ***** | ***** | ***** |
| msa238454.2{401_A909} | TAATGACTCT | TTTTAAAAAT | CTTCATAAAA | AAGGAATGAC | TATCGTCTTA |
| msa238454.2{401_H36B} | TAATGACTCT | TTTTAAAAAT | CTTCATAAAA | AAGGAATGAC | TATCGTCTTA |
| msa238454.2{401_090} | TAATGACTCT | TTTTAAAAAT | CTTCATAAAA | AAGGAATGAC | TATCGTCTTA |
| msa238454.2{401_1169NT} | TAATGACTCT | TTTTAAAAAT | CTTCATAAAA | AAGGAATGAC | TATCGTCTTA |
| msa238454.2{401_18RS21} | TAATGACTCT | TTTTAAAAAT | CTTCATAAAA | AAGGAATGAC | TATCGTCTTA |
| msa238454.2{401_2603} | TAATGACTCT | TTTTAAAAAT | CTTCATAAAA | AAGGAATGAC | TATCGTCTTA |
| msa238454.2{401_CJB110} | TAATGACTCT | TTTTAAAAAT | CTTCATAAAA | AAGGAATGAC | TATCGTCTTA |
| msa238454.2{401_COH1} | TAATGACTCT | TTTTAAAAAT | CTTCATAAAA | AAGGAATGAC | TATCGTCTTA |
| msa238454.2{401_M732} | TAATGACTCT | TTTTAAAAAT | CTTCATAAAA | AAGGAATGAC | TATCGTCTTA |
| msa238454.2{401_M781} | TAATGACTCT | TTTTAAAAAT | CTTCATAAAA | AAGGAATGAC | TATCGTCTTA |
| msa238454.2{401_JM9130013} | TAATGACTCT | TTTTAAAAAT | CTTCATAAAA | AAGGAATGAC | TATCGTCTTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa238454.2{401_A909} | GTGACTCACT | TAATGGACGA | TGTAGCGGAT | TATGCTGACT | ATGTGTATGT |
| msa238454.2{401_H36B} | GTGACTCACT | TAATGGACGA | TGTAGCGGAT | TATGCTGACT | ATGTGTATGT |
| msa238454.2{401_090} | GTGACTCACT | TAATGGACGA | TGTAGCGGAT | TATGCTGACT | ATGTGTATGT |
| msa238454.2{401_1169NT} | GTGACTCACT | TAATGGACGA | TGTAGCGGAT | TATGCTGACT | ATGTGTATGT |
| msa238454.2{401_18RS21} | GTGACTCACT | TAATGGACGA | TGTAGCGGAT | TATGCTGACT | ATGTGTATGT |
| msa238454.2{401_2603} | GTGACTCACT | TAATGGACGA | TGTAGCGGAT | TATGCTGACT | ATGTGTATGT |
| msa238454.2{401_CJB110} | GTGACTCACT | TAATGGACGA | TGTAGCGGAT | TATGCTGACT | ATGTGTATGT |
| msa238454.2{401_COH1} | GTGACTCACT | TAATGGACGA | TGTAGCGGAT | TATGCTGACT | ATGTGTATGT |
| msa238454.2{401_M732} | GTGACTCACT | TAATGGACGA | TGTAGCGGAT | TATGCTGACT | ATGTGTATGT |
| msa238454.2{401_M781} | GTGACTCACT | TAATGGACGA | TGTAGCGGAT | TATGCTGACT | ATGTGTATGT |
| msa238454.2{401_JM9130013} | GTGACTCACT | TAATGGACGA | TGTAGCGGAT | TATGCTGACT | ATGTGTATGT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa238454.2{401_A909} | TTTGAAGCA | GGGAAAGTAA | CCTTATCAGG | ACAACCAAag | CAGATTTTTC |
| msa238454.2{401_H36B} | TTTGAAGCA | GGGAAAGTAA | CCTTATCAGG | ACAACCAAag | CAGATTTTTC |
| msa238454.2{401_090} | TTTGAAGCA | GGGAAAGTAA | CCTTATCAGG | ACAACCAAa | CAGATTTTTC |
| msa238454.2{401_1169NT} | TTTGAAGCA | GGGAAAGTAA | CCTTATCAGG | ACAACCAAa | CAGATTTTTC |
| msa238454.2{401_18RS21} | TTTGAAGCA | GGGAAAGTAA | CCTTATCAGG | ACAACCAAa | CAGATTTTTC |

Table 79: Comparative Sequences relating to SAG2150

| | | | | | |
|--|------------|------------|------------|------------|------------|
| msa238454.2{401_2603} | TTTAGAAGCA | GGGAAAGTAA | CCTTATCAGG | ACAACCAAAa | CAGATTTTTC |
| msa238454.2{401_CJB110} | TTTAGAAGCA | GGGAAAGTAA | CCTTATCAGG | ACAACCAAAa | CAGATTTTTC |
| msa238454.2{401_COH1} | TTTAGAAGCA | GGGAAAGTAA | CCTTATCAGG | ACAACCAAAa | CAGATTTTTC |
| msa238454.2{401_M732} | TTTAGAAGCA | GGGAAAGTAA | CCTTATCAGG | ACAACCAAAa | CAGATTTTTC |
| msa238454.2{401_JM9130013} | TTTAGAAGCA | GGGAAAGTAA | CCTTATCAGG | ACAACCAAAa | CAGATTTTTC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 701 | | | | | |
| msa238454.2{401_A909} | AAGAAGTAGA | ACTTTTAGAA | AGTAAACAAT | TAGGAGTTCC | CAAAATCACC |
| msa238454.2{401_H36B} | AAGAAGTAGA | ACTTTTAGAA | AGTAAACAAT | TAGGAGTTCC | CAAAATCACC |
| msa238454.2{401_090} | AAGAAGTAGA | ACTTTTAGAA | AGTAAACAAT | TAGGAGTTCC | CAAAATCACC |
| msa238454.2{401_1169NT} | AAGAAGTAGA | ACTTTTAGAA | AGTAAACAAT | TAGGAGTTCC | CAAAATCACC |
| msa238454.2{401_18RS21} | AAGAAGTAGA | ACTTTTAGAA | AGTAAACAAT | TAGGAGTTCC | CAAAATCACC |
| msa238454.2{401_2603} | AAGAAGTAGA | ACTTTTAGAA | AGTAAACAAT | TAGGAGTTCC | CAAAATCACC |
| msa238454.2{401_CJB110} | AAGAAGTAGA | ACTTTTAGAA | AGTAAACAAT | TAGGAGTTCC | CAAAATCACC |
| msa238454.2{401_COH1} | AAGAAGTAGA | ACTTTTAGAA | AGTAAACAAT | TAGGAGTTCC | CAAAATCACC |
| msa238454.2{401_M732} | AAGAAGTAGA | ACTTTTAGAA | AGTAAACAAT | TAGGAGTTCC | CAAAATCACC |
| msa238454.2{401_M781} | AAGAAGTAGA | ACTTTTAGAA | AGTAAACAAT | TAGGAGTTCC | CAAAATCACC |
| msa238454.2{401_JM9130013} | AAGAAGTAGA | ACTTTTAGAA | AGTAAACAAT | TAGGAGTTCC | CAAAATCACC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 751 | | | | | |
| msa238454.2{401_A909} | AAGTTTGCTC | AAAGgCTATC | TCATAAGGGA | TTAAATTTAC | CTAGTTTACC |
| msa238454.2{401_H36B} | AAGTTTGCTC | AAAGgCTATC | TCATAAGGGA | TTAAATTTAC | CTAGTTTACC |
| msa238454.2{401_090} | AAGTTTGCTC | AAAGaCTATC | TCATAAGGGA | TTAAATTTAC | CTAGTTTACC |
| msa238454.2{401_1169NT} | AAGTTTGCTC | AAAGaCTATC | TCATAAGGGA | TTAAATTTAC | CTAGTTTACC |
| msa238454.2{401_18RS21} | AAGTTTGCTC | AAAGaCTATC | TCATAAGGGA | TTAAATTTAC | CTAGTTTACC |
| msa238454.2{401_2603} | AAGTTTGCTC | AAAGaCTATC | TCATAAGGGA | TTAAATTTAC | CTAGTTTACC |
| msa238454.2{401_CJB110} | AAGTTTGCTC | AAAGaCTATC | TCATAAGGGA | TTAAATTTAC | CTAGTTTACC |
| msa238454.2{401_COH1} | AAGTTTGCTC | AAAGaCTATC | TCATAAGGGA | TTAAATTTAC | CTAGTTTACC |
| msa238454.2{401_M732} | AAGTTTGCTC | AAAGaCTATC | TCATAAGGGA | TTAAATTTAC | CTAGTTTACC |
| msa238454.2{401_M781} | AAGTTTGCTC | AAAGaCTATC | TCATAAGGGA | TTAAATTTAC | CTAGTTTACC |
| msa238454.2{401_JM9130013} | AAGTTTGCTC | AAAGaCTATC | TCATAAGGGA | TTAAATTTAC | CTAGTTTACC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 801 | | | | | |
| msa238454.2{401_A909} | AATTACTATT | AACGAATTTG | TGGAGGCTAT | TAAGCATGGA | |
| msa238454.2{401_H36B} | AATTACTATT | AACGAATTTG | TGGAGGCTAT | TAAGCATGGA | |
| msa238454.2{401_090} | AATTACTATT | AACGAATTTG | TGGAGGCTAT | TAAGCATGGA | |
| msa238454.2{401_1169NT} | AATTACTATT | AACGAATTTG | TGGAGGCTAT | TAAGCATGGA | |
| msa238454.2{401_18RS21} | AATTACTATT | AACGAATTTG | TGGAGGCTAT | TAAGCATGGA | |
| msa238454.2{401_2603} | AATTACTATT | AACGAATTTG | TGGAGGCTAT | TAAGCATGGA | |
| msa238454.2{401_CJB110} | AATTACTATT | AACGAATTTG | TGGAGGCTAT | TAAGCATGGA | |
| msa238454.2{401_COH1} | AATTACTATT | AACGAATTTG | TGGAGGCTAT | TAAGCATGGA | |
| msa238454.2{401_M732} | AATTACTATT | AACGAATTTG | TGGAGGCTAT | TAAGCATGGA | |
| msa238454.2{401_M781} | AATTACTATT | AACGAATTTG | TGGAGGCTAT | TAAGCATGGA | |
| msa238454.2{401_JM9130013} | AATTACTATT | AACGAATTTG | TGGAGGCTAT | TAAGCATGGA | |
| Consensus | ***** | ***** | ***** | ***** | |
| 840 | | | | | |
| SEQ ID NO. 7912 | | | | | |
| STRAIN 2603 frame: 1 | | | | | |
| MGIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK | | | | | |
| GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA | | | | | |
| ERLAEEKLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR | | | | | |
| KELMTLFLKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVELLES | | | | | |
| KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG | | | | | |
| SEQ ID NO. 7913 | | | | | |
| STRAIN 090 frame: 1 | | | | | |
| GIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK | | | | | |
| GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA | | | | | |
| ERLAEEKLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR | | | | | |
| KELMTLFLKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVELLES | | | | | |
| KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG | | | | | |
| SEQ ID NO. 7914 | | | | | |
| STRAIN 090 frame: 1 | | | | | |
| GIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK | | | | | |
| GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA | | | | | |
| ERLAEEKLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR | | | | | |
| KELMTLFLKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVELLES | | | | | |
| KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG | | | | | |
| SEQ ID NO. 7915 | | | | | |
| STRAIN H36B frame: 1 | | | | | |
| GIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK | | | | | |
| GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA | | | | | |
| ERLAEEKLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR | | | | | |
| KELMTLFLKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVELLES | | | | | |
| KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG | | | | | |
| SEQ ID NO. 7916 | | | | | |

Table 79: Comparative Sequences relating to SAG2150

STRAIN 18RS21 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7917

STRAIN M732 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7918

STRAIN COH1 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7919

STRAIN M781 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7920

STRAIN CJB110 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7921

STRAIN 1169NT frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7922

STRAIN JM9130013 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKNNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

PRETTY of: /biotmp/msa238553.2{*} May 14, 2003 06:55 ..

| | | | |
|----------------------------|------------|------------|------------|
| | 1 | | 50 |
| msa238553.2{401_090} | ~GIEFKNVSY | TYQAGTPFEG | RALFDVNLKI |
| msa238553.2{401_1169NT} | ~GIEFKNVSY | TYQAGTPFEG | RALFDVNLKI |
| msa238553.2{401_18RS21} | ~GIEFKNVSY | TYQAGTPFEG | RALFDVNLKI |
| msa238553.2{401_2603} | mGIEFKNVSY | TYQAGTPFEG | RALFDVNLKI |
| msa238553.2{401_CJB110} | ~GIEFKNVSY | TYQAGTPFEG | RALFDVNLKI |
| msa238553.2{401_H36B} | ~GIEFKNVSY | TYQAGTPFEG | RALFDVNLKI |
| msa238553.2{401_JM9130013} | ~GIEFKNVSY | TYQAGTPFEG | RALFDVNLKI |
| msa238553.2{401_COH1} | ~GIEFKNVSY | TYQAGTPFEG | RALFDVNLKI |
| msa238553.2{401_M732} | ~GIEFKNVSY | TYQAGTPFEG | RALFDVNLKI |
| msa238553.2{401_M781} | ~GIEFKNVSY | TYQAGTPFEG | RALFDVNLKI |
| Consensus | ***** | ***** | ***** |
| | 51 | | 100 |
| msa238553.2{401_090} | QLLNLGHIPT | KGEVIVDDFS | IKAGDKNKEI |
| msa238553.2{401_1169NT} | QLLNLGHIPT | KGEVIVDDFS | IKAGDKNKEI |
| msa238553.2{401_18RS21} | QLLNLGHIPT | KGEVIVDDFS | IKAGDKNKEI |
| msa238553.2{401_2603} | QLLNLGHIPT | KGEVIVDDFS | IKAGDKNKEI |
| msa238553.2{401_CJB110} | QLLNLGHIPT | KGEVIVDDFS | IKAGDKNKEI |
| msa238553.2{401_H36B} | QLLNLGHIPT | KGEVIVDDFS | IKAGDKNKEI |
| msa238553.2{401_JM9130013} | QLLNLGHIPT | KGEVIVDDFS | IKAGDKNKEI |
| msa238553.2{401_COH1} | QLLNLGHIPT | KGEVIVDDFS | IKAGDKNKEI |
| msa238553.2{401_M732} | QLLNLGHIPT | KGEVIVDDFS | IKAGDKNKEI |
| msa238553.2{401_M781} | QLLNLGHIPT | KGEVIVDDFS | IKAGDKNKEI |

Table 79: Comparative Sequences relating to SAG2150

| Consensus | ***** | ***** | ***** | ***** | ***** |
|----------------------------|------------|------------|-------------|-------------|-------------|
| | 101 | | | | 150 |
| msa238553.2{401_090} | ETVLKDVAFG | PQNFGISQIE | AERLAEEKLR | LVGISEDLF | KNPFELSGGQ |
| msa238553.2{401_1169NT} | ETVLKDVAFG | PQNFGISQIE | AERLAEEKLR | LVGISEDLF | KNPFELSGGQ |
| msa238553.2{401_18RS21} | ETVLKDVAFG | PQNFGISQIE | AERLAEEKLR | LVGISEDLF | KNPFELSGGQ |
| msa238553.2{401_2603} | ETVLKDVAFG | PQNFGISQIE | AERLAEEKLR | LVGISEDLF | KNPFELSGGQ |
| msa238553.2{401_CJB110} | ETVLKDVAFG | PQNFGISQIE | AERLAEEKLR | LVGISEDLF | KNPFELSGGQ |
| msa238553.2{401_H36B} | ETVLKDVAFG | PQNFGISQIE | AERLAEEKLR | LVGISEDLF | KNPFELSGGQ |
| msa238553.2{401_JM9130013} | ETVLKDVAFG | PQNFGISQIE | AERLAEEKLR | LVGISEDLF | KNPFELSGGQ |
| msa238553.2{401_COH1} | ETVLKDVAFG | PQNFGISQIE | AERLAEEKLR | LVGISEDLF | KNPFELSGGQ |
| msa238553.2{401_M732} | ETVLKDVAFG | PQNFGISQIE | AERLAEEKLR | LVGISEDLF | KNPFELSGGQ |
| msa238553.2{401_M781} | ETVLKDVAFG | PQNFGISQIE | AERLAEEKLR | LVGISEDLF | KNPFELSGGQ |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 151 | | | | 200 |
| msa238553.2{401_090} | MRRVAIAGIL | AMEPKVLVLD | EPTAGLDPKG | RKELMTLFPK | LHKKGMTIIVL |
| msa238553.2{401_1169NT} | MRRVAIAGIL | AMEPKVLVLD | EPTAGLDPKG | RKELMTLFPK | LHKKGMTIIVL |
| msa238553.2{401_18RS21} | MRRVAIAGIL | AMEPKVLVLD | EPTAGLDPKG | RKELMTLFPK | LHKKGMTIIVL |
| msa238553.2{401_2603} | MRRVAIAGIL | AMEPKVLVLD | EPTAGLDPKG | RKELMTLFPK | LHKKGMTIIVL |
| msa238553.2{401_CJB110} | MRRVAIAGIL | AMEPKVLVLD | EPTAGLDPKG | RKELMTLFPK | LHKKGMTIIVL |
| msa238553.2{401_H36B} | MRRVAIAGIL | AMEPKVLVLD | EPTAGLDPKG | RKELMTLFPK | LHKKGMTIIVL |
| msa238553.2{401_JM9130013} | MRRVAIAGIL | AMEPKVLVLD | EPTAGLDPKG | RKELMTLFPK | LHKKGMTIIVL |
| msa238553.2{401_COH1} | MRRVAIAGIL | AMEPKVLVLD | EPTAGLDPKG | RKELMTLFPK | LHKKGMTIIVL |
| msa238553.2{401_M732} | MRRVAIAGIL | AMEPKVLVLD | EPTAGLDPKG | RKELMTLFPK | LHKKGMTIIVL |
| msa238553.2{401_M781} | MRRVAIAGIL | AMEPKVLVLD | EPTAGLDPKG | RKELMTLFPK | LHKKGMTIIVL |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 201 | | | | 250 |
| msa238553.2{401_090} | VTHLMDDVAD | YADYVYVLEA | GKVTLGSGQPK | QIFQEVLELLE | SKQLGVPKIT |
| msa238553.2{401_1169NT} | VTHLMDDVAD | YADYVYVLEA | GKVTLGSGQPK | QIFQEVLELLE | SKQLGVPKIT |
| msa238553.2{401_18RS21} | VTHLMDDVAD | YADYVYVLEA | GKVTLGSGQPK | QIFQEVLELLE | SKQLGVPKIT |
| msa238553.2{401_2603} | VTHLMDDVAD | YADYVYVLEA | GKVTLGSGQPK | QIFQEVLELLE | SKQLGVPKIT |
| msa238553.2{401_CJB110} | VTHLMDDVAD | YADYVYVLEA | GKVTLGSGQPK | QIFQEVLELLE | SKQLGVPKIT |
| msa238553.2{401_H36B} | VTHLMDDVAD | YADYVYVLEA | GKVTLGSGQPK | QIFQEVLELLE | SKQLGVPKIT |
| msa238553.2{401_JM9130013} | VTHLMDDVAD | YADYVYVLEA | GKVTLGSGQPK | QIFQEVLELLE | SKQLGVPKIT |
| msa238553.2{401_COH1} | VTHLMDDVAD | YADYVYVLEA | GKVTLGSGQPK | QIFQEVLELLE | SKQLGVPKIT |
| msa238553.2{401_M732} | VTHLMDDVAD | YADYVYVLEA | GKVTLGSGQPK | QIFQEVLELLE | SKQLGVPKIT |
| msa238553.2{401_M781} | VTHLMDDVAD | YADYVYVLEA | GKVTLGSGQPK | QIFQEVLELLE | SKQLGVPKIT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 251 | | | | 280 |
| msa238553.2{401_090} | KFAQRLSHKG | LNLPSLPITI | NEFVEAIKHG | | |
| msa238553.2{401_1169NT} | KFAQRLSHKG | LNLPSLPITI | NEFVEAIKHG | | |
| msa238553.2{401_18RS21} | KFAQRLSHKG | LNLPSLPITI | NEFVEAIKHG | | |
| msa238553.2{401_2603} | KFAQRLSHKG | LNLPSLPITI | NEFVEAIKHG | | |
| msa238553.2{401_CJB110} | KFAQRLSHKG | LNLPSLPITI | NEFVEAIKHG | | |
| msa238553.2{401_H36B} | KFAQRLSHKG | LNLPSLPITI | NEFVEAIKHG | | |
| msa238553.2{401_JM9130013} | KFAQRLSHKG | LNLPSLPITI | NEFVEAIKHG | | |
| msa238553.2{401_COH1} | KFAQRLSHKG | LNLPSLPITI | NEFVEAIKHG | | |
| msa238553.2{401_M732} | KFAQRLSHKG | LNLPSLPITI | NEFVEAIKHG | | |
| msa238553.2{401_M781} | KFAQRLSHKG | LNLPSLPITI | NEFVEAIKHG | | |
| Consensus | ***** | ***** | ***** | | |

Table 80: Comparative Sequences relating to SAG1266

SEQ ID NO. 8001

STRAIN 2603

GTGAACCACTTACTTAACTCAGTAAAGAAAATATAGCTAAAATAGATTTTGACTTTCTT
 AATGAGGCACCTTAATGCAAAATATTCGTTTGAAAGAATTAGTAGATGAACATAAAATTTCA
 AAAGAACTGGACAGTAAAGGTTGGTCCAAAAAGACTCTCGAACGATAAAAAATCTTGATAC
 GATGGCCTTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCAA
 GTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAAGGAGAAATCT
 AAAAATTATAGAAATACAACTACAGTGATTATGAAATGGAGTTAATCAATGAGGATAGG
 CAACAATTTTCAAAATATGAAACAGTTGATTTAGACCAATTGATACTTGTGTATATTTT
 AATATTGATGACTACATTTTCATCATATTTAACAATA

SEQ ID NO. 8002

STRAIN H36B

AACCACTTACTTAACTCAGTAAAGAAAATATAGCT
 AAAATAGATTTTGACTTTCTTAATGAGGCACCTTAATGCAAAATATTCGTTT
 GAAAGAAATTAGTAGATGAACATAAAATTTCAAAGAACTGGACAGTAAAG
 GTTGGTCCAAAAAGACTCTCGAACGATAAAAAATCTTGATACGATGGCCCT
 ATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCA
 AGTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAA
 GGGAGAAATCTAAAAATTATAGAAATATACAACTACAGTGATTATGAAATG
 GAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTTGA
 TTTAGACCAATTGATACTTGTGTATATTTTAATATTGATGACTACATTT
 CATCATATTTAACAATA

SEQ ID NO. 8003

STRAIN 18RS21

AACCACTTACTTAACTCAGTAAAGAAAATATAG
 CTAAAAATAGATTTTGACTTTCTTAATGAGGCACCTTAATGCAAAATATTCGTT
 TTGAAAGAAATTAGTAGATGAACATAAAATTTCAAAGAACTGGACAGTAA
 AGGTTGGTCCAAAAAGACTCTCGAACGATAAAAAATCTTGATACGATGGCC
 TTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATC
 CAAGTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGA
 AAGGGAGAAATCTAAAAATTATAGAAATATACAACTACAGTGATTATGAAA
 TGGAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTT
 GATTTAGACCAATTGATACTTGTGTATATTTTAATATTGATGACTACAT
 TTCATCATATTTAACAATA

PRETTY of: /biotmp/msa49308.2{*} February 19, 2003 07:45 ..

| | | | |
|------------------------|-------------|------------|------------|
| | 1 | | 50 |
| msa49308.2{408_18RS21} | ---AACCACCT | TACTTAACTC | CAGTAAAGAA |
| msa49308.2{408_2603} | gtgAACCACCT | TACTTAACTC | CAGTAAAGAA |
| msa49308.2{408_H36B} | ---AACCACCT | TACTTAACTC | CAGTAAAGAA |
| Consensus | ***** | ***** | ***** |
| | 51 | | 100 |
| msa49308.2{408_18RS21} | TGACTTTCTT | AATGAGGCAC | TTAATGCAAA |
| msa49308.2{408_2603} | TGACTTTCTT | AATGAGGCAC | TTAATGCAAA |
| msa49308.2{408_H36B} | TGACTTTCTT | AATGAGGCAC | TTAATGCAAA |
| Consensus | ***** | ***** | ***** |
| | 101 | | 150 |
| msa49308.2{408_18RS21} | TAGATGAACCT | AAAAATTTCA | AAAGAACTGG |
| msa49308.2{408_2603} | TAGATGAACCT | AAAAATTTCA | AAAGAACTGG |
| msa49308.2{408_H36B} | TAGATGAACCT | AAAAATTTCA | AAAGAACTGG |
| Consensus | ***** | ***** | ***** |
| | 151 | | 200 |
| msa49308.2{408_18RS21} | AAAGACTCTC | GAACGATAAA | AATCTTGTAC |
| msa49308.2{408_2603} | AAAGACTCTC | GAACGATAAA | AATCTTGTAC |
| msa49308.2{408_H36B} | AAAGACTCTC | GAACGATAAA | AATCTTGTAC |
| Consensus | ***** | ***** | ***** |
| | 201 | | 250 |
| msa49308.2{408_18RS21} | TATAGTTTCC | CTAGATCGTG | CAGATTATAA |
| msa49308.2{408_2603} | TATAGTTTCC | CTAGATCGTG | CAGATTATAA |
| msa49308.2{408_H36B} | TATAGTTTCC | CTAGATCGTG | CAGATTATAA |
| Consensus | ***** | ***** | ***** |
| | 251 | | 300 |
| msa49308.2{408_18RS21} | TTGCTAATGT | ACATGTACTA | CTGTTTTTAA |
| msa49308.2{408_2603} | TTGCTAATGT | ACATGTACTA | CTGTTTTTAA |
| msa49308.2{408_H36B} | TTGCTAATGT | ACATGTACTA | CTGTTTTTAA |
| Consensus | ***** | ***** | ***** |
| | 301 | | 350 |
| msa49308.2{408_18RS21} | AAAAATTATA | GAATATACAA | CTACAGTGAT |
| msa49308.2{408_2603} | AAAAATTATA | GAATATACAA | CTACAGTGAT |
| msa49308.2{408_H36B} | AAAAATTATA | GAATATACAA | CTACAGTGAT |
| Consensus | ***** | ***** | ***** |

Table 80: Comparative Sequences relating to SAG1266

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351                                     400
msa49308.2{408_18RS21} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
msa49308.2{408_2603} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
msa49308.2{408_H36B} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
Consensus *****

401                                     450
msa49308.2{408_18RS21} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
msa49308.2{408_2603} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
msa49308.2{408_H36B} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
Consensus *****

451
msa49308.2{408_18RS21} ACAATA
msa49308.2{408_2603} ACAATA
msa49308.2{408_H36B} ACAATA
Consensus *****

SEQ ID NO. 8004
STRAIN 2603 frame: 1
VNHLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILY
DGLINKHIVSLDRADYNI IQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDR
QQFSKYETVDLDQLILVDIFNIDDISSYLTII

SEQ ID NO. 8005
STRAIN H36B frame: 1
NHLLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNI IQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDRQ
QQFSKYETVDLDQLILVDIFNIDDISSYLTII

SEQ ID NO. 8006
STRAIN 18RS21 frame: 1
NHLLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNI IQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDRQ
QQFSKYETVDLDQLILVDIFNIDDISSYLTII

PRETTY of: /biotmp/msa49418.2{*} February 19, 2003 07:47 ..

1                                     50
msa49418.2{408_18RS21} -NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
msa49418.2{408_2603} vNHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
msa49418.2{408_H36B} -NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
Consensus *****

51                                     100
msa49418.2{408_18RS21} KDSRTIKILY DGLINKHIVS LDRADYNI IQ VIPFANVHVL LFLIPERENS
msa49418.2{408_2603} KDSRTIKILY DGLINKHIVS LDRADYNI IQ VIPFANVHVL LFLIPERENS
msa49418.2{408_H36B} KDSRTIKILY DGLINKHIVS LDRADYNI IQ VIPFANVHVL LFLIPERENS
Consensus *****

101                                    150
msa49418.2{408_18RS21} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
msa49418.2{408_2603} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
msa49418.2{408_H36B} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
Consensus *****

151
msa49418.2{408_18RS21} TI
msa49418.2{408_2603} TI
msa49418.2{408_H36B} TI
Consensus **

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Table 81: Comparative Sequences relating to SAG0011

SEQ ID NO. 8101

STRAIN 090

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
 ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTGCTAGCAAAACAATAAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGCGAAATGATTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8102

STRAIN A909

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATA
 TATTAAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCG
 TTTAATGGGTTGGGTTCTTATTTTGTCTATGCTtttATTTATTTTACCCACTTATAATTT
 AGTTAAGAGTTACAGAACTTTACAAGAAGTCGTCAAGAAGTTGTAAAATTAACGAAAGA
 CTATCAGACATTAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAA
 TCCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGCGAAAT
 GATTTACCCATTACCAGACCT

SEQ ID NO. 8103

STRAIN H36B

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
 ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGCGAAATGATTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8104

STRAIN 18RS21

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATATATTAACGATGAGAATCTAAAAAA
 CGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTT
 GTCATGCTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAA
 GAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAACTAATAGAACT
 GAGAACCAGAAGTTGCTAGCAAAACAATAAAAAATCCAGATTACGTTCAAAAATATGCT
 CGAGCTAAGTATTATTTCTCTAAGACCGCGAAATGATTTACCCATTACCAGACCTTTTA
 CCAAAA

SEQ ID NO. 8105

STRAIN M732

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
 ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGAC
 CGCGAAATGATTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8106

STRAIN COH1

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATGCTttt
 ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAAG
 AACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAACT
 AATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAATCCAGA
 TTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGACCGCG
 AATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8107

STRAIN M781

AGCaAGCCTAATGTTGTTTCAGTT
 AAATAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTG
 AGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATGCT
 ATGCTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACA
 TTTACAAGAAGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAACT
 CATTAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAA
 AATCCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGACCGCG
 GACCGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8108

STRAIN CJB110

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATGCTttt
 ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAAG

Table 81: Comparative Sequences relating to SAG0011

AACGTCGTCAGAAAGTTGTAAAATTAACGAAAGACTATCAGACATTAAC
 AATAGAACTGAGAACCCAGAAGTTGCTAGCAAAACAACTAAAAATCCAGA
 TTACGTTCAAAAATATGCTCGAGCTAAGTATTATTCTTAAGACCGGCG
 AAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8109

STRAIN 1169NT

AGCAAGCCTAATGTTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTT
 ACAAGAAGCTCGTCAAGAAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCCAGAAGTTACTAGCAAAACAACTAAAAAT
 CCGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTCTCTAAGAC
 CGCGGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8110

STRAIN JM9130013

AGCAAGCCTAATGTTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTT
 ACAAGAAGCTCGTCAAGAAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCCAGAAGTTACTAGCAAAACAACTAAAAAT
 CCGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTCTCTAAGAC
 TGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8111

STRAIN 2603

agcaagcctaagtgtgttcagttaataatcaatatattaacgatgagaa
 tctaaaaaacgttacgaagctgaggagttacgccgaaaaaatcgtttaa
 tgggttgggttcttattttgtcatgcttttatttttaccacttat
 aatttagttaagagttacagaactttacaagaagctcgtaagaagttgt
 aaaattaacgaagactatcagacattaactaatagaactgagaaccaga
 agttgctagcaaaacaactaaaaatccagattacgttcaaaaatgatgct
 cgagctaagtattatttctctaagaccggcgaaatgatttaccattacc
 agaccttttaccaaaa

PRETTY of: /biotmp/msa25643.2{*} . April 29, 2002 05:59 ..

| | | | |
|---------------------------|------------|------------|----------------------------------|
| | 1 | | 50 |
| msa25643.2{418_COH1} | AGCAAGCCTA | ATGTTGTTCA | GTTAAATAAT CAATATATTA ACGATGAGAA |
| msa25643.2{418_M732} | AGCAAGCCTA | ATGTTGTTCA | GTTAAATAAT CAATATATTA ACGATGAGAA |
| msa25643.2{418_M781} | AGCAAGCCTA | ATGTTGTTCA | GTTAAATAAT CAATATATTA ACGATGAGAA |
| msa25643.2{418_JM9130013} | AGCAAGCCTA | ATGTTGTTCA | GTTAAATAAT CAATATATTA ACGATGAGAA |
| msa25643.2{418_090} | AGCAAGCCTA | ATGTTGTTCA | GTTAAATAAT CAATATATTA ACGATGAGAA |
| msa25643.2{418_18RS21} | AGCAAGCCTA | ATGTTGTTCA | GTTAAATAAT CAATATATTA ACGATGAGAA |
| msa25643.2{418_2603} | AGCAAGCCTA | ATGTTGTTCA | GTTAAATAAT CAATATATTA ACGATGAGAA |
| msa25643.2{418_CJB110} | AGCAAGCCTA | ATGTTGTTCA | GTTAAATAAT CAATATATTA ACGATGAGAA |
| msa25643.2{418_1169NT} | AGCAAGCCTA | ATGTTGTTCA | GTTAAATAAT CAATATATTA ACGATGAGAA |
| msa25643.2{418_A909} | AGCAAGCCTA | ATGTTGTTCA | GTTAAATAAT CAATATATTA ACGATGAGAA |
| msa25643.2{418_H36B} | AGCAAGCCTA | ATGTTGTTCA | GTTAAATAAT CAATATATTA ACGATGAGAA |
| Consensus | ***** | ***** | ***** |
| | 51 | | 100 |
| msa25643.2{418_COH1} | TCTAAAAAAA | CGTTACGAAG | CTGAGGAGTT ACGCCGAAAA AATCGTTTAA |
| msa25643.2{418_M732} | TCTAAAAAAA | CGTTACGAAG | CTGAGGAGTT ACGCCGAAAA AATCGTTTAA |
| msa25643.2{418_M781} | TCTAAAAAAA | CGTTACGAAG | CTGAGGAGTT ACGCCGAAAA AATCGTTTAA |
| msa25643.2{418_JM9130013} | TCTAAAAAAA | CGTTACGAAG | CTGAGGAGTT ACGCCGAAAA AATCGTTTAA |
| msa25643.2{418_090} | TCTAAAAAAA | CGTTACGAAG | CTGAGGAGTT ACGCCGAAAA AATCGTTTAA |
| msa25643.2{418_18RS21} | TCTAAAAAAA | CGTTACGAAG | CTGAGGAGTT ACGCCGAAAA AATCGTTTAA |
| msa25643.2{418_2603} | TCTAAAAAAA | CGTTACGAAG | CTGAGGAGTT ACGCCGAAAA AATCGTTTAA |
| msa25643.2{418_CJB110} | TCTAAAAAAA | CGTTACGAAG | CTGAGGAGTT ACGCCGAAAA AATCGTTTAA |
| msa25643.2{418_1169NT} | TCTAAAAAAA | CGTTACGAAG | CTGAGGAGTT ACGCCGAAAA AATCGTTTAA |
| msa25643.2{418_A909} | TCTAAAAAAA | CGTTACGAAG | CTGAGGAGTT ACGCCGAAAA AATCGTTTAA |
| msa25643.2{418_H36B} | TCTAAAAAAA | CGTTACGAAG | CTGAGGAGTT ACGCCGAAAA AATCGTTTAA |
| Consensus | ***** | ***** | ***** |
| | 101 | | 150 |
| msa25643.2{418_COH1} | TGGGTTGGGT | TCCTATTTT | GTCATGCTTT TATTTATTTT ACCCACTTAT |
| msa25643.2{418_M732} | TGGGTTGGGT | TCCTATTTT | GTCATGCTTT TATTTATTTT ACCCACTTAT |
| msa25643.2{418_M781} | TGGGTTGGGT | TCCTATTTT | GTCATGCTTT TATTTATTTT ACCCACTTAT |
| msa25643.2{418_JM9130013} | TGGGTTGGGT | TCCTATTTT | GTCATGCTTT TATTTATTTT ACCCACTTAT |
| msa25643.2{418_090} | TGGGTTGGGT | TCCTATTTT | GTCATGCTTT TATTTATTTT ACCCACTTAT |
| msa25643.2{418_18RS21} | TGGGTTGGGT | TCCTATTTT | GTCATGCTTT TATTTATTTT ACCCACTTAT |
| msa25643.2{418_2603} | TGGGTTGGGT | TCCTATTTT | GTCATGCTTT TATTTATTTT ACCCACTTAT |
| msa25643.2{418_CJB110} | TGGGTTGGGT | TCCTATTTT | GTCATGCTTT TATTTATTTT ACCCACTTAT |
| msa25643.2{418_1169NT} | TGGGTTGGGT | TCCTATTTT | GTCATGCTTT TATTTATTTT ACCCACTTAT |
| msa25643.2{418_A909} | TGGGTTGGGT | TCCTATTTT | GTCATGCTTT TATTTATTTT ACCCACTTAT |
| msa25643.2{418_H36B} | TGGGTTGGGT | TCCTATTTT | GTCATGCTTT TATTTATTTT ACCCACTTAT |
| Consensus | ***** | ***** | ***** |

Table 81: Comparative Sequences relating to SAG0011

| | | | |
|---------------------------|------------|-------------|------------|
| | 151 | | 200 |
| msa25643.2{418_COH1} | AATTTAGTTA | AGAGTTACAG | AACTTTACAA |
| msa25643.2{418_M732} | AATTTAGTTA | AGAGTTACAG | AACTTTACAA |
| msa25643.2{418_M781} | AATTTAGTTA | AGAGTTACAG | AACTTTACAA |
| msa25643.2{418_JM9130013} | AATTTAGTTA | AGAGTTACAG | AACTTTACAA |
| msa25643.2{418_090} | AATTTAGTTA | AGAGTTACAG | AACTTTACAA |
| msa25643.2{418_18RS21} | AATTTAGTTA | AGAGTTACAG | AACTTTACAA |
| msa25643.2{418_2603} | AATTTAGTTA | AGAGTTACAG | AACTTTACAA |
| msa25643.2{418_CJB110} | AATTTAGTTA | AGAGTTACAG | AACTTTACAA |
| msa25643.2{418_1169NT} | AATTTAGTTA | AGAGTTACAG | AACTTTACAA |
| msa25643.2{418_A909} | AATTTAGTTA | AGAGTTACAG | AACTTTACAA |
| msa25643.2{418_H36B} | AATTTAGTTA | AGAGTTACAG | AACTTTACAA |
| Consensus | ***** | ***** | ***** |
| | 201 | | 250 |
| msa25643.2{418_COH1} | AAAATTAACG | AAAGACTATC | AGACATTAAC |
| msa25643.2{418_M732} | AAAATTAACG | AAAGACTATC | AGACATTAAC |
| msa25643.2{418_M781} | AAAATTAACG | AAAGACTATC | AGACATTAAC |
| msa25643.2{418_JM9130013} | AAAATTAACG | AAAGACTATC | AGACATTAAC |
| msa25643.2{418_090} | AAAATTAACG | AAAGACTATC | AGACATTAAC |
| msa25643.2{418_18RS21} | AAAATTAACG | AAAGACTATC | AGACATTAAC |
| msa25643.2{418_2603} | AAAATTAACG | AAAGACTATC | AGACATTAAC |
| msa25643.2{418_CJB110} | AAAATTAACG | AAAGACTATC | AGACATTAAC |
| msa25643.2{418_1169NT} | AAAATTAACG | AAAGACTATC | AGACATTAAC |
| msa25643.2{418_A909} | AAAATTAACG | AAAGACTATC | AGACATTAAC |
| msa25643.2{418_H36B} | AAAATTAACG | AAAGACTATC | AGACATTAAC |
| Consensus | ***** | ***** | ***** |
| | 251 | | 300 |
| msa25643.2{418_COH1} | AGTTACTAGC | AAAACAACCTA | AAAAATCCAG |
| msa25643.2{418_M732} | AGTTACTAGC | AAAACAACCTA | AAAAATCCAG |
| msa25643.2{418_M781} | AGTTACTAGC | AAAACAACCTA | AAAAATCCAG |
| msa25643.2{418_JM9130013} | AGTTACTAGC | AAAACAACCTA | AAAAATCCAG |
| msa25643.2{418_090} | AGTTACTAGC | AAAACAACCTA | AAAAATCCAG |
| msa25643.2{418_18RS21} | AGTTACTAGC | AAAACAACCTA | AAAAATCCAG |
| msa25643.2{418_2603} | AGTTACTAGC | AAAACAACCTA | AAAAATCCAG |
| msa25643.2{418_CJB110} | AGTTACTAGC | AAAACAACCTA | AAAAATCCAG |
| msa25643.2{418_1169NT} | AGTTACTAGC | AAAACAACCTA | AAAAATCCAG |
| msa25643.2{418_A909} | AGTTACTAGC | AAAACAACCTA | AAAAATCCAG |
| msa25643.2{418_H36B} | AGTTACTAGC | AAAACAACCTA | AAAAATCCAG |
| Consensus | ****-**** | ***** | ***** |
| | 301 | | 350 |
| msa25643.2{418_COH1} | CGAGCGAAGT | ATTATTTCTC | TAAGACcGGC |
| msa25643.2{418_M732} | CGAGCGAAGT | ATTATTTCTC | TAAGACcGGC |
| msa25643.2{418_M781} | CGAGCGAAGT | ATTATTTCTC | TAAGACcGGC |
| msa25643.2{418_JM9130013} | CGAGCGAAGT | ATTATTTCTC | TAAGACcGGC |
| msa25643.2{418_090} | CGAGCGAAGT | ATTATTTCTC | TAAGACcGGC |
| msa25643.2{418_18RS21} | CGAGCGAAGT | ATTATTTCTC | TAAGACcGGC |
| msa25643.2{418_2603} | CGAGCGAAGT | ATTATTTCTC | TAAGACcGGC |
| msa25643.2{418_CJB110} | CGAGCGAAGT | ATTATTTCTC | TAAGACcGGC |
| msa25643.2{418_1169NT} | CGAGCGAAGT | ATTATTTCTC | TAAGACcGGC |
| msa25643.2{418_A909} | CGAGCGAAGT | ATTATTTCTC | TAAGACcGGC |
| msa25643.2{418_H36B} | CGAGCGAAGT | ATTATTTCTC | TAAGACcGGC |
| Consensus | ***** | ***** | ***** |
| | 351 | | 366 |
| msa25643.2{418_COH1} | AGACCTttta | ccaaaa | |
| msa25643.2{418_M732} | AGACCTttta | ccaaaa | |
| msa25643.2{418_M781} | AGACCTttta | ccaaaa | |
| msa25643.2{418_JM9130013} | AGACCTttta | ccaaaa | |
| msa25643.2{418_090} | AGACCTttta | ccaaaa | |
| msa25643.2{418_18RS21} | AGACCTttta | ccaaaa | |
| msa25643.2{418_2603} | AGACCTttta | ccaaaa | |
| msa25643.2{418_CJB110} | AGACCTttta | ccaaaa | |
| msa25643.2{418_1169NT} | AGACCTttta | ccaaaa | |
| msa25643.2{418_A909} | AGACCTttta | ccaaaa | |
| msa25643.2{418_H36B} | AGACCTttta | ccaaaa | |
| Consensus | ***** | ***** | |

SEQ ID NO. 8112

STRAIN 090

SKPNVQLNNQYINDENLKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVKLTKDYQTLTNRTNENQKLLAKQLKNPDYVQKYARAKYFSKTGEM
 IYPLDLLPK

SEQ ID NO. 8113

STRAIN A909

SKPNVQLNNQYINDENLKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVKLTKDYQTLTNRTNENQKLLAKQLKNPDYVQKYARAKYFSKTGEM

Table 81: Comparative Sequences relating to SAG0011

IYPLPD

SEQ ID NO. 8114

STRAIN H36B

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8115

STRAIN 18RS21

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVKSYRTLQ
 ERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM IYPLPDLL
 PK

SEQ ID NO. 8116

STRAIN M732

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8117

STRAIN COH1

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVK
 SYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM IY
 PLPDLLPK

SEQ ID NO. 8118

STRAIN M781

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 LVKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGE
 MIYPLPDLLPK

SEQ ID NO. 8119

STRAIN CJB110

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVK
 SYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM IY
 PLPDLLPK

SEQ ID NO. 8120

STRAIN 1169NT

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8121

STRAIN JM9130013

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8122

STRAIN 2603

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVKSYRTLQ
 ERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM IYPLPDLL
 PK

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa20122.2{*} April 29, 2002 06:08 ..

| | | | |
|---------------------------|-------------|------------------------|-----------------------|
| | 1 | | 50 |
| msa20122.2{418_090} | SKPNVVQLNN | QYINDENLKK RYEAEELRRK | NRLMGWVLIF VMLLFILPTY |
| msa20122.2{418_A909} | SKPNVVQLNN | QYINDENLKK RYEAEELRRK | NRLMGWVLIF VMLLFILPTY |
| msa20122.2{418_1169NT} | SKPNVVQLNN | QYINDENLKK RYEAEELRRK | NRLMGWVLIF VMLLFILPTY |
| msa20122.2{418_18RS21} | SKPNVVQLNN | QYINDENLKK RYEAEELRRK | NRLMGWVLIF VMLLFILPTY |
| msa20122.2{418_2603} | SKPNVVQLNN | QYINDENLKK RYEAEELRRK | NRLMGWVLIF VMLLFILPTY |
| msa20122.2{418_CJB110} | SKPNVVQLNN | QYINDENLKK RYEAEELRRK | NRLMGWVLIF VMLLFILPTY |
| msa20122.2{418_COH1} | SKPNVVQLNN | QYINDENLKK RYEAEELRRK | NRLMGWVLIF VMLLFILPTY |
| msa20122.2{418_H36B} | SKPNVVQLNN | QYINDENLKK RYEAEELRRK | NRLMGWVLIF VMLLFILPTY |
| msa20122.2{418_JM9130013} | SKPNVVQLNN | QYINDENLKK RYEAEELRRK | NRLMGWVLIF VMLLFILPTY |
| msa20122.2{418_M732} | SKPNVVQLNN | QYINDENLKK RYEAEELRRK | NRLMGWVLIF VMLLFILPTY |
| msa20122.2{418_M781} | SKPNVVQLNN | QYINDENLKK RYEAEELRRK | NRLMGWVLIF VMLLFILPTY |
| Consensus | ***** | ***** | ***** |
| | 51 | | 100 |
| msa20122.2{418_090} | NLVKSRYRTLQ | ERRQEVVVKLT KDYQTLTNRT | ENQKLLAKQL KNPDYVQKYA |
| msa20122.2{418_A909} | NLVKSRYRTLQ | ERRQEVVVKLT KDYQTLTNRT | ENQKLLAKQL KNPDYVQKYA |

Table 81: Comparative Sequences relating to SAG0011

| | | | | | |
|---------------------------|------------|------------|------------|------------|------------|
| msa20122.2{418_1169NT} | NLVKSYRTLQ | ERRQEVVKLT | KDYQTLTNRT | ENQKLLAKQL | KNPDYVQKYA |
| msa20122.2{418_18RS21} | NLVKSYRTLQ | ERRQEVVKLT | KDYQTLTNRT | ENQKLLAKQL | KNPDYVQKYA |
| msa20122.2{418_2603} | NLVKSYRTLQ | ERRQEVVKLT | KDYQTLTNRT | ENQKLLAKQL | KNPDYVQKYA |
| msa20122.2{418_CJB110} | NLVKSYRTLQ | ERRQEVVKLT | KDYQTLTNRT | ENQKLLAKQL | KNPDYVQKYA |
| msa20122.2{418_COH1} | NLVKSYRTLQ | ERRQEVVKLT | KDYQTLTNRT | ENQKLLAKQL | KNPDYVQKYA |
| msa20122.2{418_H36B} | NLVKSYRTLQ | ERRQEVVKLT | KDYQTLTNRT | ENQKLLAKQL | KNPDYVQKYA |
| msa20122.2{418_JM9130013} | NLVKSYRTLQ | ERRQEVVKLT | KDYQTLTNRT | ENQKLLAKQL | KNPDYVQKYA |
| msa20122.2{418_M732} | NLVKSYRTLQ | ERRQEVVKLT | KDYQTLTNRT | ENQKLLAKQL | KNPDYVQKYA |
| msa20122.2{418_M781} | NLVKSYRTLQ | ERRQEVVKLT | KDYQTLTNRT | ENQKLLAKQL | KNPDYVQKYA |
| Consensus | ***** | ***** | ***** | ***** | ***** |

| | 101 | 122 |
|---------------------------|------------|---------------|
| msa20122.2{418_090} | RAKYFFSKTG | EMIYPLPD11 pk |
| msa20122.2{418_A909} | RAKYFFSKTG | EMIYPLPD-- -- |
| msa20122.2{418_1169NT} | RAKYFFSKTG | EMIYPLPD11 pk |
| msa20122.2{418_18RS21} | RAKYFFSKTG | EMIYPLPD11 pk |
| msa20122.2{418_2603} | RAKYFFSKTG | EMIYPLPD11 pk |
| msa20122.2{418_CJB110} | RAKYFFSKTG | EMIYPLPD11 pk |
| msa20122.2{418_COH1} | RAKYFFSKTG | EMIYPLPD11 pk |
| msa20122.2{418_H36B} | RAKYFFSKTG | EMIYPLPD11 pk |
| msa20122.2{418_JM9130013} | RAKYFFSKTG | EMIYPLPD11 pk |
| msa20122.2{418_M732} | RAKYFFSKTG | EMIYPLPD11 pk |
| msa20122.2{418_M781} | RAKYFFSKTG | EMIYPLPD11 pk |
| Consensus | ***** | *****-- -- |

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8201

STRAIN 2603

ATGAAAAATTATTGTTAAAAATGTAAGGATAAGAAGGTTAAAGCATTTCACATTTTAGAA
 TGTTTGGTAGCATTGGTTACAATCACAGGAGCTTTACTAGTTTATCAAGGACTGACAAAA
 TTGTTGGCTCAACAGATAGTAGTGATGCTTCTCCAGTCAGTCTGAATGGGTGTTATTA
 AcTCAGCAACTAAATGCAGAATTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAA
 CTTTATTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTC
 CGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAGACAATTGT
 CAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTTTTATTTTAAAGGACGGGTTAAAA
 AGGACATTTTACTATGATTTTAAAGAAGAACTTAA

SEQ ID NO. 8202

STRAIN 090

AATTCTGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTTA
 CGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTT
 CCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGT
 TAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACTTGTTT
 TATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGA
 AACT

SEQ ID NO. 8203

STRAIN A909

CAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
 TTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATG
 GGTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTT
 TTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
 AGAACT

SEQ ID NO. 8204

STRAIN H36B

ATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTT
 TATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGA
 TGATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTT
 ATGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTT
 GTTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAA
 AGAAGAACT

SEQ ID NO. 8205

STRAIN 18RS21

AGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTTATT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGG
 GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTT
 TTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAA
 GAACT

SEQ ID NO. 8206

STRAIN M732

CAGAATTTGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
 TTTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATG
 GGTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTT
 TTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
 AGAACT

SEQ ID NO. 8207

STRAIN COH1

GAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTT
 ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGGG
 TTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTT
 TTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAG
 AACT

SEQ ID NO. 8208

STRAIN M781

AGAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGG
 GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTT
 TTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAA
 GAACT

SEQ ID NO. 8209

STRAIN CJB110

GAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTT
 ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGG
 TTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACTTGTTT
 TTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAG
 AACT

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8210

STRAIN 1169NT

TCGAAGGCGCTCACTTGGAAATATTTAAGACAGAACAACTTTATTACGT
 AAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAGATGATTTTCG
 TAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAG
 ACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAACTTGTTTTAT
 TTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGAAAC
 T

SEQ ID NO. 8211

STRAIN JM9130013

TGCAGAAITTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTT
 ATTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAGAT
 GATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTA
 TGGGTTAGACAAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTG
 TTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAA
 GAAGAACT

PRETTY of: /biotmp/msa128189.2{*} February 7, 2003 08:19 ..

| | | | | | |
|--------------------------|------------|------------|------------|------------|------------|
| | 1 | | | | 50 |
| msa128189.2{6_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_2603} | atgaaaaatt | tattgttaaa | atgtaaggat | aagaaggtta | aagcatttac |
| msa128189.2{6_A909} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_H36B} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_M732} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_M781} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_090} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_CJB110} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_1169NT} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 51 | | | | 100 |
| msa128189.2{6_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_2603} | acttttagaa | tgtttgtag | cattgggtac | aatcacagga | gctttactag |
| msa128189.2{6_A909} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_H36B} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_M732} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_M781} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_090} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_CJB110} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_1169NT} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 101 | | | | 150 |
| msa128189.2{6_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_2603} | tttatcaagg | actgacaaaa | ttgttggtc | aacagatagt | agtgatgtct |
| msa128189.2{6_A909} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_H36B} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_M732} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_M781} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_090} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_CJB110} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_1169NT} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 151 | | | | 200 |
| msa128189.2{6_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_2603} | tcttccagtc | agtctgaatg | ggtgttatta | actcagcaac | taaATGCaga |
| msa128189.2{6_A909} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_H36B} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_M732} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_M781} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_090} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_CJB110} | ----- | ----- | ----- | ----- | ----- |
| msa128189.2{6_1169NT} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 201 | | | | 250 |
| msa128189.2{6_18RS21} | atTtGAAGGC | GCTCAtcTGG | AATATTTAAG | ACAGAACAAA | CITTATTTAC |
| msa128189.2{6_2603} | atTtGAAGGC | GCTCAtcTGG | AATATTTAAG | ACAGAACAAA | CITTATTTAC |
| msa128189.2{6_A909} | atTtGAAGGC | GCTCAtcTGG | AATATTTAAG | ACAGAACAAA | CITTATTTAC |
| msa128189.2{6_H36B} | atTtGAAGGC | GCTCAtcTGG | AATATTTAAG | ACAGAACAAA | CITTATTTAC |

Table 82: Comparative Sequences relating to SAG0165

| | | | | | |
|--------------------------|------------|------------|------------|------------|------------|
| msa128189.2{6_JM9130013} | atTtGAAGGC | GCTCAtcTGG | AATATTTAAG | ACAGAACAAA | CTTTATTAC |
| msa128189.2{6_COH1} | atTcGAAGGC | GCTCActTGG | AATATTTAAG | ACAGAACAAA | CTTTATTAC |
| msa128189.2{6_M732} | atTcGAAGGC | GCTCActTGG | AATATTTAAG | ACAGAACAAA | CTTTATTAC |
| msa128189.2{6_M781} | atTcGAAGGC | GCTCActTGG | AATATTTAAG | ACAGAACAAA | CTTTATTAC |
| msa128189.2{6_CJB110} | atTcGAAGGC | GCTCActTGG | AATATTTAAG | ACAGAACAAA | CTTTATTAC |
| msa128189.2{6_1169NT} | ~TcGAAGGC | GCTCActTGG | AATATTTAAG | ACAGAACAAA | CTTTATTAC |
| Consensus | ~*~***** | *****--*** | ***** | ***** | ***** |
| 251 | | | | | |
| msa128189.2{6_18RS21} | GTAAGCAAGA | TAAGATTGTA | ACCTTTGGCA | AATCTAATAA | AGATGATTTC |
| msa128189.2{6_2603} | GTAAGCAAGA | TAAGATTGTA | ACCTTTGGCA | AATCTAATAA | AGATGATTTC |
| msa128189.2{6_A909} | GTAAGCAAGA | TAAGATTGTA | ACCTTTGGCA | AATCTAATAA | AGATGATTTC |
| msa128189.2{6_H36B} | GTAAGCAAGA | TAAGATTGTA | ACCTTTGGCA | AATCTAATAA | AGATGATTTC |
| msa128189.2{6_JM9130013} | GTAAGCAAGA | TAAGATTGTA | ACCTTTGGCA | AATCTAATAA | AGATGATTTC |
| msa128189.2{6_COH1} | GTAAGCAAGA | TAAGATTGTA | ACCTTTGGCA | AATCTAATAA | AGATGATTTC |
| msa128189.2{6_M732} | GTAAGCAAGA | TAAGATTGTA | ACCTTTGGCA | AATCTAATAA | AGATGATTTC |
| msa128189.2{6_M781} | GTAAGCAAGA | TAAGATTGTA | ACCTTTGGCA | AATCTAATAA | AGATGATTTC |
| msa128189.2{6_090} | GTAAGCAAGA | TAAGATTGTA | ACCTTTGGCA | AATCTAATAA | AGATGATTTC |
| msa128189.2{6_CJB110} | GTAAGCAAGA | TAAGATTGTA | ACCTTTGGCA | AATCTAATAA | AGATGATTTC |
| msa128189.2{6_1169NT} | GTAAGCAAGA | TAAGATTGTA | ACCTTTGGCA | AATCTAATAA | AGATGATTTC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 301 | | | | | |
| msa128189.2{6_18RS21} | CGTAAGACAG | GTTATgATGG | TCGAGGTTAT | CAACCAATGG | TTTATGGGTT |
| msa128189.2{6_2603} | CGTAAGACAG | GTTATgATGG | TCGAGGTTAT | CAACCAATGG | TTTATGGGTT |
| msa128189.2{6_A909} | CGTAAGACAG | GTTATgATGG | TCGAGGTTAT | CAACCAATGG | TTTATGGGTT |
| msa128189.2{6_H36B} | CGTAAGACAG | GTTATgATGG | TCGAGGTTAT | CAACCAATGG | TTTATGGGTT |
| msa128189.2{6_JM9130013} | CGTAAGACAG | GTTATgATGG | TCGAGGTTAT | CAACCAATGG | TTTATGGGTT |
| msa128189.2{6_COH1} | CGTAAGACAG | GTTATaATGG | TCGAGGTTAT | CAACCAATGG | TTTATGGGTT |
| msa128189.2{6_M732} | CGTAAGACAG | GTTATaATGG | TCGAGGTTAT | CAACCAATGG | TTTATGGGTT |
| msa128189.2{6_M781} | CGTAAGACAG | GTTATaATGG | TCGAGGTTAT | CAACCAATGG | TTTATGGGTT |
| msa128189.2{6_090} | CGTAAGACAG | GTTATgATGG | TCGAGGTTAT | CAACCAATGG | TTTATGGGTT |
| msa128189.2{6_CJB110} | CGTAAGACAG | GTTATgATGG | TCGAGGTTAT | CAACCAATGG | TTTATGGGTT |
| msa128189.2{6_1169NT} | CGTAAGACAG | GTTATgATGG | TCGAGGTTAT | CAACCAATGG | TTTATGGGTT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 351 | | | | | |
| msa128189.2{6_18RS21} | AGACAATTGT | CAAATGAGTC | AgACCAAAAG | TATGGTAAAA | CTTGTITTTT |
| msa128189.2{6_2603} | AGACAATTGT | CAAATGAGTC | AgACCAAAAG | TATGGTAAAA | CTTGTITTTT |
| msa128189.2{6_A909} | AGACAATTGT | CAAATGAGTC | AgACCAAAAG | TATGGTAAAA | CTTGTITTTT |
| msa128189.2{6_H36B} | AGACAATTGT | CAAATGAGTC | AgACCAAAAG | TATGGTAAAA | CTTGTITTTT |
| msa128189.2{6_JM9130013} | AGACAATTGT | CAAATGAGTC | AgACCAAAAG | TATGGTAAAA | CTTGTITTTT |
| msa128189.2{6_COH1} | AGACAATTGT | CAAATGAGTC | AgACCAAAAG | TATGGTAAAA | CTTGTITTTT |
| msa128189.2{6_M732} | AGACAATTGT | CAAATGAGTC | AgACCAAAAG | TATGGTAAAA | CTTGTITTTT |
| msa128189.2{6_M781} | AGACAATTGT | CAAATGAGTC | AgACCAAAAG | TATGGTAAAA | CTTGTITTTT |
| msa128189.2{6_090} | AGACAATTGT | CAAATGAGTC | AaACCAAAAG | TATGGTAAAA | CTTGTITTTT |
| msa128189.2{6_CJB110} | AGACAATTGT | CAAATGAGTC | AaACCAAAAG | TATGGTAAAA | CTTGTITTTT |
| msa128189.2{6_1169NT} | AGACAATTGT | CAAATGAGTC | AaACCAAAAG | TATGGTAAAA | CTTGTITTTT |
| Consensus | ***** | ***** | *~***** | ***** | ***** |
| 401 | | | | | |
| msa128189.2{6_18RS21} | ATTTTAAGGA | CGGGTTAAAA | AGGACATTTT | ACTATGATTT | TAAAGAAGAA |
| msa128189.2{6_2603} | ATTTTAAGGA | CGGGTTAAAA | AGGACATTTT | ACTATGATTT | TAAAGAAGAA |
| msa128189.2{6_A909} | ATTTTAAGGA | CGGGTTAAAA | AGGACATTTT | ACTATGATTT | TAAAGAAGAA |
| msa128189.2{6_H36B} | ATTTTAAGGA | CGGGTTAAAA | AGGACATTTT | ACTATGATTT | TAAAGAAGAA |
| msa128189.2{6_JM9130013} | ATTTTAAGGA | CGGGTTAAAA | AGGACATTTT | ACTATGATTT | TAAAGAAGAA |
| msa128189.2{6_COH1} | ATTTTAAGGA | CGGGTTAAAA | AGGACATTTT | ACTATGATTT | TAAAGAAGAA |
| msa128189.2{6_M732} | ATTTTAAGGA | CGGGTTAAAA | AGGACATTTT | ACTATGATTT | TAAAGAAGAA |
| msa128189.2{6_M781} | ATTTTAAGGA | CGGGTTAAAA | AGGACATTTT | ACTATGATTT | TAAAGAAGAA |
| msa128189.2{6_090} | ATTTTAAGGA | CGGGTTAAAA | AGGACATTTT | ACTATGATTT | TAAAGAAGAA |
| msa128189.2{6_CJB110} | ATTTTAAGGA | CGGGTTAAAA | AGGACATTTT | ACTATGATTT | TAAAGAAGAA |
| msa128189.2{6_1169NT} | ATTTTAAGGA | CGGGTTAAAA | AGGACATTTT | ACTATGATTT | TAAAGAAGAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 451 | | | | | |
| msa128189.2{6_18RS21} | ACT--- | | | | |
| msa128189.2{6_2603} | ACTtaa | | | | |
| msa128189.2{6_A909} | ACT--- | | | | |
| msa128189.2{6_H36B} | ACT--- | | | | |
| msa128189.2{6_JM9130013} | ACT--- | | | | |
| msa128189.2{6_COH1} | ACT--- | | | | |
| msa128189.2{6_M732} | ACT--- | | | | |
| msa128189.2{6_M781} | ACT--- | | | | |
| msa128189.2{6_090} | ACT--- | | | | |
| msa128189.2{6_CJB110} | ACT--- | | | | |
| msa128189.2{6_1169NT} | ACT--- | | | | |
| Consensus | ***** | | | | |

SEQ ID NO. 8212

STRAIN 2603 frame: 1

MKNLLKCKDKKVKAFPTLLECLVALVTITGALLVYQGLTKLLAQQIVVMSSSSQSEWVLL
 TQQLNAEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNC

Table 82: Comparative Sequences relating to SAG0165

QMSQTKSMVKLVFYFKDGLKRTFYDFKEET.

SEQ ID NO. 8213

STRAIN 090 frame: 3

EFEGAHLLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKS
MVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8214

STRAIN A909 frame: 3

EFEGAHLLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8215

STRAIN H36B frame: 3

AEFEGAHLLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8216

STRAIN 18RS21 frame: 2

EFEGAHLLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8217

STRAIN M732 frame: 3

EFEGAHLLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8218

STRAIN COH1 frame: 1

EFEGAHLLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8219

STRAIN M781 frame: 2

EFEGAHLLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8220

STRAIN CJB110 frame: 1

EFEGAHLLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8221

STRAIN 1169NT frame: 3

EGAHLLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKSM
VKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8222

STRAIN JM9130013 frame: 2

AEFEGAHLLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFYDFKEET

PRETTY of: /biotmp/msa128319.2{*} February 7, 2003 08:27 ..

| | | | | | |
|--------------------------|------------|------------|------------|------------|------------|
| | 1 | | | | 50 |
| msa128319.2{6_090} | ----- | ----- | ----- | ----- | ----- |
| msa128319.2{6_1169NT} | ----- | ----- | ----- | ----- | ----- |
| msa128319.2{6_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa128319.2{6_2603} | mknlllkckd | kkvkaftlle | clvalvtitg | allvyggltk | llaqqivvms |
| msa128319.2{6_H36B} | ----- | ----- | ----- | ----- | ----- |
| msa128319.2{6_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa128319.2{6_A909} | ----- | ----- | ----- | ----- | ----- |
| msa128319.2{6_CJB110} | ----- | ----- | ----- | ----- | ----- |
| msa128319.2{6_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa128319.2{6_M732} | ----- | ----- | ----- | ----- | ----- |
| msa128319.2{6_M781} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 51 | | | | 100 |
| msa128319.2{6_090} | ----- | -----fEG | AHLEYLRQNK | LYLRKQDKIV | TFGKSNKDDF |
| msa128319.2{6_1169NT} | ----- | -----EG | AHLEYLRQNK | LYLRKQDKIV | TFGKSNKDDF |
| msa128319.2{6_18RS21} | ----- | -----EfEG | AHLEYLRQNK | LYLRKQDKIV | TFGKSNKDDF |
| msa128319.2{6_2603} | sssqsewvll | tqqlnAEfEG | AHLEYLRQNK | LYLRKQDKIV | TFGKSNKDDF |
| msa128319.2{6_H36B} | ----- | -----AEfEG | AHLEYLRQNK | LYLRKQDKIV | TFGKSNKDDF |
| msa128319.2{6_JM9130013} | ----- | -----AEfEG | AHLEYLRQNK | LYLRKQDKIV | TFGKSNKDDF |
| msa128319.2{6_A909} | ----- | -----EfEG | AHLEYLRQNK | LYLRKQDKIV | TFGKSNKDDF |
| msa128319.2{6_CJB110} | ----- | -----EfEG | AHLEYLRQNK | LYLRKQDKIV | TFGKSNKDDF |
| msa128319.2{6_COH1} | ----- | -----EfEG | AHLEYLRQNK | LYLRKQDKIV | TFGKSNKDDF |
| msa128319.2{6_M732} | ----- | -----EfEG | AHLEYLRQNK | LYLRKQDKIV | TFGKSNKDDF |
| msa128319.2{6_M781} | ----- | -----EfEG | AHLEYLRQNK | LYLRKQDKIV | TFGKSNKDDF |
| Consensus | ***** | *****_** | ***** | ***** | ***** |

Table 82: Comparative Sequences relating to SAG0165

| | | | | |
|--------------------------|------------|------------|------------|-----------------------|
| | 101 | | | 150 |
| msa128319.2{6_090} | RKTGYdGRGY | QPMVYGLDNC | QMSQTKSMVK | LVFYFKDGLK RTFYFDKKEE |
| msa128319.2{6_1169NT} | RKTGYdGRGY | QPMVYGLDNC | QMSQTKSMVK | LVFYFKDGLK RTFYFDKKEE |
| msa128319.2{6_18RS21} | RKTGYdGRGY | QPMVYGLDNC | QMSQTKSMVK | LVFYFKDGLK RTFYFDKKEE |
| msa128319.2{6_2603} | RKTGYdGRGY | QPMVYGLDNC | QMSQTKSMVK | LVFYFKDGLK RTFYFDKKEE |
| msa128319.2{6_H36B} | RKTGYdGRGY | QPMVYGLDNC | QMSQTKSMVK | LVFYFKDGLK RTFYFDKKEE |
| msa128319.2{6_JM9130013} | RKTGYdGRGY | QPMVYGLDNC | QMSQTKSMVK | LVFYFKDGLK RTFYFDKKEE |
| msa128319.2{6_A909} | RKTGYdGRGY | QPMVYGLDNC | QMSQTKSMVK | LVFYFKDGLK RTFYFDKKEE |
| msa128319.2{6_CJB110} | RKTGYdGRGY | QPMVYGLDNC | QMSQTKSMVK | LVFYFKDGLK RTFYFDKKEE |
| msa128319.2{6_COH1} | RKTGYnGRGY | QPMVYGLDNC | QMSQTKSMVK | LVFYFKDGLK RTFYFDKKEE |
| msa128319.2{6_M732} | RKTGYnGRGY | QPMVYGLDNC | QMSQTKSMVK | LVFYFKDGLK RTFYFDKKEE |
| msa128319.2{6_M781} | RKTGYnGRGY | QPMVYGLDNC | QMSQTKSMVK | LVFYFKDGLK RTFYFDKKEE |
| Consensus | ***** | ***** | ***** | ***** |
| | 151 | | | |
| msa128319.2{6_090} | T~ | | | |
| msa128319.2{6_1169NT} | T~ | | | |
| msa128319.2{6_18RS21} | T~ | | | |
| msa128319.2{6_2603} | T~ | | | |
| msa128319.2{6_H36B} | T~ | | | |
| msa128319.2{6_JM9130013} | T~ | | | |
| msa128319.2{6_A909} | T~ | | | |
| msa128319.2{6_CJB110} | T~ | | | |
| msa128319.2{6_COH1} | T~ | | | |
| msa128319.2{6_M732} | T~ | | | |
| msa128319.2{6_M781} | T~ | | | |
| Consensus | ** | | | |

Table 83: Comparative Sequences relating to SAG0108

SEQ ID NO. 8301

STRAIN 2603

atgaaaaagattcgattatcaaagtttattaaaatgattgttgttattttgtttttaatt
 agtgtagcagctagttttattttttccacgttgcccaagttcgagatgataaatccttt
 atttcaaatgggtcaacgttaagcctggaaactctttatatgtctatgataaatcctttgat
 aagctattaaagcaaaaaatagaaatgacaaacaaaataaaagcaagttgcttggat
 gtctcgtgctgtaagaaaactcataagacagctgttgcgttcaggttttgcgaatagc
 aaagagaatatgaaggcatatgggtggctgtttcataagttaggatataaatgttcttatg
 cctgacaatattgcacatgggtgaaagtcatgggcagttgataggctatggctggaacgac
 cgcgagaacattatcaaatggacagaaatgatagttgataagaatccatcaagccaaatt
 actttatttgggtgttcaatgggtggagcaacagtcagtgaggctagtggtgaaaaatta
 cctagtcaggtgtttaatcatctgaagattgcggttattctagtggttggatgaatta
 aaatttcaggctaaagagatgtatgggttaccagccttcccactcttatatgaagtttca
 caaatttctaaaatcagagcaggttttctgtatggacaagcaagtagtgctgaacaattg
 aaaaagaataatttaccagccctctttattcatggtgataaggataatttgtttcaaca
 agtatgggttatgacaactataaagctacagcaggttaagaaagagctttatattgtaaaa
 ggggcaaacatgcgaatcttttgaacagagccagaaaaatatgagaaacgtatctct
 agttttttgaaaaatatgaaaaa

SEQ ID NO. 8302

STRAIN 090

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCC
 AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTT
 TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAATAGAA
 ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAA
 GAAACTCATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAAG
 AGAATATGAAGGCATATGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTATGCTTACCAATATGACATGCTGGAAGTTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCAATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTACTTTaTTTGGTGTTCATGGGT
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
 TAATATCATTTGAAGATTGCGGTTATTCTAGTGTTCGGATGAATTAAT
 TTCAGGCTAAAGAGATGATGGTTTACCAGCCTTCCCCTCTTATATGAA
 GTTTCAACAATTTCTAAATCAGAGCAGGTTTTCTGTATGGACAAGCAAG
 TAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATG
 GTGATAAGGATAATTTTGTCCAAAGATATGGTTTATGACAACTATAAAA
 GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAGGGGCAAAACATGC
 GAAATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGA AAAAATATGAAAAA

SEQ ID NO. 8303

STRAIN A909

AATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTTTATATGCT
 TATGATAAATCCTTTGATAAGCTATTAAAGCAAAAATAGAAATGACAAA
 CCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTC
 ATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGAGAATATG
 AAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCC
 TGACAAACATGACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCT
 GGAACGACCGCGAAGCAATTTCAAATGGACAGAAATGATAGTTGATAAG
 AATTCTCAAGCCAAATTACTTTATTGGTGTTCATGGGTGGAGCAAC
 AGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCA
 TTGAAGATGCGGTTATTCTGGTGTTCGGGATGAATTAATTTTACAGGCT
 AAAGAGATGATGGTTTACCAGCCTTCCCCTCTTATATGAAGTTTCAAC
 AATTTCTAAATCAGAGCAGGTTTTCTGTATGGACAAGCAAGTAGTGTG
 AACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGGTGATAAG
 GATAATTTTGTTCACCAAGATAGGTTTATGACAACTATAAGCTACAGC
 AGGTAAGAAAGAGCTTTATATTGTAAAGGGGCAAAACATGCGAAATCTT
 TTGAAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAA
 AATATGAAAAA

SEQ ID NO. 8304

STRAIN H36B

AGTTTTTATTTTTTCCACGTTGCCCAAGTTTCGAGATGATAAATCCTTTAT
 TTCAAATGGTCAACGTAAGCCTGGAACTCTTTATATGCTTATGATAAAT
 CCTTTGATAAGCTATTAAAGCAAAAATAGAAATGACAAACCAAAATATA
 AAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTCATAAGACAGC
 GTTGTGCTTCATGGTTTTTGGCAATAGCAAAGAGAATATGAAGGCATATG
 GTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCTTGACAACATT
 GCACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCTGGAACGACCG
 CGAGAACATTATCAAATGGACAGAAATGATAGTTGATAAGAAATTCATCAA
 GCCAAATTACTTTATTGGTGTTCATGGGTGGAGCAACAGTCATGATG
 GCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCATTGAAGATTG
 CGGTTATTCTGGTGTTCGGGATGAATTAATTTTACAGGCTAAAGAGATGT
 ATGGTTTACCAGCCTTCCCCTCTTATATGAAGTTTCAACAATTTCTAAA
 ATCAGAGCAGGTTTTCTGTATGGACAAGCAAGTAGTGTGCAACAAATTGAA
 AAAGAATAATTTACCAGCCCTCTTTATTCATGGTGATAAGGATAATTTTG
 TTCCAACAAGTATGGTTTATGACAACTATAAGCTACAGCAGGTAAGAAA
 GAGCTTTATATTGTAAAGGGGCAAAACATGCGAAATCTTTTGAACAGA
 GCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAAAAATATGAAA
 AA

SEQ ID NO. 8305

STRAIN 18RS21

Table 83: Comparative Sequences relating to SAG0108

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTTT
 ATATGCTTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGTTAAG
 AAAACTCATAAGACAGCTGTGTGCTTCATGGTTTTGCGAATAGCAAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTTC
 TTATGCTTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTGCGGTTATTCTAGTGTGGGATGAATTAAAAAT
 TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTTCATGG
 TGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
 AAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8306

STRAIN M732

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTTT
 ATATGCTTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGCTAAG
 AAAACTCATAAGACAGTTGTTGTGCTTCATGGTTTTGCGAATAGCAAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTTC
 TTATGCTTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 GGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTGTGGTTATTCTAGTGTGGGATGAATTAAAAAT
 TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTTCATGG
 TGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
 AAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8307

STRAIN COH1

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCG
 GAGATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCT
 TTATATGCTTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
 AATGaCAAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGCTA
 AGAAAACTCATAAGACAGTTGTTGTGCTTCATGGTTTTGCGAATAGCAAAA
 GAGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGT
 TCTTATGCTTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAG
 CTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATA
 GTGGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 TGGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTG
 TTAATATCATTGAAGATTGTGGTTATTCTAGTGTGGGATGAATTAAAAA
 TTTCAAGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
 AGTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAA
 GTAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTTCAT
 GGTGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAA
 AGCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
 CGAAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT
 TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8308

STRAIN M781

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCG
 AGATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTT
 TATATGCTTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
 ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGCTAA
 GAAACTCATAAGACAGTTGTTGTGCTTCATGGTTTTGCGAATAGCAAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTATGCTTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAG
 TGGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGTG
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 TAAATATCATTGAAGATTGTGGTTATTCTAGTGTGGGATGAATTAAAAAT
 TTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
 GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
 TAgTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTTCATG
 GTGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACATAA
 GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
 GAAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT
 TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8309

Table 83: Comparative Sequences relating to SAG0108

STRAIN CJB110

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGAG
 ATGATAAATCCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTA
 TATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAAT
 GACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGA
 AAACCTATAAGACAGCTGTTGCTGTTTCATGGTTTTGCGAATAGCAAAGAG
 AATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCT
 TATGCTGTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGCT
 ATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGTT
 GATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGG
 AGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTA
 ATATCATTGAAGATTGCGGTTATTCTAGTGTTTGGGATGAATTAATAATTT
 CAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAGT
 TTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGTA
 GTGTGGAACAATTGAAAAAGAAATAATTACCAGCCCTCTTTATTCATGGT
 GATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAGC
 TACAGCAGGTAAGAAAGAGCTTTATATTTGTAAGGGGGCAAAACATGCGA
 AATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTT
 TTGAAAAAATATGAAAA

SEQ ID NO. 8310

STRAIN 1169NT

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAATCCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
 ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCcAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAG
 AAAACCTATAAGACAGCTGTTGCTGTTTCATGGTTTTGCGAATAGCAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCT
 TTATACCTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTGCGGTTATTCTAGTGTTTGGGATGAATTAATAAT
 TCAGGCTAaAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTAGAACAAATTGAAAAAGAAATAATTACCAGCCCTCTTTATTCATGG
 TGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTTGTAAGGGGGCAAAACATGCG
 AATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTT
 TTTGAAAAAATATGAAAA

SEQ ID NO. 8311

STRAIN JM9130013

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
 AGATGATAAATCCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
 ATGaCAAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGTTAA
 GAAAACTCATAAGACAGCTGTTGCTGTTTCATGGTTTTGCGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTATGCTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCaAATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGT
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
 TAATATCATTGAAGATTGCGGTTATTCTAGTGTTTGGGATGAATTAATAAT
 TTCAAGCTAaAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
 TAGTGTGGAACAATTGAAAAAGAAATAATTACCAGCCCTCTTTATTCATG
 GTGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAA
 GCTACAGCAGGTAAGAAAGAGCTTTATATTTGTAAGGGGGCAAAACATGCG
 GAAATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGAAAAAATATGAAAA

PRETTY of: /biotmp/msa286608.2{*} February 24, 2003 06:26 ..

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| | 1 | | | | 50 |
| msa286608.2{662_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa286608.2{662_M732} | ----- | ----- | ----- | ----- | ----- |
| msa286608.2{662_M781} | ----- | ----- | ----- | ----- | ----- |
| msa286608.2{662_A909} | ----- | ----- | ----- | ----- | ----- |
| msa286608.2{662_H36B} | ----- | ----- | ----- | ----- | ----- |
| msa286608.2{662_090} | ----- | ----- | ----- | ----- | ----- |
| msa286608.2{662_CJB110} | ----- | ----- | ----- | ----- | ----- |
| msa286608.2{662_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa286608.2{662_2603} | atgaaaaaga | ttcgattatc | aaagtttatt | aaaatgattg | ttgtattttt |
| msa286608.2{662_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa286608.2{662_1169NT} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ***** | ***** | ***** |

| | | | | | |
|-----------------------|--------|------------|------------|------------|-----|
| | 51 | | | | 100 |
| msa286608.2{662_COH1} | -----g | ctagttttta | ttttttccac | gttgcccaag | |
| msa286608.2{662_M732} | -----g | ctagttttta | ttttttccac | gttgcccaag | |
| msa286608.2{662_M781} | -----g | ctagttttta | ttttttccac | gttgcccaag | |

Table 83: Comparative Sequences relating to SAG0108

| | | | | | |
|----------------------------|------------|-------------|-------------|------------|------------|
| msa286608.2{662_A909} | ----- | ----- | ----- | ----- | ----- |
| msa286608.2{662_H36B} | ----- | ----- | --agtttttta | ttttttccac | gttgcccaag |
| msa286608.2{662_090} | ----- | ----- | ctagtttttta | ttttttccac | gttgcccaag |
| msa286608.2{662_CJB110} | ----- | ----- | ctagtttttta | ttttttccac | gttgcccaag |
| msa286608.2{662_18RS21} | ----- | ----- | ctagtttttta | ttttttccac | gttgcccaag |
| msa286608.2{662_2603} | gtttttaatt | agtgttagcag | ctagtttttta | ttttttccac | gttgcccaag |
| msa286608.2{662_JM9130013} | ----- | ----- | ctagtttttta | ttttttccac | gttgcccaag |
| msa286608.2{662_1169NT} | ----- | ----- | ctagtttttta | ttttttccac | gttgcccaag |
| Consensus | ***** | ***** | ----- | ----- | ----- |
| 101 | | | | | |
| msa286608.2{662_COH1} | ttcgagatga | taAATCCTTT | ATTTCAAATG | GTCACGTAA | GCCTGGAAAC |
| msa286608.2{662_M732} | ttcgagatga | taAATCCTTT | ATTTCAAATG | GTCACGTAA | GCCTGGAAAC |
| msa286608.2{662_M781} | ttcgagatga | taAATCCTTT | ATTTCAAATG | GTCACGTAA | GCCTGGAAAC |
| msa286608.2{662_A909} | ----- | --AATCCTTT | ATTTCAAATG | GTCACGTAA | GCCTGGAAAC |
| msa286608.2{662_H36B} | ttcgagatga | taAATCCTTT | ATTTCAAATG | GTCACGTAA | GCCTGGAAAC |
| msa286608.2{662_090} | ttcgagatga | taAATCCTTT | ATTTCAAATG | GTCACGTAA | GCCTGGAAAC |
| msa286608.2{662_CJB110} | ttcgagatga | taAATCCTTT | ATTTCAAATG | GTCACGTAA | GCCTGGAAAC |
| msa286608.2{662_18RS21} | ttcgagatga | taAATCCTTT | ATTTCAAATG | GTCACGTAA | GCCTGGAAAC |
| msa286608.2{662_2603} | ttcgagatga | taAATCCTTT | ATTTCAAATG | GTCACGTAA | GCCTGGAAAC |
| msa286608.2{662_JM9130013} | ttcgagatga | taAATCCTTT | ATTTCAAATG | GTCACGTAA | GCCTGGAAAC |
| msa286608.2{662_1169NT} | ttcgagatga | taAATCCTTT | ATTTCAAATG | GTCACGTAA | GCCTGGAAAC |
| Consensus | ----- | ***** | ***** | ***** | ***** |
| 151 | | | | | |
| msa286608.2{662_COH1} | TCTTTATATG | CTTATGATAA | ATCCTTTGAT | AAGCTATTAA | AGCAAAAAAT |
| msa286608.2{662_M732} | TCTTTATATG | CTTATGATAA | ATCCTTTGAT | AAGCTATTAA | AGCAAAAAAT |
| msa286608.2{662_M781} | TCTTTATATG | CTTATGATAA | ATCCTTTGAT | AAGCTATTAA | AGCAAAAAAT |
| msa286608.2{662_A909} | TCTTTATATG | CTTATGATAA | ATCCTTTGAT | AAGCTATTAA | AGCAAAAAAT |
| msa286608.2{662_H36B} | TCTTTATATG | CTTATGATAA | ATCCTTTGAT | AAGCTATTAA | AGCAAAAAAT |
| msa286608.2{662_090} | TCTTTATATG | CTTATGATAA | ATCCTTTGAT | AAGCTATTAA | AGCAAAAAAT |
| msa286608.2{662_CJB110} | TCTTTATATG | CTTATGATAA | ATCCTTTGAT | AAGCTATTAA | AGCAAAAAAT |
| msa286608.2{662_18RS21} | TCTTTATATG | CTTATGATAA | ATCCTTTGAT | AAGCTATTAA | AGCAAAAAAT |
| msa286608.2{662_2603} | TCTTTATATG | CTTATGATAA | ATCCTTTGAT | AAGCTATTAA | AGCAAAAAAT |
| msa286608.2{662_JM9130013} | TCTTTATATG | CTTATGATAA | ATCCTTTGAT | AAGCTATTAA | AGCAAAAAAT |
| msa286608.2{662_1169NT} | TCTTTATATG | CTTATGATAA | ATCCTTTGAT | AAGCTATTAA | AGCAAAAAAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 201 | | | | | |
| msa286608.2{662_COH1} | AGAAATGACA | AACCAAAATA | TAAAGCAAGT | TGCTTGGTAT | GTTCTGCTG |
| msa286608.2{662_M732} | AGAAATGACA | AACCAAAATA | TAAAGCAAGT | TGCTTGGTAT | GTTCTGCTG |
| msa286608.2{662_M781} | AGAAATGACA | AACCAAAATA | TAAAGCAAGT | TGCTTGGTAT | GTTCTGCTG |
| msa286608.2{662_A909} | AGAAATGACA | AACCAAAATA | TAAAGCAAGT | TGCTTGGTAT | GTTCTGCTG |
| msa286608.2{662_H36B} | AGAAATGACA | AACCAAAATA | TAAAGCAAGT | TGCTTGGTAT | GTTCTGCTG |
| msa286608.2{662_090} | AGAAATGACA | AACCAAAATA | TAAAGCAAGT | TGCTTGGTAT | GTTCTGCTG |
| msa286608.2{662_CJB110} | AGAAATGACA | AACCAAAATA | TAAAGCAAGT | TGCTTGGTAT | GTTCTGCTG |
| msa286608.2{662_18RS21} | AGAAATGACA | AACCAAAATA | TAAAGCAAGT | TGCTTGGTAT | GTTCTGCTG |
| msa286608.2{662_2603} | AGAAATGACA | AACCAAAATA | TAAAGCAAGT | TGCTTGGTAT | GTTCTGCTG |
| msa286608.2{662_JM9130013} | AGAAATGACA | AACCAAAATA | TAAAGCAAGT | TGCTTGGTAT | GTTCTGCTG |
| msa286608.2{662_1169NT} | AGAAATGACA | AACCAAAATA | TAAAGCAAGT | TGCTTGGTAT | GTTCTGCTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 251 | | | | | |
| msa286608.2{662_COH1} | cTAAGAAAAC | TCATAAGACA | GcTGTGTGCG | TTCATGGTTT | TGCGAATAGC |
| msa286608.2{662_M732} | cTAAGAAAAC | TCATAAGACA | GcTGTGTGCG | TTCATGGTTT | TGCGAATAGC |
| msa286608.2{662_M781} | cTAAGAAAAC | TCATAAGACA | GcTGTGTGCG | TTCATGGTTT | TGCGAATAGC |
| msa286608.2{662_A909} | cTAAGAAAAC | TCATAAGACA | GcTGTGTGCG | TTCATGGTTT | TGCGAATAGC |
| msa286608.2{662_H36B} | cTAAGAAAAC | TCATAAGACA | GcTGTGTGCG | TTCATGGTTT | TGCGAATAGC |
| msa286608.2{662_090} | cTAAGAAAAC | TCATAAGACA | GcTGTGTGCG | TTCATGGTTT | TGCGAATAGC |
| msa286608.2{662_CJB110} | cTAAGAAAAC | TCATAAGACA | GcTGTGTGCG | TTCATGGTTT | TGCGAATAGC |
| msa286608.2{662_18RS21} | cTAAGAAAAC | TCATAAGACA | GcTGTGTGCG | TTCATGGTTT | TGCGAATAGC |
| msa286608.2{662_2603} | cTAAGAAAAC | TCATAAGACA | GcTGTGTGCG | TTCATGGTTT | TGCGAATAGC |
| msa286608.2{662_JM9130013} | cTAAGAAAAC | TCATAAGACA | GcTGTGTGCG | TTCATGGTTT | TGCGAATAGC |
| msa286608.2{662_1169NT} | cTAAGAAAAC | TCATAAGACA | GcTGTGTGCG | TTCATGGTTT | TGCGAATAGC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 301 | | | | | |
| msa286608.2{662_COH1} | AAAGAGAATA | TGAAGGCATA | TGGTTGGCTG | TTTCATAAGT | TAGGATACAA |
| msa286608.2{662_M732} | AAAGAGAATA | TGAAGGCATA | TGGTTGGCTG | TTTCATAAGT | TAGGATACAA |
| msa286608.2{662_M781} | AAAGAGAATA | TGAAGGCATA | TGGTTGGCTG | TTTCATAAGT | TAGGATACAA |
| msa286608.2{662_A909} | AAAGAGAATA | TGAAGGCATA | TGGTTGGCTG | TTTCATAAGT | TAGGATACAA |
| msa286608.2{662_H36B} | AAAGAGAATA | TGAAGGCATA | TGGTTGGCTG | TTTCATAAGT | TAGGATACAA |
| msa286608.2{662_090} | AAAGAGAATA | TGAAGGCATA | TGGTTGGCTG | TTTCATAAGT | TAGGATACAA |
| msa286608.2{662_CJB110} | AAAGAGAATA | TGAAGGCATA | TGGTTGGCTG | TTTCATAAGT | TAGGATACAA |
| msa286608.2{662_18RS21} | AAAGAGAATA | TGAAGGCATA | TGGTTGGCTG | TTTCATAAGT | TAGGATACAA |
| msa286608.2{662_2603} | AAAGAGAATA | TGAAGGCATA | TGGTTGGCTG | TTTCATAAGT | TAGGATACAA |
| msa286608.2{662_JM9130013} | AAAGAGAATA | TGAAGGCATA | TGGTTGGCTG | TTTCATAAGT | TAGGATACAA |
| msa286608.2{662_1169NT} | AAAGAGAATA | TGAAGGCATA | TGGTTGGCTG | TTTCATAAGT | TAGGATACAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 351 | | | | | |
| msa286608.2{662_COH1} | TGTTCTTATg | CCTGACAAcA | TTGCACATGG | TGAAAGTCAT | GGGCAGTTGA |
| msa286608.2{662_M732} | TGTTCTTATg | CCTGACAAcA | TTGCACATGG | TGAAAGTCAT | GGGCAGTTGA |
| 400 | | | | | |

Table 83: Comparative Sequences relating to SAG0108

| | | | | | | |
|----------------------------|-------------|-------------|------------|-------------|-------------|-----|
| msa286608.2{662_M781} | TGTTCTTTATg | CCTGACAAcA | TTGCACATGG | TGAAAGTCAT | GGGCAGTTGA | |
| msa286608.2{662_A909} | TGTTCTTTATg | CCTGACAAcA | TTGCACATGG | TGAAAGTCAT | GGGCAGTTGA | |
| msa286608.2{662_H36B} | TGTTCTTTATg | CCTGACAAcA | TTGCACATGG | TGAAAGTCAT | GGGCAGTTGA | |
| msa286608.2{662_090} | TGTTCTTTATg | CCTGACAAcA | TTGCACATGG | TGAAAGTCAT | GGGCAGTTGA | |
| msa286608.2{662_CJB110} | TGTTCTTTATg | CCTGACAAcA | TTGCACATGG | TGAAAGTCAT | GGGCAGTTGA | |
| msa286608.2{662_18RS21} | TGTTCTTTATg | CCTGACAAcA | TTGCACATGG | TGAAAGTCAT | GGGCAGTTGA | |
| msa286608.2{662_2603} | TGTTCTTTATg | CCTGACAAcA | TTGCACATGG | TGAAAGTCAT | GGGCAGTTGA | |
| msa286608.2{662_JM9130013} | TGTTCTTTATg | CCTGACAAcA | TTGCACATGG | TGAAAGTCAT | GGGCAGTTGA | |
| msa286608.2{662_1169NT} | TGTTCTTTATa | CCTGACAAcA | TTGCACATGG | TGAAAGTCAT | GGGCAGTTGA | |
| Consensus | *****-* | *****-* | ***** | ***** | ***** | |
| 401 | | | | | | 450 |
| msa286608.2{662_COH1} | TAGGCTATGG | CTGGAACGAC | CGCGAGAACA | TTATCAAATG | GACAGAAATG | |
| msa286608.2{662_M732} | TAGGCTATGG | CTGGAACGAC | CGCGAGAACA | TTATCAAATG | GACAGAAATG | |
| msa286608.2{662_M781} | TAGGCTATGG | CTGGAACGAC | CGCGAGAACA | TTATCAAATG | GACAGAAATG | |
| msa286608.2{662_A909} | TAGGCTATGG | CTGGAACGAC | CGCGAGAACA | TTATCAAATG | GACAGAAATG | |
| msa286608.2{662_H36B} | TAGGCTATGG | CTGGAACGAC | CGCGAGAACA | TTATCAAATG | GACAGAAATG | |
| msa286608.2{662_090} | TAGGCTATGG | CTGGAACGAC | CGCGAGAACA | TTATCAAATG | GACAGAAATG | |
| msa286608.2{662_CJB110} | TAGGCTATGG | CTGGAACGAC | CGCGAGAACA | TTATCAAATG | GACAGAAATG | |
| msa286608.2{662_18RS21} | TAGGCTATGG | CTGGAACGAC | CGCGAGAACA | TTATCAAATG | GACAGAAATG | |
| msa286608.2{662_2603} | TAGGCTATGG | CTGGAACGAC | CGCGAGAACA | TTATCAAATG | GACAGAAATG | |
| msa286608.2{662_JM9130013} | TAGGCTATGG | CTGGAACGAC | CGCGAGAACA | TTATCAAATG | GACAGAAATG | |
| msa286608.2{662_1169NT} | TAGGCTATGG | CTGGAACGAC | CGCGAGAACA | TTATCAAATG | GACAGAAATG | |
| Consensus | ***** | ***** | ***** | ***** | ***** | |
| 451 | | | | | | 500 |
| msa286608.2{662_COH1} | ATAGTgGATA | AGAATcCATC | AAGCCAAATT | ACTTTATTtTG | GTGTTTCAAT | |
| msa286608.2{662_M732} | ATAGTgGATA | AGAATcCATC | AAGCCAAATT | ACTTTATTtTG | GTGTTTCAAT | |
| msa286608.2{662_M781} | ATAGTgGATA | AGAATcCATC | AAGCCAAATT | ACTTTATTtTG | GTGTTTCAAT | |
| msa286608.2{662_A909} | ATAGTtGATA | AGAATtCATC | AAGCCAAATT | ACTTTATTtTG | GTGTTTCAAT | |
| msa286608.2{662_H36B} | ATAGTtGATA | AGAATtCATC | AAGCCAAATT | ACTTTATTtTG | GTGTTTCAAT | |
| msa286608.2{662_090} | ATAGTtGATA | AGAATtCATC | AAGCCAAATT | ACTTTATTtTG | GTGTTTCAAT | |
| msa286608.2{662_CJB110} | ATAGTtGATA | AGAATtCATC | AAGCCAAATT | ACTTTATTtTG | GTGTTTCAAT | |
| msa286608.2{662_18RS21} | ATAGTtGATA | AGAATtCATC | AAGCCAAATT | ACTTTATTtTG | GTGTTTCAAT | |
| msa286608.2{662_2603} | ATAGTtGATA | AGAATtCATC | AAGCCAAATT | ACTTTATTtTG | GTGTTTCAAT | |
| msa286608.2{662_JM9130013} | ATAGTtGATA | AGAATtCATC | AAGCCAAATT | ACTTTATTtTG | GTGTTTCAAT | |
| msa286608.2{662_1169NT} | ATAGTtGATA | AGAATtCATC | AAGCCAAATT | ACTTTATTtTG | GTGTTTCAAT | |
| Consensus | *****-***** | *****-***** | ***** | ***** | ***** | |
| 501 | | | | | | 550 |
| msa286608.2{662_COH1} | GGGTGGAGCA | ACAGTCATGA | TGGCTAGTGG | TGAAAAATTA | CCTAGTCAGG | |
| msa286608.2{662_M732} | GGGTGGAGCA | ACAGTCATGA | TGGCTAGTGG | TGAAAAATTA | CCTAGTCAGG | |
| msa286608.2{662_M781} | GGGTGGAGCA | ACAGTCATGA | TGGCTAGTGG | TGAAAAATTA | CCTAGTCAGG | |
| msa286608.2{662_A909} | GGGTGGAGCA | ACAGTCATGA | TGGCTAGTGG | TGAAAAATTA | CCTAGTCAGG | |
| msa286608.2{662_H36B} | GGGTGGAGCA | ACAGTCATGA | TGGCTAGTGG | TGAAAAATTA | CCTAGTCAGG | |
| msa286608.2{662_090} | GGGTGGAGCA | ACAGTCATGA | TGGCTAGTGG | TGAAAAATTA | CCTAGTCAGG | |
| msa286608.2{662_CJB110} | GGGTGGAGCA | ACAGTCATGA | TGGCTAGTGG | TGAAAAATTA | CCTAGTCAGG | |
| msa286608.2{662_18RS21} | GGGTGGAGCA | ACAGTCATGA | TGGCTAGTGG | TGAAAAATTA | CCTAGTCAGG | |
| msa286608.2{662_2603} | GGGTGGAGCA | ACAGTCATGA | TGGCTAGTGG | TGAAAAATTA | CCTAGTCAGG | |
| msa286608.2{662_JM9130013} | GGGTGGAGCA | ACAGTCATGA | TGGCTAGTGG | TGAAAAATTA | CCTAGTCAGG | |
| msa286608.2{662_1169NT} | GGGTGGAGCA | ACAGTCATGA | TGGCTAGTGG | TGAAAAATTA | CCTAGTCAGG | |
| Consensus | ***** | ***** | ***** | ***** | ***** | |
| 551 | | | | | | 600 |
| msa286608.2{662_COH1} | TTGTTAATAT | CATTGAAGAT | TGcGGTTATT | CTaGTGTTTg | GGATGAATTA | |
| msa286608.2{662_M732} | TTGTTAATAT | CATTGAAGAT | TGcGGTTATT | CTaGTGTTTg | GGATGAATTA | |
| msa286608.2{662_M781} | TTGTTAATAT | CATTGAAGAT | TGcGGTTATT | CTaGTGTTTg | GGATGAATTA | |
| msa286608.2{662_A909} | TTGTTAATAT | CATTGAAGAT | TGcGGTTATT | CTgGTGTTTg | GGATGAATTA | |
| msa286608.2{662_H36B} | TTGTTAATAT | CATTGAAGAT | TGcGGTTATT | CTgGTGTTTg | GGATGAATTA | |
| msa286608.2{662_090} | TTGTTAATAT | CATTGAAGAT | TGcGGTTATT | CTaGTGTTTg | GGATGAATTA | |
| msa286608.2{662_CJB110} | TTGTTAATAT | CATTGAAGAT | TGcGGTTATT | CTaGTGTTTg | GGATGAATTA | |
| msa286608.2{662_18RS21} | TTGTTAATAT | CATTGAAGAT | TGcGGTTATT | CTaGTGTTTg | GGATGAATTA | |
| msa286608.2{662_2603} | TTGTTAATAT | CATTGAAGAT | TGcGGTTATT | CTaGTGTTTg | GGATGAATTA | |
| msa286608.2{662_JM9130013} | TTGTTAATAT | CATTGAAGAT | TGcGGTTATT | CTaGTGTTTg | GGATGAATTA | |
| msa286608.2{662_1169NT} | TTGTTAATAT | CATTGAAGAT | TGcGGTTATT | CTaGTGTTTg | GGATGAATTA | |
| Consensus | ***** | ***** | **..***** | **..***** | ***** | |
| 601 | | | | | | 650 |
| msa286608.2{662_COH1} | AAATTTcAGG | CTAAAGAGAT | GTATGGTTTA | CCAGCCTTCC | CACCTCTTATA | |
| msa286608.2{662_M732} | AAATTTcAGG | CTAAAGAGAT | GTATGGTTTA | CCAGCCTTCC | CACCTCTTATA | |
| msa286608.2{662_M781} | AAATTTcAGG | CTAAAGAGAT | GTATGGTTTA | CCAGCCTTCC | CACCTCTTATA | |
| msa286608.2{662_A909} | AAATTTcAGG | CTAAAGAGAT | GTATGGTTTA | CCAGCCTTCC | CACCTCTTATA | |
| msa286608.2{662_H36B} | AAATTTcAGG | CTAAAGAGAT | GTATGGTTTA | CCAGCCTTCC | CACCTCTTATA | |
| msa286608.2{662_090} | AAATTTcAGG | CTAAAGAGAT | GTATGGTTTA | CCAGCCTTCC | CACCTCTTATA | |
| msa286608.2{662_CJB110} | AAATTTcAGG | CTAAAGAGAT | GTATGGTTTA | CCAGCCTTCC | CACCTCTTATA | |
| msa286608.2{662_18RS21} | AAATTTcAGG | CTAAAGAGAT | GTATGGTTTA | CCAGCCTTCC | CACCTCTTATA | |
| msa286608.2{662_2603} | AAATTTcAGG | CTAAAGAGAT | GTATGGTTTA | CCAGCCTTCC | CACCTCTTATA | |
| msa286608.2{662_JM9130013} | AAATTTcAGG | CTAAAGAGAT | GTATGGTTTA | CCAGCCTTCC | CACCTCTTATA | |
| msa286608.2{662_1169NT} | AAATTTcAGG | CTAAAGAGAT | GTATGGTTTA | CCAGCCTTCC | CACCTCTTATA | |
| Consensus | ***** | ***** | ***** | ***** | ***** | |
| 651 | | | | | | 700 |
| msa286608.2{662_COH1} | TGAAGTTTCA | ACAATTCTA | AAATCAGAGC | AGGTTTTCG | TATGGACAAG | |

Table 83: Comparative Sequences relating to SAG0108

| | | | | | |
|----------------------------|------------|------------|------------|------------|-------------|
| msa286608.2{662_M732} | TGAAGTTTCA | ACAATTTCTA | AAATCAGAGC | AGGTTTTTCG | TATGGACAAG |
| msa286608.2{662_M781} | TGAAGTTTCA | ACAATTTCTA | AAATCAGAGC | AGGTTTTTCG | TATGGACAAG |
| msa286608.2{662_A909} | TGAAGTTTCA | ACAATTTCTA | AAATCAGAGC | AGGTTTTTCG | TATGGACAAG |
| msa286608.2{662_H36B} | TGAAGTTTCA | ACAATTTCTA | AAATCAGAGC | AGGTTTTTCG | TATGGACAAG |
| msa286608.2{662_090} | TGAAGTTTCA | ACAATTTCTA | AAATCAGAGC | AGGTTTTTCG | TATGGACAAG |
| msa286608.2{662_CJB110} | TGAAGTTTCA | ACAATTTCTA | AAATCAGAGC | AGGTTTTTCG | TATGGACAAG |
| msa286608.2{662_18RS21} | TGAAGTTTCA | ACAATTTCTA | AAATCAGAGC | AGGTTTTTCG | TATGGACAAG |
| msa286608.2{662_2603} | TGAAGTTTCA | ACAATTTCTA | AAATCAGAGC | AGGTTTTTCG | TATGGACAAG |
| msa286608.2{662_JM9130013} | TGAAGTTTCA | ACAATTTCTA | AAATCAGAGC | AGGTTTTTCG | TATGGACAAG |
| msa286608.2{662_1169NT} | TGAAGTTTCA | ACAATTTCTA | AAATCAGAGC | AGGTTTTTCG | TATGGACAAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa286608.2{662_COH1} | CAAGTAGTGT | cGAACAATTG | AAAAAGAATA | ATTACCAGC | CCTCTTTATT |
| msa286608.2{662_M732} | CAAGTAGTGT | cGAACAATTG | AAAAAGAATA | ATTACCAGC | CCTCTTTATT |
| msa286608.2{662_M781} | CAAGTAGTGT | cGAACAATTG | AAAAAGAATA | ATTACCAGC | CCTCTTTATT |
| msa286608.2{662_A909} | CAAGTAGTGT | cGAACAATTG | AAAAAGAATA | ATTACCAGC | CCTCTTTATT |
| msa286608.2{662_H36B} | CAAGTAGTGT | cGAACAATTG | AAAAAGAATA | ATTACCAGC | CCTCTTTATT |
| msa286608.2{662_090} | CAAGTAGTGT | cGAACAATTG | AAAAAGAATA | ATTACCAGC | CCTCTTTATT |
| msa286608.2{662_CJB110} | CAAGTAGTGT | cGAACAATTG | AAAAAGAATA | ATTACCAGC | CCTCTTTATT |
| msa286608.2{662_18RS21} | CAAGTAGTGT | cGAACAATTG | AAAAAGAATA | ATTACCAGC | CCTCTTTATT |
| msa286608.2{662_2603} | CAAGTAGTGT | cGAACAATTG | AAAAAGAATA | ATTACCAGC | CCTCTTTATT |
| msa286608.2{662_JM9130013} | CAAGTAGTGT | cGAACAATTG | AAAAAGAATA | ATTACCAGC | CCTCTTTATT |
| msa286608.2{662_1169NT} | CAAGTAGTGT | cGAACAATTG | AAAAAGAATA | ATTACCAGC | CCTCTTTATT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa286608.2{662_COH1} | CATGGTGATA | AGGATAATTT | TGTTCCAACA | AGTATGGTTT | ATGACAACCTA |
| msa286608.2{662_M732} | CATGGTGATA | AGGATAATTT | TGTTCCAACA | AGTATGGTTT | ATGACAACCTA |
| msa286608.2{662_M781} | CATGGTGATA | AGGATAATTT | TGTTCCAACA | AGTATGGTTT | ATGACAACCTA |
| msa286608.2{662_A909} | CATGGTGATA | AGGATAATTT | TGTTCCAACA | AGTATGGTTT | ATGACAACCTA |
| msa286608.2{662_H36B} | CATGGTGATA | AGGATAATTT | TGTTCCAACA | AGTATGGTTT | ATGACAACCTA |
| msa286608.2{662_090} | CATGGTGATA | AGGATAATTT | TGTTCCAACA | AGTATGGTTT | ATGACAACCTA |
| msa286608.2{662_CJB110} | CATGGTGATA | AGGATAATTT | TGTTCCAACA | AGTATGGTTT | ATGACAACCTA |
| msa286608.2{662_18RS21} | CATGGTGATA | AGGATAATTT | TGTTCCAACA | AGTATGGTTT | ATGACAACCTA |
| msa286608.2{662_2603} | CATGGTGATA | AGGATAATTT | TGTTCCAACA | AGTATGGTTT | ATGACAACCTA |
| msa286608.2{662_JM9130013} | CATGGTGATA | AGGATAATTT | TGTTCCAACA | AGTATGGTTT | ATGACAACCTA |
| msa286608.2{662_1169NT} | CATGGTGATA | AGGATAATTT | TGTTCCAACA | AGTATGGTTT | ATGACAACCTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa286608.2{662_COH1} | TAAAGCTACA | GCAGGTAAGA | AAGAGCTTTA | TATTGTAAAA | GGGGCAAAAC |
| msa286608.2{662_M732} | TAAAGCTACA | GCAGGTAAGA | AAGAGCTTTA | TATTGTAAAA | GGGGCAAAAC |
| msa286608.2{662_M781} | TAAAGCTACA | GCAGGTAAGA | AAGAGCTTTA | TATTGTAAAA | GGGGCAAAAC |
| msa286608.2{662_A909} | TAAAGCTACA | GCAGGTAAGA | AAGAGCTTTA | TATTGTAAAA | GGGGCAAAAC |
| msa286608.2{662_H36B} | TAAAGCTACA | GCAGGTAAGA | AAGAGCTTTA | TATTGTAAAA | GGGGCAAAAC |
| msa286608.2{662_090} | TAAAGCTACA | GCAGGTAAGA | AAGAGCTTTA | TATTGTAAAA | GGGGCAAAAC |
| msa286608.2{662_CJB110} | TAAAGCTACA | GCAGGTAAGA | AAGAGCTTTA | TATTGTAAAA | GGGGCAAAAC |
| msa286608.2{662_18RS21} | TAAAGCTACA | GCAGGTAAGA | AAGAGCTTTA | TATTGTAAAA | GGGGCAAAAC |
| msa286608.2{662_2603} | TAAAGCTACA | GCAGGTAAGA | AAGAGCTTTA | TATTGTAAAA | GGGGCAAAAC |
| msa286608.2{662_JM9130013} | TAAAGCTACA | GCAGGTAAGA | AAGAGCTTTA | TATTGTAAAA | GGGGCAAAAC |
| msa286608.2{662_1169NT} | TAAAGCTACA | GCAGGTAAGA | AAGAGCTTTA | TATTGTAAAA | GGGGCAAAAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa286608.2{662_COH1} | ATGCGAAATC | TTTTGAAACA | GAGCCAGAAA | AATATGAGAA | ACGTATCTCT |
| msa286608.2{662_M732} | ATGCGAAATC | TTTTGAAACA | GAGCCAGAAA | AATATGAGAA | ACGTATCTCT |
| msa286608.2{662_M781} | ATGCGAAATC | TTTTGAAACA | GAGCCAGAAA | AATATGAGAA | ACGTATCTCT |
| msa286608.2{662_A909} | ATGCGAAATC | TTTTGAAACA | GAGCCAGAAA | AATATGAGAA | ACGTATCTCT |
| msa286608.2{662_H36B} | ATGCGAAATC | TTTTGAAACA | GAGCCAGAAA | AATATGAGAA | ACGTATCTCT |
| msa286608.2{662_090} | ATGCGAAATC | TTTTGAAACA | GAGCCAGAAA | AATATGAGAA | ACGTATCTCT |
| msa286608.2{662_CJB110} | ATGCGAAATC | TTTTGAAACA | GAGCCAGAAA | AATATGAGAA | ACGTATCTCT |
| msa286608.2{662_18RS21} | ATGCGAAATC | TTTTGAAACA | GAGCCAGAAA | AATATGAGAA | ACGTATCTCT |
| msa286608.2{662_2603} | ATGCGAAATC | TTTTGAAACA | GAGCCAGAAA | AATATGAGAA | ACGTATCTCT |
| msa286608.2{662_JM9130013} | ATGCGAAATC | TTTTGAAACA | GAGCCAGAAA | AATATGAGAA | ACGTATCTCT |
| msa286608.2{662_1169NT} | ATGCGAAATC | TTTTGAAACA | GAGCCAGAAA | AATATGAGAA | ACGTATCTCT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa286608.2{662_COH1} | AGTTTTTTGA | AAAAATATGA | AAAA | | |
| msa286608.2{662_M732} | AGTTTTTTGA | AAAAATATGA | AAAA | | |
| msa286608.2{662_M781} | AGTTTTTTGA | AAAAATATGA | AAAA | | |
| msa286608.2{662_A909} | AGTTTTTTGA | AAAAATATGA | AAAA | | |
| msa286608.2{662_H36B} | AGTTTTTTGA | AAAAATATGA | AAAA | | |
| msa286608.2{662_090} | AGTTTTTTGA | AAAAATATGA | AAAA | | |
| msa286608.2{662_CJB110} | AGTTTTTTGA | AAAAATATGA | AAAA | | |
| msa286608.2{662_18RS21} | AGTTTTTTGA | AAAAATATGA | AAAA | | |
| msa286608.2{662_2603} | AGTTTTTTGA | AAAAATATGA | AAAA | | |
| msa286608.2{662_JM9130013} | AGTTTTTTGA | AAAAATATGA | AAAA | | |
| msa286608.2{662_1169NT} | AGTTTTTTGA | AAAAATATGA | AAAA | | |
| Consensus | ***** | ***** | ***** | | |

SEQ ID NO. 8312

Table 83: Comparative Sequences relating to SAG0108

STRAIN 2603 frame: 1

MKKIRLSKFIKMIIVILFLISVAASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFD
KLLKQKIEMTNQNIKQVAVYVPAVKKTKHTAVVHGFANSKENMKAYGWLPHKLGYNVLM
PDNIAHGESHGQLIGYGWNDRENI IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKL
PSQVVNI IEDCGYSSVWDELKFKQAKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQL
KKNLPALEFIHGDKDNFVPTSMVYDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRIS
SFLKKYEK

SEQ ID NO. 8313

STRAIN 090 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8314

STRAIN A909 frame: 3

SFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPAKKTHKTAVVHGFAN
SKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDRENI IKWTEMIVDKNSSS
QITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQAKEMYGLPAFPLLYE
VSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMVYDNYKATAGKKELYI
VKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8315

STRAIN H36B frame: 1

SFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
KKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNSSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8316

STRAIN 18RS21 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
VKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8317

STRAIN M732 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8318

STRAIN COH1 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8319

STRAIN M781 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8320

STRAIN CJB110 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8321

STRAIN 1169NT frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLI PDNIAHGESHGQLIGYGWNDREN
I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

SEQ ID NO. 8322

Table 83: Comparative Sequences relating to SAG0108

STRAIN JM9130013 frame: 1

ASFFYFFHVAQVRDDKSF ISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
 VKKTHKTAVVVHGFANSKENMKAYGWL FHLGYNVLPDNIAGHESHGQLIGYGWDRN
 IKWTMIIVDKNPSSQITLFGVSMGGATVMMASGEKLPQVNNI IEDCGYSSVWDELKFO
 AKEMYGLPAFPLLYEVSTISKIRAGFSYQASSVEQLKKNLPALEI HGDKNFVPTSMV
 YDNYKATAGKELYIVGAKHAKSFETEPEKYEKRISFLKKYK

PRETTY of: /biotmp/msa286876.2{*} February 24, 2003 06:46 ..

| | | | | | |
|----------------------------|------------|------------|--------------|------------|-------------|
| | 1 | | | | 50 |
| msa286876.2{662_A909} | ----- | ----- | ----- | -----SF | ISNGQRKPGN |
| msa286876.2{662_H36B} | ----- | ----- | -----SFYFFH | VAQVRDDKSF | ISNGQRKPGN |
| msa286876.2{662_COH1} | ----- | ----- | -----ASFYFFH | VAQVRDDKSF | ISNGQRKPGN |
| msa286876.2{662_M732} | ----- | ----- | -----ASFYFFH | VAQVRDDKSF | ISNGQRKPGN |
| msa286876.2{662_M781} | ----- | ----- | -----ASFYFFH | VAQVRDDKSF | ISNGQRKPGN |
| msa286876.2{662_18RS21} | ----- | ----- | -----ASFYFFH | VAQVRDDKSF | ISNGQRKPGN |
| msa286876.2{662_2603} | mkkirlskfi | kmivvilfli | svaASFYFFH | VAQVRDDKSF | ISNGQRKPGN |
| msa286876.2{662_JM9130013} | ----- | ----- | -----ASFYFFH | VAQVRDDKSF | ISNGQRKPGN |
| msa286876.2{662_090} | ----- | ----- | -----ASFYFFH | VAQVRDDKSF | ISNGQRKPGN |
| msa286876.2{662_CJB110} | ----- | ----- | -----ASFYFFH | VAQVRDDKSF | ISNGQRKPGN |
| msa286876.2{662_1169NT} | ----- | ----- | -----ASFYFFH | VAQVRDDKSF | ISNGQRKPGN |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 51 | | | | 100 |
| msa286876.2{662_A909} | SLYAYDKSFD | KLLKQKIEMT | NONIKQVAVY | VPAaKKTHTK | avVVHGFANS |
| msa286876.2{662_H36B} | SLYAYDKSFD | KLLKQKIEMT | NONIKQVAVY | VPAaKKTHTK | avVVHGFANS |
| msa286876.2{662_COH1} | SLYAYDKSFD | KLLKQKIEMT | NONIKQVAVY | VPAaKKTHTK | avVVHGFANS |
| msa286876.2{662_M732} | SLYAYDKSFD | KLLKQKIEMT | NONIKQVAVY | VPAaKKTHTK | avVVHGFANS |
| msa286876.2{662_M781} | SLYAYDKSFD | KLLKQKIEMT | NONIKQVAVY | VPAaKKTHTK | avVVHGFANS |
| msa286876.2{662_18RS21} | SLYAYDKSFD | KLLKQKIEMT | NONIKQVAVY | VPAaKKTHTK | avVVHGFANS |
| msa286876.2{662_2603} | SLYAYDKSFD | KLLKQKIEMT | NONIKQVAVY | VPAaKKTHTK | avVVHGFANS |
| msa286876.2{662_JM9130013} | SLYAYDKSFD | KLLKQKIEMT | NONIKQVAVY | VPAaKKTHTK | avVVHGFANS |
| msa286876.2{662_090} | SLYAYDKSFD | KLLKQKIEMT | NONIKQVAVY | VPAaKKTHTK | avVVHGFANS |
| msa286876.2{662_CJB110} | SLYAYDKSFD | KLLKQKIEMT | NONIKQVAVY | VPAaKKTHTK | avVVHGFANS |
| msa286876.2{662_1169NT} | SLYAYDKSFD | KLLKQKIEMT | NONIKQVAVY | VPAaKKTHTK | avVVHGFANS |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 101 | | | | 150 |
| msa286876.2{662_A909} | KENMKAYGWL | FHLGYNVLM | PDNIAHGES | GQLIGYGWND | RENI IKWTEM |
| msa286876.2{662_H36B} | KENMKAYGWL | FHLGYNVLM | PDNIAHGES | GQLIGYGWND | RENI IKWTEM |
| msa286876.2{662_COH1} | KENMKAYGWL | FHLGYNVLM | PDNIAHGES | GQLIGYGWND | RENI IKWTEM |
| msa286876.2{662_M732} | KENMKAYGWL | FHLGYNVLM | PDNIAHGES | GQLIGYGWND | RENI IKWTEM |
| msa286876.2{662_M781} | KENMKAYGWL | FHLGYNVLM | PDNIAHGES | GQLIGYGWND | RENI IKWTEM |
| msa286876.2{662_18RS21} | KENMKAYGWL | FHLGYNVLM | PDNIAHGES | GQLIGYGWND | RENI IKWTEM |
| msa286876.2{662_2603} | KENMKAYGWL | FHLGYNVLM | PDNIAHGES | GQLIGYGWND | RENI IKWTEM |
| msa286876.2{662_JM9130013} | KENMKAYGWL | FHLGYNVLM | PDNIAHGES | GQLIGYGWND | RENI IKWTEM |
| msa286876.2{662_090} | KENMKAYGWL | FHLGYNVLM | PDNIAHGES | GQLIGYGWND | RENI IKWTEM |
| msa286876.2{662_CJB110} | KENMKAYGWL | FHLGYNVLM | PDNIAHGES | GQLIGYGWND | RENI IKWTEM |
| msa286876.2{662_1169NT} | KENMKAYGWL | FHLGYNVLM | PDNIAHGES | GQLIGYGWND | RENI IKWTEM |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 151 | | | | 200 |
| msa286876.2{662_A909} | IVDKNsSSQI | TLFGVSMGGA | TVMASGEKL | PSQVNNIED | CGYSgVWDEL |
| msa286876.2{662_H36B} | IVDKNsSSQI | TLFGVSMGGA | TVMASGEKL | PSQVNNIED | CGYSgVWDEL |
| msa286876.2{662_COH1} | IVDKNpSSQI | TLFGVSMGGA | TVMASGEKL | PSQVNNIED | CGYSsVWDEL |
| msa286876.2{662_M732} | IVDKNpSSQI | TLFGVSMGGA | TVMASGEKL | PSQVNNIED | CGYSsVWDEL |
| msa286876.2{662_M781} | IVDKNpSSQI | TLFGVSMGGA | TVMASGEKL | PSQVNNIED | CGYSsVWDEL |
| msa286876.2{662_18RS21} | IVDKNpSSQI | TLFGVSMGGA | TVMASGEKL | PSQVNNIED | CGYSsVWDEL |
| msa286876.2{662_2603} | IVDKNpSSQI | TLFGVSMGGA | TVMASGEKL | PSQVNNIED | CGYSsVWDEL |
| msa286876.2{662_JM9130013} | IVDKNpSSQI | TLFGVSMGGA | TVMASGEKL | PSQVNNIED | CGYSsVWDEL |
| msa286876.2{662_090} | IVDKNpSSQI | TLFGVSMGGA | TVMASGEKL | PSQVNNIED | CGYSsVWDEL |
| msa286876.2{662_CJB110} | IVDKNpSSQI | TLFGVSMGGA | TVMASGEKL | PSQVNNIED | CGYSsVWDEL |
| msa286876.2{662_1169NT} | IVDKNpSSQI | TLFGVSMGGA | TVMASGEKL | PSQVNNIED | CGYSsVWDEL |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 201 | | | | 250 |
| msa286876.2{662_A909} | KFQAKEMYGL | PAFPLLYEVS | TISKIRAGFS | YQASSVEQL | KKNLPALEI |
| msa286876.2{662_H36B} | KFQAKEMYGL | PAFPLLYEVS | TISKIRAGFS | YQASSVEQL | KKNLPALEI |
| msa286876.2{662_COH1} | KFQAKEMYGL | PAFPLLYEVS | TISKIRAGFS | YQASSVEQL | KKNLPALEI |
| msa286876.2{662_M732} | KFQAKEMYGL | PAFPLLYEVS | TISKIRAGFS | YQASSVEQL | KKNLPALEI |
| msa286876.2{662_M781} | KFQAKEMYGL | PAFPLLYEVS | TISKIRAGFS | YQASSVEQL | KKNLPALEI |
| msa286876.2{662_18RS21} | KFQAKEMYGL | PAFPLLYEVS | TISKIRAGFS | YQASSVEQL | KKNLPALEI |
| msa286876.2{662_2603} | KFQAKEMYGL | PAFPLLYEVS | TISKIRAGFS | YQASSVEQL | KKNLPALEI |
| msa286876.2{662_JM9130013} | KFQAKEMYGL | PAFPLLYEVS | TISKIRAGFS | YQASSVEQL | KKNLPALEI |
| msa286876.2{662_090} | KFQAKEMYGL | PAFPLLYEVS | TISKIRAGFS | YQASSVEQL | KKNLPALEI |
| msa286876.2{662_CJB110} | KFQAKEMYGL | PAFPLLYEVS | TISKIRAGFS | YQASSVEQL | KKNLPALEI |
| msa286876.2{662_1169NT} | KFQAKEMYGL | PAFPLLYEVS | TISKIRAGFS | YQASSVEQL | KKNLPALEI |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 251 | | | | 300 |
| msa286876.2{662_A909} | HGDKDNFVPT | SMVYDNYKAT | AGKKELYIVK | GAKHAKSFET | EPEKYEKRIS |
| msa286876.2{662_H36B} | HGDKDNFVPT | SMVYDNYKAT | AGKKELYIVK | GAKHAKSFET | EPEKYEKRIS |
| msa286876.2{662_COH1} | HGDKDNFVPT | SMVYDNYKAT | AGKKELYIVK | GAKHAKSFET | EPEKYEKRIS |

Table 83: Comparative Sequences relating to SAG0108

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| msa286876.2{662_M732} | HGDKDNFVPT | SMVYDNYKAT | AGKKELYIVK | GAKHAKSFET | EPEKYEKRIS |
| msa286876.2{662_M781} | HGDKDNFVPT | SMVYDNYKAT | AGKKELYIVK | GAKHAKSFET | EPEKYEKRIS |
| msa286876.2{662_18RS21} | HGDKDNFVPT | SMVYDNYKAT | AGKKELYIVK | GAKHAKSFET | EPEKYEKRIS |
| msa286876.2{662_2603} | HGDKDNFVPT | SMVYDNYKAT | AGKKELYIVK | GAKHAKSFET | EPEKYEKRIS |
| msa286876.2{662_JM9130013} | HGDKDNFVPT | SMVYDNYKAT | AGKKELYIVK | GAKHAKSFET | EPEKYEKRIS |
| msa286876.2{662_090} | HGDKDNFVPT | SMVYDNYKAT | AGKKELYIVK | GAKHAKSFET | EPEKYEKRIS |
| msa286876.2{662_CJB110} | HGDKDNFVPT | SMVYDNYKAT | AGKKELYIVK | GAKHAKSFET | EPEKYEKRIS |
| msa286876.2{662_1169NT} | HGDKDNFVPT | SMVYDNYKAT | AGKKELYIVK | GAKHAKSFET | EPEKYEKRIS |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 301 | | | | | |
| msa286876.2{662_A909} | SFLKKYEK | | | | |
| msa286876.2{662_H36B} | SFLKKYEK | | | | |
| msa286876.2{662_COH1} | SFLKKYEK | | | | |
| msa286876.2{662_M732} | SFLKKYEK | | | | |
| msa286876.2{662_M781} | SFLKKYEK | | | | |
| msa286876.2{662_18RS21} | SFLKKYEK | | | | |
| msa286876.2{662_2603} | SFLKKYEK | | | | |
| msa286876.2{662_JM9130013} | SFLKKYEK | | | | |
| msa286876.2{662_090} | SFLKKYEK | | | | |
| msa286876.2{662_CJB110} | SFLKKYEK | | | | |
| msa286876.2{662_1169NT} | SFLKKYEK | | | | |
| Consensus | ***** | | | | |

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8401

STRAIN 2603

ATGATGAAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACTAAAC
 AATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAAATCATAGCATTAAATTTG
 ATGCCAGCCATTGATTTTAAATGCAATCAATTGATTAGAACCTCAAGATTGGACCGT
 ATCGTAGTAGCAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTACAGCA
 AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTA
 ACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGATGCACGACGTAATAAT
 GTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAGACTGTACACTTCTCTT
 GAAGAAGTCTTACAAGAGGTGGGAATAAAGCCAATGTTTATTGTCGGAGAGGTTGCA
 GCATTTTGTGATCAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAAACCTTTACCT
 TGTGCAGTAGCAATTGGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATGCGTTT
 GTTCCACGATACTTAAAAAGTGTGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTGTGAA
 ACGAATACAGAAGATATATTAAAGAGAGTT

SEQ ID NO. 8402

STRAIN 090

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACT
 AAAAATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAAATC
 ATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGCAATCAATTGAT
 TTAGAACCTCAAGATTGGAGCCGATCGTAGTGGCAGAGGGTCCAGGATC
 TTATACGGGCTTACGTGTAGCTGTTGTACAGCAAAAATGCTAGCTTATA
 CGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTAAACAAAT
 GGATTTTCAGAAAATGATTTGTTGGTACCCTTATAGATGCACGACGTAA
 CAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAGACT
 GTACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGAATAAAGCCAAT
 GTTCATTTTGTGGAGAGGTTGCAGCATTTTGTGATCAGATTAAAGAAAGC
 CTTACCACATGCTAAAATTACAGAAACCTTTACCTTGTGCAGTGGCAATTG
 GCGCAAAAGGACAAAAATGGAAGCGTTAATGTAGATGCGTTTGTTCAC
 CGATACTTAAACAGAGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTG
 TGAACGAAT

SEQ ID NO. 8403

STRAIN A909

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAG
 TGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATATC
 AAAAAAGAAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGCA
 ATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAGG
 GTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTCTACAGCAAAAATG
 CTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGC
 TTTAAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGATG
 CACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGTT
 AAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGAA
 TAAAGCCAATGTTTATTTGTTCGGAGAGGTTGCAGCATTTGTTTGACCAGA
 TTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 GCGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATGC
 GTTTGTTCCACGATACTTAAAAAGTGTGTTGAAGCTGAGGAAAATTGGTTAA
 GAAACCACTGTGAACGAAT

SEQ ID NO. 8404

STRAIN H36B

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
 TAAACAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTATTTGTTCGGAGAGGTTGCAGCATTTGTTTGACCAG
 ATTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACTTAAAAAGTGTGTTGAAGCTGAGGAAAATTGGTTA
 AGAAACCACTGTGAACGAATACAGAAGATATATTAAAGAGAGTT

SEQ ID NO. 8405

STRAIN 18RS21

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
 TAAACAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTATTTGTTCGGAGAGGTTGCAGCATTTTGTGACCAG
 ATTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACTTAAAAAGTGTGTTGAAGCTGAGGAAAATTGGTTA
 AGAAACCACTGTGAACGAATACAGAAGATATATTAAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8406

STRAIN M732

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATCTGT
 TAAACCAAGCTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTGATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGAnn
 CGTTTGTTCACGATACCTTAAACGTTGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8407

STRAIN COH1

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCAC
 TATCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATC
 AATATCAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTT
 AATGCAATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAG
 CAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCA
 AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCT
 GTACGCTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACCTTA
 TAGATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGAT
 ACTGTTAAACCAAGCTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGT
 GGGGAATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTG
 ATCAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCT
 TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGT
 AGATGCGTTTGTTCACGATACCTTAAACGTTGTTGAAGCTGAGGAAAATT
 GGTAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8408

STRAIN M781

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTA
 TCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAA
 TATCAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAA
 TGCAATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTATCA
 GAGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAA
 AATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGT
 ACGCTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACCTTATA
 GATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATACT
 TGTTAAACCAAGCTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGG
 GGAATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTGAT
 CAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTG
 TGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAG
 ATGCGTTTGTTCACGATACCTTAAACGTTGTTGAAGCTGAGGAAAATTGG
 TAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8409

STRAIN CJB110

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTGGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTGTTGGTACCACCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATCTGT
 TAAACCAAGCTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTgATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACCTTAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8410

STRAIN I169NT

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATCTGT
 TAAACCAAGCTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTGTGACG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACCTTAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267

AGTGGCAATTGGGCGCAAAGGACAAAAATGGAAGCGTTAATGTAGATG
CGTTTGTTCACGATACCTTAAACGTGTTGAAGCTGAGGAAATTTGGTTA
AAAAACCACTGTGAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO.: 8411

STRAIN JM9130013

AAAGTTTTAGCCTTTGATACCTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTAATGC
AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
gCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAAATGGATTTCAGAAAATGATTTATTGGTACCCTTATAGAT
GCACGACGTAAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
TAAACCAAGCTGTCACTTCTCTTGAAGAAGCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTGTTGACCAG
ATTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAGCGTTAATGTAGATG
CGTTTGTTCACGATACCTTAAACGTGTTGAAGCTGAGGAAATTTGGTTA
AGAAACCACTGTGAACGAATACAGAAGAATATATTAAAGAGAGTT

PRETTY of: /biotmp/msa521675.2{*} March 10, 2003 08:34 ..

| | | | |
|---------------------------|------------|------------|----------------------------------|
| | 1 | | 50 |
| msa521675.2{69_A909} | -----AAAG | TTTTAGCCTT | TGATACTTCA AGCAAAGCAC TATCAGTGGC |
| msa521675.2{69_H36B} | -----AAAG | TTTTAGCCTT | TGATACTTCA AGCAAAGCAC TATCAGTGGC |
| msa521675.2{69_JM9130013} | -----AAAG | TTTTAGCCTT | TGATACTTCA AGCAAAGCAC TATCAGTGGC |
| msa521675.2{69_1169NT} | -----AAAG | TTTTAGCCTT | TGATACTTCA AGCAAAGCAC TATCAGTGGC |
| msa521675.2{69_090} | -----AAAG | TTTTAGCCTT | TGATACTTCA AGCAAAGCAC TATCAGTGGC |
| msa521675.2{69_CJB110} | -----AAAG | TTTTAGCCTT | TGATACTTCA AGCAAAGCAC TATCAGTGGC |
| msa521675.2{69_18RS21} | -----AAAG | TTTTAGCCTT | TGATACTTCA AGCAAAGCAC TATCAGTGGC |
| msa521675.2{69_2603} | atgatgAAAG | TTTTAGCCTT | TGATACTTCA AGCAAAGCAC TATCAGTGGC |
| msa521675.2{69_COH1} | -----AAAG | TTTTAGCCTT | TGATACTTCA AGCAAAGCAC TATCAGTGGC |
| msa521675.2{69_M732} | -----AAAG | TTTTAGCCTT | TGATACTTCA AGCAAAGCAC TATCAGTGGC |
| msa521675.2{69_M781} | -----AAAG | TTTTAGCCTT | TGATACTTCA AGCAAAGCAC TATCAGTGGC |
| Consensus | ***** | ***** | ***** |

| | | | |
|---------------------------|------------|------------|---------------------------------|
| | 51 | | 100 |
| msa521675.2{69_A909} | TGTACTAAAC | AATATGGAAT | GTTTAGCGAC TGTCACATC AATATCAAAA |
| msa521675.2{69_H36B} | TGTACTAAAC | AATATGGAAT | GTTTAGCGAC TGTCACATC AATATCAAAA |
| msa521675.2{69_JM9130013} | TGTACTAAAC | AATATGGAAT | GTTTAGCGAC TGTCACATC AATATCAAAA |
| msa521675.2{69_1169NT} | TGTACTAAAC | AATATGGAAT | GTTTAGCGAC TGTCACATC AATATCAAAA |
| msa521675.2{69_090} | TGTACTAAAC | AATATGGAAT | GTTTAGCGAC TGTCACATC AATATCAAAA |
| msa521675.2{69_CJB110} | TGTACTAAAC | AATATGGAAT | GTTTAGCGAC TGTCACATC AATATCAAAA |
| msa521675.2{69_18RS21} | TGTACTAAAC | AATATGGAAT | GTTTAGCGAC TGTCACATC AATATCAAAA |
| msa521675.2{69_2603} | TGTACTAAAC | AATATGGAAT | GTTTAGCGAC TGTCACATC AATATCAAAA |
| msa521675.2{69_COH1} | TGTACTAAAC | AATATGGAAT | GTTTAGCGAC TGTCACATC AATATCAAAA |
| msa521675.2{69_M732} | TGTACTAAAC | AATATGGAAT | GTTTAGCGAC TGTCACATC AATATCAAAA |
| msa521675.2{69_M781} | TGTACTAAAC | AATATGGAAT | GTTTAGCGAC TGTCACATC AATATCAAAA |
| Consensus | ***** | ***** | ***** |

| | | | |
|---------------------------|------------|-----------|----------------------------------|
| | 101 | | 150 |
| msa521675.2{69_A909} | AGAATCATAG | CATTAATTG | ATGCCAGCCA TTGATTTTTT AATGCAATCA |
| msa521675.2{69_H36B} | AGAATCATAG | CATTAATTG | ATGCCAGCCA TTGATTTTTT AATGCAATCA |
| msa521675.2{69_JM9130013} | AGAATCATAG | CATTAATTG | ATGCCAGCCA TTGATTTTTT AATGCAATCA |
| msa521675.2{69_1169NT} | AGAATCATAG | CATTAATTG | ATGCCAGCCA TTGATTTTTT AATGCAATCA |
| msa521675.2{69_090} | AGAATCATAG | CATTAATTG | ATGCCAGCCA TTGATTTTTT AATGCAATCA |
| msa521675.2{69_CJB110} | AGAATCATAG | CATTAATTG | ATGCCAGCCA TTGATTTTTT AATGCAATCA |
| msa521675.2{69_18RS21} | AGAATCATAG | CATTAATTG | ATGCCAGCCA TTGATTTTTT AATGCAATCA |
| msa521675.2{69_2603} | AGAATCATAG | CATTAATTG | ATGCCAGCCA TTGATTTTTT AATGCAATCA |
| msa521675.2{69_COH1} | AGAATCATAG | CATTAATTG | ATGCCAGCCA TTGATTTTTT AATGCAATCA |
| msa521675.2{69_M732} | AGAATCATAG | CATTAATTG | ATGCCAGCCA TTGATTTTTT AATGCAATCA |
| msa521675.2{69_M781} | AGAATCATAG | CATTAATTG | ATGCCAGCCA TTGATTTTTT AATGCAATCA |
| Consensus | ***** | ***** | ***** |

| | | | |
|---------------------------|-----------|------------|---------------------------------|
| | 151 | | 200 |
| msa521675.2{69_A909} | ATTGATTAG | AACCTCAAGA | TTTGGACCGT ATCGTAGTg CAGAGGGTCC |
| msa521675.2{69_H36B} | ATTGATTAG | AACCTCAAGA | TTTGGACCGT ATCGTAGTg CAGAGGGTCC |
| msa521675.2{69_JM9130013} | ATTGATTAG | AACCTCAAGA | TTTGGACCGT ATCGTAGTg CAGAGGGTCC |
| msa521675.2{69_1169NT} | ATTGATTAG | AACCTCAAGA | TTTGGACCGT ATCGTAGTg CAGAGGGTCC |
| msa521675.2{69_090} | ATTGATTAG | AACCTCAAGA | TTTGGACCGT ATCGTAGTg CAGAGGGTCC |
| msa521675.2{69_CJB110} | ATTGATTAG | AACCTCAAGA | TTTGGACCGT ATCGTAGTg CAGAGGGTCC |
| msa521675.2{69_18RS21} | ATTGATTAG | AACCTCAAGA | TTTGGACCGT ATCGTAGTg CAGAGGGTCC |
| msa521675.2{69_2603} | ATTGATTAG | AACCTCAAGA | TTTGGACCGT ATCGTAGTg CAGAGGGTCC |
| msa521675.2{69_COH1} | ATTGATTAG | AACCTCAAGA | TTTGGACCGT ATCGTAGTg CAGAGGGTCC |
| msa521675.2{69_M732} | ATTGATTAG | AACCTCAAGA | TTTGGACCGT ATCGTAGTg CAGAGGGTCC |
| msa521675.2{69_M781} | ATTGATTAG | AACCTCAAGA | TTTGGACCGT ATCGTAGTg CAGAGGGTCC |
| Consensus | ***** | ***** | ***** |

| | | | |
|----------------------|------------|------------|----------------------------------|
| | 201 | | 250 |
| msa521675.2{69_A909} | AGGATCTTAT | ACGGGCTTAC | GTGTAGCTGT TGCTACAGCA AAAATGCTAG |
| msa521675.2{69_H36B} | AGGATCTTAT | ACGGGCTTAC | GTGTAGCTGT TGCTACAGCA AAAATGCTAG |

Table 84: Comparative Sequences relating to SAG0267

| | | | | | |
|---------------------------|-------------|------------|------------|-------------|-------------|
| msa521675.2{69_JM9130013} | AGGATCTTAT | ACGGGCTTAC | GTGTAGCTGT | TGCTACAGCA | AAAAATGCTAG |
| msa521675.2{69_1169NT} | AGGATCTTAT | ACGGGCTTAC | GTGTAGCTGT | TGCTACAGCA | AAAAATGCTAG |
| msa521675.2{69_090} | AGGATCTTAT | ACGGGCTTAC | GTGTAGCTGT | TGCTACAGCA | AAAAATGCTAG |
| msa521675.2{69_CJB110} | AGGATCTTAT | ACGGGCTTAC | GTGTAGCTGT | TGCTACAGCA | AAAAATGCTAG |
| msa521675.2{69_18RS21} | AGGATCTTAT | ACGGGCTTAC | GTGTAGCTGT | TGCTACAGCA | AAAAATGCTAG |
| msa521675.2{69_2603} | AGGATCTTAT | ACGGGCTTAC | GTGTAGCTGT | TGCTACAGCA | AAAAATGCTAG |
| msa521675.2{69_COH1} | AGGATCTTAT | ACGGGCTTAC | GTGTAGCTGT | TGCTACAGCA | AAAAATGCTAG |
| msa521675.2{69_M732} | AGGATCTTAT | ACGGGCTTAC | GTGTAGCTGT | TGCTACAGCA | AAAAATGCTAG |
| msa521675.2{69_M781} | AGGATCTTAT | ACGGGCTTAC | GTGTAGCTGT | TGCTACAGCA | AAAAATGCTAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 251 | | | | | |
| msa521675.2{69_A909} | CTTATACGCT | TAAGATTGAC | TTAGTTGGAG | TATCTAGCCT | GTACGCTTTA |
| msa521675.2{69_H36B} | CTTATACGCT | TAAGATTGAC | TTAGTTGGAG | TATCTAGCCT | GTACGCTTTA |
| msa521675.2{69_JM9130013} | CTTATACGCT | TAAGATTGAC | TTAGTTGGAG | TATCTAGCCT | GTACGCTTTA |
| msa521675.2{69_1169NT} | CTTATACGCT | TAAGATTGAC | TTAGTTGGAG | TATCTAGCCT | GTACGCTTTA |
| msa521675.2{69_090} | CTTATACGCT | TAAGATTGAC | TTAGTTGGAG | TATCTAGCCT | GTACGCTTTA |
| msa521675.2{69_CJB110} | CTTATACGCT | TAAGATTGAC | TTAGTTGGAG | TATCTAGCCT | GTACGCTTTA |
| msa521675.2{69_18RS21} | CTTATACGCT | TAAGATTGAC | TTAGTTGGAG | TATCTAGCCT | GTACGCTTTA |
| msa521675.2{69_2603} | CTTATACGCT | TAAGATTGAC | TTAGTTGGAG | TATCTAGCCT | GTACGCTTTA |
| msa521675.2{69_COH1} | CTTATACGCT | TAAGATTGAC | TTAGTTGGAG | TATCTAGCCT | GTACGCTTTA |
| msa521675.2{69_M732} | CTTATACGCT | TAAGATTGAC | TTAGTTGGAG | TATCTAGCCT | GTACGCTTTA |
| msa521675.2{69_M781} | CTTATACGCT | TAAGATTGAC | TTAGTTGGAG | TATCTAGCCT | GTACGCTTTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 301 | | | | | |
| msa521675.2{69_A909} | ACAAATGGAT | TTTCAGAAAA | TGATTTaTTG | GTACCACITTA | TAGATGCACG |
| msa521675.2{69_H36B} | ACAAATGGAT | TTTCAGAAAA | TGATTTaTTG | GTACCACITTA | TAGATGCACG |
| msa521675.2{69_JM9130013} | ACAAATGGAT | TTTCAGAAAA | TGATTTaTTG | GTACCACITTA | TAGATGCACG |
| msa521675.2{69_1169NT} | ACAAATGGAT | TTTCAGAAAA | TGATTTaTTG | GTACCACITTA | TAGATGCACG |
| msa521675.2{69_090} | ACAAATGGAT | TTTCAGAAAA | TGATTTaTTG | GTACCACITTA | TAGATGCACG |
| msa521675.2{69_CJB110} | ACAAATGGAT | TTTCAGAAAA | TGATTTaTTG | GTACCACITTA | TAGATGCACG |
| msa521675.2{69_18RS21} | ACAAATGGAT | TTTCAGAAAA | TGATTTaTTG | GTACCACITTA | TAGATGCACG |
| msa521675.2{69_2603} | ACAAATGGAT | TTTCAGAAAA | TGATTTaTTG | GTACCACITTA | TAGATGCACG |
| msa521675.2{69_COH1} | ACAAATGGAT | TTTCAGAAAA | TGATTTaTTG | GTACCACITTA | TAGATGCACG |
| msa521675.2{69_M732} | ACAAATGGAT | TTTCAGAAAA | TGATTTaTTG | GTACCACITTA | TAGATGCACG |
| msa521675.2{69_M781} | ACAAATGGAT | TTTCAGAAAA | TGATTTaTTG | GTACCACITTA | TAGATGCACG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 351 | | | | | |
| msa521675.2{69_A909} | ACGTAAcAAT | GTTTATGTTG | GTTTCTATCA | AAATGGaGAT | ACTGTTAAAC |
| msa521675.2{69_H36B} | ACGTAAcAAT | GTTTATGTTG | GTTTCTATCA | AAATGGaGAT | ACTGTTAAAC |
| msa521675.2{69_JM9130013} | ACGTAAcAAT | GTTTATGTTG | GTTTCTATCA | AAATGGaGAT | ACTGTTAAAC |
| msa521675.2{69_1169NT} | ACGTAAcAAT | GTTTATGTTG | GTTTCTATCA | AAATGGtGAT | ACTGTTAAAC |
| msa521675.2{69_090} | ACGTAAcAAT | GTTTATGTTG | GTTTCTATCA | AAATGGtGAT | ACTGTTAAAC |
| msa521675.2{69_CJB110} | ACGTAAcAAT | GTTTATGTTG | GTTTCTATCA | AAATGGtGAT | ACTGTTAAAC |
| msa521675.2{69_18RS21} | ACGTAAcAAT | GTTTATGTTG | GTTTCTATCA | AAATGGtGAT | ACTGTTAAAC |
| msa521675.2{69_2603} | ACGTAAcAAT | GTTTATGTTG | GTTTCTATCA | AAATGGtGAT | ACTGTTAAAC |
| msa521675.2{69_COH1} | ACGTAAcAAT | GTTTATGTTG | GTTTCTATCA | AAATGGtGAT | ACTGTTAAAC |
| msa521675.2{69_M732} | ACGTAAcAAT | GTTTATGTTG | GTTTCTATCA | AAATGGtGAT | ACTGTTAAAC |
| msa521675.2{69_M781} | ACGTAAcAAT | GTTTATGTTG | GTTTCTATCA | AAATGGtGAT | ACTGTTAAAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 401 | | | | | |
| msa521675.2{69_A909} | CAGACTGTCA | CACCTTCTCT | GAAGAAGTCT | TACAAGAGGT | GGGGAATAAA |
| msa521675.2{69_H36B} | CAGACTGTCA | CACCTTCTCT | GAAGAAGTCT | TACAAGAGGT | GGGGAATAAA |
| msa521675.2{69_JM9130013} | CAGACTGTCA | CACCTTCTCT | GAAGAAGTCT | TACAAGAGGT | GGGGAATAAA |
| msa521675.2{69_1169NT} | CAGACTGTCA | CACCTTCTCT | GAAGAAGTCT | TACAAGAGGT | GGGGAATAAA |
| msa521675.2{69_090} | CAGACTGTCA | CACCTTCTCT | GAAGAAGTCT | TACAAGAGGT | GGGGAATAAA |
| msa521675.2{69_CJB110} | CAGACTGTCA | CACCTTCTCT | GAAGAAGTCT | TACAAGAGGT | GGGGAATAAA |
| msa521675.2{69_18RS21} | CAGACTGTCA | CACCTTCTCT | GAAGAAGTCT | TACAAGAGGT | GGGGAATAAA |
| msa521675.2{69_2603} | CAGACTGTCA | CACCTTCTCT | GAAGAAGTCT | TACAAGAGGT | GGGGAATAAA |
| msa521675.2{69_COH1} | CAGACTGTCA | CACCTTCTCT | GAAGAAGTCT | TACAAGAGGT | GGGGAATAAA |
| msa521675.2{69_M732} | CAGACTGTCA | CACCTTCTCT | GAAGAAGTCT | TACAAGAGGT | GGGGAATAAA |
| msa521675.2{69_M781} | CAGACTGTCA | CACCTTCTCT | GAAGAAGTCT | TACAAGAGGT | GGGGAATAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 451 | | | | | |
| msa521675.2{69_A909} | GCCAAATGTTT | ATTTTGTGCG | AGAGGTTGCA | GCATTtGTTG | AcCAGATTAA |
| msa521675.2{69_H36B} | GCCAAATGTTT | ATTTTGTGCG | AGAGGTTGCA | GCATTtGTTG | AcCAGATTAA |
| msa521675.2{69_JM9130013} | GCCAAATGTTT | ATTTTGTGCG | AGAGGTTGCA | GCATTtGTTG | AcCAGATTAA |
| msa521675.2{69_1169NT} | GCCAAATGTTT | ATTTTGTGCG | AGAGGTTGCA | GCATTtGTTG | AcCAGATTAA |
| msa521675.2{69_090} | GCCAAATGTTT | ATTTTGTGCG | AGAGGTTGCA | GCATTtGTTG | AcCAGATTAA |
| msa521675.2{69_CJB110} | GCCAAATGTTT | ATTTTGTGCG | AGAGGTTGCA | GCATTtGTTG | AcCAGATTAA |
| msa521675.2{69_18RS21} | GCCAAATGTTT | ATTTTGTGCG | AGAGGTTGCA | GCATTtGTTG | AcCAGATTAA |
| msa521675.2{69_2603} | GCCAAATGTTT | ATTTTGTGCG | AGAGGTTGCA | GCATTtGTTG | AcCAGATTAA |
| msa521675.2{69_COH1} | GCCAAATGTTT | ATTTTGTGCG | AGAGGTTGCA | GCATTtGTTG | AcCAGATTAA |
| msa521675.2{69_M732} | GCCAAATGTTT | ATTTTGTGCG | AGAGGTTGCA | GCATTtGTTG | AcCAGATTAA |
| msa521675.2{69_M781} | GCCAAATGTTT | ATTTTGTGCG | AGAGGTTGCA | GCATTtGTTG | AcCAGATTAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 501 | | | | | |
| msa521675.2{69_A909} | GAAAGtTTTA | CCACATGCTA | AAATTACAGA | AACTTTACCT | TGTGCAgTgG |
| 550 | | | | | |

Table 84: Comparative Sequences relating to SAG0267

| | | | | | |
|---------------------------|-------------|------------|------------|------------|------------|
| msa521675.2{69_H36B} | GAAAGcttTA | CCACATGCTA | AAATTACAGA | AACTTTACCT | TGTGCAGTgG |
| msa521675.2{69_JM9130013} | GAAAGcttTA | CCACATGCTA | AAATTACAGA | AACTTTACCT | TGTGCAGTgG |
| msa521675.2{69_1169NT} | GAAAGcttTA | CCACATGCTA | AAATTACAGA | AACTTTACCT | TGTGCAGTgG |
| msa521675.2{69_090} | GAAAGccTtTA | CCACATGCTA | AAATTACAGA | AACTTTACCT | TGTGCAGTgG |
| msa521675.2{69_CJB110} | GAAAGccTtTA | CCACATGCTA | AAATTACAGA | AACTTTACCT | TGTGCAGTgG |
| msa521675.2{69_18RS21} | GAAAGccTtTA | CCACATGCTA | AAATTACAGA | AACTTTACCT | TGTGCAGTgG |
| msa521675.2{69_2603} | GAAAGccTtTA | CCACATGCTA | AAATTACAGA | AACTTTACCT | TGTGCAGTgG |
| msa521675.2{69_COH1} | GAAAGccTtTA | CCACATGCTA | AAATTACAGA | AACTTTACCT | TGTGCAGTgG |
| msa521675.2{69_M732} | GAAAGccTtTA | CCACATGCTA | AAATTACAGA | AACTTTACCT | TGTGCAGTgG |
| msa521675.2{69_M781} | GAAAGccTtTA | CCACATGCTA | AAATTACAGA | AACTTTACCT | TGTGCAGTgG |
| Consensus | *****-*** | ***** | ***** | ***** | ***** |
| msa521675.2{69_A909} | CAATTGGGCG | CAAAGGACAA | AAAATGaAAA | GCGTTAATGT | AGAtgCGTTT |
| msa521675.2{69_H36B} | CAATTGGGCG | CAAAGGACAA | AAAATGaAAA | GCGTTAATGT | AGAtgCGTTT |
| msa521675.2{69_JM9130013} | CAATTGGGCG | CAAAGGACAA | AAAATGaAAA | GCGTTAATGT | AGAtgCGTTT |
| msa521675.2{69_1169NT} | CAATTGGGCG | CAAAGGACAA | AAAATGaAAA | GCGTTAATGT | AGAtgCGTTT |
| msa521675.2{69_090} | CAATTGGGCG | CAAAGGACAA | AAAATGaAAA | GCGTTAATGT | AGAtgCGTTT |
| msa521675.2{69_CJB110} | CAATTGGGCG | CAAAGGACAA | AAAATGaAAA | GCGTTAATGT | AGAtgCGTTT |
| msa521675.2{69_18RS21} | CAATTGGGCG | CAAAGGACAA | AAAATGaAAA | GCGTTAATGT | AGAtgCGTTT |
| msa521675.2{69_2603} | CAATTGGGCG | CAAAGGACAA | AAAATGaAAA | GCGTTAATGT | AGAtgCGTTT |
| msa521675.2{69_COH1} | CAATTGGGCG | CAAAGGACAA | AAAATGaAAA | GCGTTAATGT | AGAtgCGTTT |
| msa521675.2{69_M732} | CAATTGGGCG | CAAAGGACAA | AAAATGaAAA | GCGTTAATGT | AGAtgCGTTT |
| msa521675.2{69_M781} | CAATTGGGCG | CAAAGGACAA | AAAATGaAAA | GCGTTAATGT | AGAtgCGTTT |
| Consensus | ***** | ***** | *****-*** | ***** | ***** |
| msa521675.2{69_A909} | GTTCACGAT | ACTTAAAACG | tGTTGAAGCT | GAGGAAAATT | GGTTAAgAAA |
| msa521675.2{69_H36B} | GTTCACGAT | ACTTAAAACG | tGTTGAAGCT | GAGGAAAATT | GGTTAAgAAA |
| msa521675.2{69_JM9130013} | GTTCACGAT | ACTTAAAACG | tGTTGAAGCT | GAGGAAAATT | GGTTAAgAAA |
| msa521675.2{69_1169NT} | GTTCACGAT | ACTTAAAACG | tGTTGAAGCT | GAGGAAAATT | GGTTAAaAAA |
| msa521675.2{69_090} | GTTCACGAT | ACTTAAAACG | aGTTGAAGCT | GAGGAAAATT | GGTTAAaAAA |
| msa521675.2{69_CJB110} | GTTCACGAT | ACTTAAAACG | aGTTGAAGCT | GAGGAAAATT | GGTTAAaAAA |
| msa521675.2{69_18RS21} | GTTCACGAT | ACTTAAAACG | tGTTGAAGCT | GAGGAAAATT | GGTTAAaAAA |
| msa521675.2{69_2603} | GTTCACGAT | ACTTAAAACG | tGTTGAAGCT | GAGGAAAATT | GGTTAAaAAA |
| msa521675.2{69_COH1} | GTTCACGAT | ACTTAAAACG | tGTTGAAGCT | GAGGAAAATT | GGTTAAaAAA |
| msa521675.2{69_M732} | GTTCACGAT | ACTTAAAACG | tGTTGAAGCT | GAGGAAAATT | GGTTAAaAAA |
| msa521675.2{69_M781} | GTTCACGAT | ACTTAAAACG | tGTTGAAGCT | GAGGAAAATT | GGTTAAaAAA |
| Consensus | ***** | ***** | -***** | ***** | *****-*** |
| msa521675.2{69_A909} | CCACTGTGAA | ACGAAT---- | ----- | ----- | 690 |
| msa521675.2{69_H36B} | CCACTGTGAA | ACGAATACAG | AAGAATATAT | TAAGAGAGTT | |
| msa521675.2{69_JM9130013} | CCACTGTGAA | ACGAATACAG | AAGAATATAT | TAAGAGAGTT | |
| msa521675.2{69_1169NT} | CCACTGTGAA | ACGAATACAG | AAGAATATAT | TAAGAGAGTT | |
| msa521675.2{69_090} | CCACTGTGAA | ACGAAT---- | ----- | ----- | |
| msa521675.2{69_CJB110} | CCACTGTGAA | ACGAATACAG | AAGAATATAT | TAAGAGAGTT | |
| msa521675.2{69_18RS21} | CCACTGTGAA | ACGAATACAG | AAGAATATAT | TAAGAGAGTT | |
| msa521675.2{69_2603} | CCACTGTGAA | ACGAATACAG | AAGAATATAT | TAAGAGAGTT | |
| msa521675.2{69_COH1} | CCACTGTGAA | ACGAATACAG | AAGAATATAT | TAAGAGAGTT | |
| msa521675.2{69_M732} | CCACTGTGAA | ACGAATACAG | AAGAATATAT | TAAGAGAGTT | |
| msa521675.2{69_M781} | CCACTGTGAA | ACGAATACAG | AAGAATATAT | TAAGAGAGTT | |
| Consensus | ***** | ***** | ***** | ***** | |

SEQ ID NO. 8412

STRAIN 2603 frame: 1

MMKVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDR
 IVVAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENDLLVPLIDARRNN
 VYVGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 CAVAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETNTTEEYIKRV

SEQ ID NO. 8413

STRAIN 090 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETN

SEQ ID NO. 8414

STRAIN A909 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETN

SEQ ID NO. 8415

STRAIN H36B frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETNTTEEYIKRV

SEQ ID NO. 8416

Table 84: Comparative Sequences relating to SAG0267

STRAIN 18RS21 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVDAFVPRYLKRVEAENWLKNHCETNTEEYIKRV

SEQ ID NO. 8417

STRAIN M732 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVXXFVPRYLKRVEAENWLKNHCETNTEEYIKRV

SEQ ID NO. 8418

STRAIN COH1 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVDAFVPRYLKRVEAENWLKNHCETNTEEYIKRV

SEQ ID NO. 8419

STRAIN M781 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VSEGPSTYGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVDAFVPRYLKRVEAENWLKNHCETNTEEYIKRV

SEQ ID NO. 8420

STRAIN CJB110 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVDAFVPRYLKRVEAENWLKNHCETNTEEYIKRV

SEQ ID NO. 8421

STRAIN 1169NT frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVDAFVPRYLKRVEAENWLKNHCETNTEEYIKRV

SEQ ID NO. 8422

STRAIN JM9130013 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKMSVNVDAFVPRYLKRVEAENWLKNHCETNTEEYIKRV

PRETTY of: /biotmp/msa521982.2{*} March 10, 2003 08:40 ..

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1                                     50
msa521982.2{69_A909} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_H36B} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_JM9130013} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_090} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_CJB110} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_18RS21} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_2603} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_COH1} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_M781} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_1169NT} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_M732} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
Consensus *****
51                                     100
msa521982.2{69_A909} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_H36B} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_JM9130013} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_090} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_CJB110} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_18RS21} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_2603} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_COH1} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M781} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_1169NT} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M732} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
Consensus *****
101                                     150
msa521982.2{69_A909} TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK
msa521982.2{69_H36B} TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK

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Table 84: Comparative Sequences relating to SAG0267

| | | | | | |
|---------------------------|------------|------------|------------|------------|------------|
| msa521982.2{69_JM9130013} | TNGFSENDLL | VPLIDARRNN | VYVGFYQNGD | TVKPDCHTSL | EEVLQEVGNK |
| msa521982.2{69_090} | TNGFSENDLL | VPLIDARRNN | VYVGFYQNGD | TVKPDCHTSL | EEVLQEVGNK |
| msa521982.2{69_CJB110} | TNGFSENDLL | VPLIDARRNN | VYVGFYQNGD | TVKPDCHTSL | EEVLQEVGNK |
| msa521982.2{69_18RS21} | TNGFSENDLL | VPLIDARRNN | VYVGFYQNGD | TVKPDCHTSL | EEVLQEVGNK |
| msa521982.2{69_2603} | TNGFSENDLL | VPLIDARRNN | VYVGFYQNGD | TVKPDCHTSL | EEVLQEVGNK |
| msa521982.2{69_COH1} | TNGFSENDLL | VPLIDARRNN | VYVGFYQNGD | TVKPDCHTSL | EEVLQEVGNK |
| msa521982.2{69_M781} | TNGFSENDLL | VPLIDARRNN | VYVGFYQNGD | TVKPDCHTSL | EEVLQEVGNK |
| msa521982.2{69_1169NT} | TNGFSENDLL | VPLIDARRNN | VYVGFYQNGD | TVKPDCHTSL | EEVLQEVGNK |
| msa521982.2{69_M732} | TNGFSENDLL | VPLIDARRNN | VYVGFYQNGD | TVKPDCHTSL | EEVLQEVGNK |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 151 | | | | | |
| msa521982.2{69_A909} | ANVHFVGEVA | AFvDQIKKvL | PHAKITETLP | CAVAIGRKGQ | KMkSVNVdaF |
| msa521982.2{69_H36B} | ANVHFVGEVA | AFvDQIKKvL | PHAKITETLP | CAVAIGRKGQ | KMkSVNVdaF |
| msa521982.2{69_JM9130013} | ANVHFVGEVA | AFvDQIKKvL | PHAKITETLP | CAVAIGRKGQ | KMkSVNVdaF |
| msa521982.2{69_090} | ANVHFVGEVA | AFvDQIKKaL | PHAKITETLP | CAVAIGRKGQ | KMeSVNVdaF |
| msa521982.2{69_CJB110} | ANVHFVGEVA | AFvDQIKKaL | PHAKITETLP | CAVAIGRKGQ | KMeSVNVdaF |
| msa521982.2{69_18RS21} | ANVHFVGEVA | AFvDQIKKaL | PHAKITETLP | CAVAIGRKGQ | KMkSVNVdaF |
| msa521982.2{69_2603} | ANVHFVGEVA | AFvDQIKKaL | PHAKITETLP | CAVAIGRKGQ | KMkSVNVdaF |
| msa521982.2{69_COH1} | ANVHFVGEVA | AFvDQIKKaL | PHAKITETLP | CAVAIGRKGQ | KMkSVNVdaF |
| msa521982.2{69_M781} | ANVHFVGEVA | AFvDQIKKaL | PHAKITETLP | CAVAIGRKGQ | KMkSVNVdaF |
| msa521982.2{69_1169NT} | ANVHFVGEVA | AFvDQIKKaL | PHAKITETLP | CAVAIGRKGQ | KMeSVNVdaF |
| msa521982.2{69_M732} | ANVHFVGEVA | AFvDQIKKaL | PHAKITETLP | CAVAIGRKGQ | KMkSVNVxxF |
| Consensus | ***** | **_*****_* | ***** | ***** | **_*****_* |
| 201 | | | | | |
| msa521982.2{69_A909} | VPRYLKRVEA | EENWLrNHCE | TN----- | | 230 |
| msa521982.2{69_H36B} | VPRYLKRVEA | EENWLrNHCE | TNTEEYIKRV | | |
| msa521982.2{69_JM9130013} | VPRYLKRVEA | EENWLrNHCE | TNTEEYIKRV | | |
| msa521982.2{69_090} | VPRYLKRVEA | EENWLkNHCE | TN----- | | |
| msa521982.2{69_CJB110} | VPRYLKRVEA | EENWLkNHCE | TNTEEYIKRV | | |
| msa521982.2{69_18RS21} | VPRYLKRVEA | EENWLkNHCE | TNTEEYIKRV | | |
| msa521982.2{69_2603} | VPRYLKRVEA | EENWLkNHCE | TNTEEYIKRV | | |
| msa521982.2{69_COH1} | VPRYLKRVEA | EENWLkNHCE | TNTEEYIKRV | | |
| msa521982.2{69_M781} | VPRYLKRVEA | EENWLkNHCE | TNTEEYIKRV | | |
| msa521982.2{69_1169NT} | VPRYLKRVEA | EENWLkNHCE | TNTEEYIKRV | | |
| msa521982.2{69_M732} | VPRYLKRVEA | EENWLkNHCE | TNTEEYIKRV | | |
| Consensus | ***** | ***** | ***** | | |

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8501

STRAIN 2603

atgagtaaaccgacaaaatttaggaattagtaaaaaaggagcaattatatcagggctctca
 gtggcactaattgtagtaaataggtgggtttttatgggtacaatctcaacctaatagagt
 gcagtaaaaactaactacaaagtttttatgttagagaaggaggtgttcgtcctcaact
 cttttgacaggaaggctaaggtcaatcaagaacagtatgtgtattttgatgctaataaa
 ggttaatcgagcaactgtcacagttaaagtggtgataaaatcacagctggtcagcagtta
 gttcaabatgatacaacaactgcacaagcagcctacgacactgctaactcgtcaattaaat
 aaagttagcgcgtcagatttaataatctaagacaaacaggaagcttccagctatggaatca
 agtgatcaatcttctcatcatcacaaaggacaagggactcaatcgactagtggtgagcag
 aatcgctctacagcaaaattatcaaagtcagctaatgcttcatacaaccaacaactcaa
 gatttgaatgatgcttatgcagatgcacagcgagaaagtaataaagcacaanaagcattg
 aatgatactgttattacaagtgacgtatcagggacagttgttgaagttaatagtgatatt
 gatccagcttcaaaaactagtcaggtacttgtccatgtgacaaactgaaggtaaactcaa
 gtacaaggaacgatgagtgagtgatgtttggctaatgttaaaaaagaccaggtgttaaa
 ataaaatctaaggtctatcctgacaaggaatgggaaggtaaaatttcatatctcaaat
 tatccagaagcagaagcaacaacaatgactctaataacgggtctagtgtgttaaatat
 aaatataaagtagattacttagccctctcgatgcattaaaacaaggttttaccgtatca
 gttgaagtagtttaaggagataagcaccttatgtccctacaagttctgtgataaaca
 gataataaacactttgtttgggtatacaatgatttctaactcgtaaaatttccaaagttgaa
 gtcaaaattggtaagctgtagtgaagacacaagaatttttatcaggtttgaaagcagga
 caaatcggtggttactaatccaagtaaaccttcaaggatgggcaaaaattgataatatt
 gaatcaatcgatcttaactctaataagaatcagaggtgaaa

SEQ ID NO. 8502

STRAIN 090

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
 CAAAGTTTTTAAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACAGTCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
 ATCATACAAGGACAAGGACTCAATCGACTAGTGGTGGCAGCAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAAACTT
 CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAATAAAGC
 ACAAAAAGCATTTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTCAAGTA
 CTTGCTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTTAAAAAAGACCAAGCTGTTAAATAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAAAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTTTACCCTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATGTCTCCTACAAGTTCTGTGATAAAACAAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
 GGACAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAATCTAATAAGAAATCAGAGG

SEQ ID NO. 8503

STRAIN A909

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAA
 CTACAAAGTTTTTAAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTT
 TGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCT
 AATAAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCAC
 AGCTGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCT
 ACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAAT
 CTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTC
 ATCATCATACAAGGACAAGGGCTCAATCGACTAGTGGTGGCAGCAATC
 GTCTACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAA
 CTTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAATAA
 AGCACAAAAGCATTTGAATGATACTGTTATTACAAGTGACGTATCAGGGA
 CAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTCAAGTCA
 GTACTTGTCCATGTAGCAACTGAGGGTAACTCCAAGTACAAGGAACGAT
 GAGTGATGATGATTTGGCTAATGTTAAAAAAGACCAAGTCTGTTAAATAA
 AATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTATATATC
 TCAAAATTATCCAGAAGCAGAAGCAAAACAATGACTCTAATAACGGCTC
 TAGTGCTGTAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATG
 CATTAACAAAGGTTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAG
 CACCTTATGTTCTTACAAGTTCTGTGACAAAACAAAGATAATAAACACTT
 TGTTTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCA
 AAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAG
 GCAGGACAATCGTGGTTACTAATCCAAGCAAACTTCAAGGATGGGCA
 AAAAATTGATAATATTGAATCAATAGATCTTAAGTCTAATAAGAAATCAG
 AGGTGAAA

SEQ ID NO. 8504

STRAIN H36B

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
 CAAAGTTTTTAAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC

Table 85: Comparative Sequences relating to SAG1361

TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
ATCATCACAAGGACAAGGGAAGTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAAACCAACTT
CAAGATTGTAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAGCATTGAATGATCTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATGATCCAGCTTCAAAAAGTCAAGTA
CTTGTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTGGCTAATGTAAAAAAGACAGGCTGTTAAATAAAAT
CTAAGGCTATCTCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
AATTATCCAGAAGCAGAAGCAACCAACATGACTCTAATAACGGCTCTAG
TGCTGTAAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAAAACAAGTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATGTTCTTACAAGTTCTGTGACAAACAAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTAGTTACTAATCCAAGTAAAGCTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TG

SEQ ID NO. 8505

STRAIN 18RS21

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCTTC
ATCATCACAAGGACAAGGGAAGTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAAACCAACTT
CAAGATTGTAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAGCATTGAATGATGATGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATGATCCAGCTTCAAAAAGTCAAGTA
CTTGTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTGGCTAATGTAAAAAAGACAGGCTGTTAAATAAAAT
CTAAGGCTCTATCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
AATTATCCAGAAGCAGAAGCAACCAACATGACTCTAATAACGGCTCTAG
TGCTGTAAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAAAACAAGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATGTTCTTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAG

SEQ ID NO. 8506

STRAIN M732

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGGAGTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
ATCATCACAAGGACAAGGGAAGTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAAACCAACTT
CAAGATTGTAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAGCATTGAATGATGATGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATGATCCAGCTTCAAAAAGTCAAGTA
CTTGTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTGGCTAATGTAAAAAAGATCAGGCTGTTAAATAAAAT
CTAAGGCTCTATCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
AATTATCCAGAAGCAGAAGCAACCAACATGACTCTAATAACGGCTCTAG
TGCTGTAAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAAAACAAGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATGTTCTTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTGGTTACTAATCCAAGCAAACTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TGAA

SEQ ID NO. 8507

STRAIN COH1

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAAC
TAATTACAAGTTTAAATGTTAGAGAAGGAAGTGTTCGTCTCAACTC
TTTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTGAT
GCTAATAAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAAT
CACAGCTGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAG
CCTACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAAT
AATCTAAAGACAACAGGAGTTTTCAGCTATGGAATCAAGTGATCAATC

Table 85: Comparative Sequences relating to SAG1361

TTCATCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGA
 ATCGTCTACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAA
 CAACCTTCAAGATTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAA
 TAAAGCACAAAAGCATTTGAATGATAGTCTTATTAACAAGTGACGTATCAG
 GGACAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTAGT
 CAAGTACTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAAC
 GATGAGTGAGTATGATTGGCTAATGTTAAAAAAGATCAGGCTGTTAAAA
 TAAAAATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTATAT
 ATCTCAAATTTATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGG
 CTCTAGTGTCTGTAATTTATAATATAAAGTAGATATTACTAGCCCTCTCG
 ATGCATTAAAAACAGGTTTACCGTATCAGTTGAAGTAGTTAATGGAGAT
 AAGCACCTTATTGTCCCTACAAGTTCTGTGATAAAACAAGATAATAAACA
 CTTTGTGTTGGGTATACAATGATTTCTAATCGTAAATTTCCAAGTTGAAG
 TCAAAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTG
 AAAGCAGGACAAATCGTGGTTACTAATCCAAGCAAACTTTCAAGGATGG
 GCAAAAAATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAAT
 CAGAGGTGAA

SEQ ID NO. 8507

STRAIN M781

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCGAGTAAAACTAATTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
 ACACGTCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAAATAATCTA
 AAGACAACAGGGAGTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCT
 CAAGATTTGAATGATGCTTATGCGATGCACAGGCAGAAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATGCTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTAGTCAAGTA
 CTTGTCCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAAAAGATCAGGCTGTTAAATAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGCAAACTTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TGAA

SEQ ID NO. 8508

STRAIN CJB110

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCGAGTAAAACTAATTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
 ACACGTCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
 ATCATCACAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCT
 CAAGATTTGAATGATGCTTATGCGATGCACAGGCAGAAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATGCTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTAGTCAAGTA
 CTTGTCCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAAAAGACCAGGCTGTTAAATAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGTAAACCTTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TGA

SEQ ID NO. 8509

STRAIN I169NT

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCGAGTAAAACT
 AACTACAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCT
 TTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATG
 CTAATAAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATC
 ACAGCTGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGC
 CTACGACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAAATA
 ATCTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCT
 TCTTCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAAA
 TCGTCTACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAAC

Table 85: Comparative Sequences relating to SAG1361

AACTTCAAGATTGTAATGATGCTTATGCAGATGCACAGGCAGAAGTAAT
AAAGCACAAAAGTGAATGAATGATATGTTATTACAAGTGACGTATCAGG
CAGAGTTTGAAGTTAATAGTGATATTGTCAGCTTCAAAAACTAGTC
AAGTACTTGTCCATGTAGCACTGAAGGTAACCTCCAAGTACAAGGAACG
ATGAGTGAGTATGATTTGGCTAATGTTAAAAAAGCAGCGCTGTTTAAAT
AAAACTAAGGTCATCTCTGACAAAGGAATGGGAAGGTAATAATTCATTA
TCTCAAATTTATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGC
TCTAGTGCTGTAAATATAAATATAAGATAGATATTACTAGCCCTCTCGA
TGCTATAAAAACAGGTTTATCCGTTATCAGTTGAAGTAGTTATGGAGATA
AGCACTTATTTGCCCTACAAGTTCTGTGATAAACAAAGATAATTAACAC
TTTGTTTGGGTATAACAATGATTTCTAATCGTAAATTTCCAAAGTTGAAGT
CAAAATTTGTAAGCTGATGCTAAGACAGAGAAATTTTATCAGGTTTGA
AAGCAGGACAATTCGTGGTTACTAATCAAAGTAAACCTTCAAGGATGGG
CAAAAATTGATAATTTGAATCAATCGATCTTAACCTTAATAAGAAATC
AGAGGTGAA

SEQ ID NO. 8510

STRAIN JM9130013

TTTTTATGGGTACAATCTCAACCTTAATAAGAGTGCAGTAAAACTAACTCA
CAAAGTTTTAATGCTTAGAGCAAGGAAGTGTTCGTCTCAACTCTTTTGA
CAGGAAAAGCTTAGGCTAATCAAGAAGCAGTATGCTGTTATTGTAGTCGAA
AAAGTGAATTCGAGCAACTGCTTAGCATGTAAAGTGGGTGATAAAAATCACAGC
TGGTCAGCACTTAGTTCAATATGATACAACACTGCACAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAAATAATCTA
AAGACAACAGGAAGTCTTCAGCATTTGAATCAAGTGATCAATCTTCATCT
ATCATCAACAGGACAGGGGGCTCAATCGACTAGTGTGGCAGCAATCGTC
TACAGCAAAATTAACAACTCAAGCTAGTATGCTTCTACAACCAACAACTT
CAAGAAATTGAATGATGCTTATGCAAGTGCACAGGCAGAGTAATAAAGC
ACAAAAGCATTGAATGATATCTGTTATTACAAGTACGCTATCAGGACAG
TTGTTGAAGTAAATAGTGATTAATGATCAGCTCAAAAACATGTCGAAGTA
CTTGTCTAGTGTACCAACTGAGGGTTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGACCAGTCTGTTAAAAATAAAAT
CTAAGGTCTATGCTGACAAGGAATGGGAAGTGTAATTTCATATATCTCA
AATTATCAGAAGCAGCAAGACAACCAATAGCTCAATTAACCGCTCTAG
TGCTGTAAATTAATAAATATAAAGTAGATATTATGACCCCTCTCATAGTAT
TAAAAACAAGGTTTACTGTATCAGTTGAAGTAGTTAATGGAGATGACAC
CTTATTGTTCTCAACAGTTCTGTGACAAACAAGATAATAAACACTTTGT
TTGGGTATCAATGATTTCTAATCGTAAAAATTTCCAAGTGTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACAAGAAATTTTATCAGGTTTGAAGACA
GGACAATCGTGGTTACTAATCCAAGCAAAACTTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATAGATCTTAAGTCTAATAAGAAATCAGAG
TGAAA

PRETTY of: /biotmp/msa363690.2{*} March 31, 2003 07:01 ..

| | 1 | | | | | 50 |
|----------------------------|------------|------------|------------|------------|------------|----|
| msa363690.2{690_COH1} | ~ | ~ | ~ | ~ | ~ | ~ |
| msa363690.2{690_M732} | ~ | ~ | ~ | ~ | ~ | ~ |
| msa363690.2{690_M781} | ~ | ~ | ~ | ~ | ~ | ~ |
| msa363690.2{690_090} | ~ | ~ | ~ | ~ | ~ | ~ |
| msa363690.2{690_CJB110} | ~ | ~ | ~ | ~ | ~ | ~ |
| msa363690.2{690_1169NT} | ~ | ~ | ~ | ~ | ~ | ~ |
| msa363690.2{690_18RS21} | ~ | ~ | ~ | ~ | ~ | ~ |
| msa363690.2{690_2603} | atgagtaaac | gacaaaattt | aggaattagt | aaaaaaggag | caattatatt | |
| msa363690.2{690_A909} | ~ | ~ | ~ | ~ | ~ | ~ |
| msa363690.2{690_JM9130013} | ~ | ~ | ~ | ~ | ~ | ~ |
| msa363690.2{690_H36B} | ~ | ~ | ~ | ~ | ~ | ~ |
| Consensus | ***** | ***** | ***** | ***** | ***** | |

| | 51 | | | 100 |
|----------------------------|-------------|------------|------------|-----------------------|
| msa363690.2{690_COH1} | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~TTT TTATGGGTAC |
| msa363690.2{690_M732} | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~TTT TTATGGGTAC |
| msa363690.2{690_M781} | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~TTT TTATGGGTAC |
| msa363690.2{690_090} | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~TTT TTATGGGTAC |
| msa363690.2{690_CJB110} | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~TTT TTATGGGTAC |
| msa363690.2{690_1169NT} | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~TTT TTATGGGTAC |
| msa363690.2{690_18RS21} | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~TTT TTATGGGTAC |
| msa363690.2{690_2603} | agggcctctca | gtggcactaa | ttgtagtaat | aggtggcTTT TTATGGGTAC |
| msa363690.2{690_A909} | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~TTT TTATGGGTAC |
| msa363690.2{690_JM9130013} | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~TTT TTATGGGTAC |
| msa363690.2{690_H36B} | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~TTT TTATGGGTAC |
| Consensus | ***** | ***** | ***** | ***** |

| | | |
|-------------------------|----------------------------------|-------------------------|
| | 101 | 150 |
| msa363690.2{690_COH1} | AATCTCAACC TAATAAGAGT GCAGTAAAAA | CTAAatTACAA AGTTTTTAAAT |
| msa363690.2{690_M732} | AATCTCAACC TAATAAGAGT GCAGTAAAAA | CTAAatTACAA AGTTTTTAAAT |
| msa363690.2{690_M781} | AATCTCAACC TAATAAGAGT GCAGTAAAAA | CTAAatTACAA AGTTTTTAAAT |
| msa363690.2{690_O90} | AATCTCAACC TAATAAGAGT GCAGTAAAAA | CTAAatTACAA AGTTTTTAAAT |
| msa363690.2{690_CJB110} | AATCTCAACC TAATAAGAGT GCAGTAAAAA | CTAAatTACAA AGTTTTTAAAT |
| msa363690.2{690_1169NT} | AATCTCAACC TAATAAGAGT GCAGTAAAAA | CTAAatTACAA AGTTTTTAAAT |
| msa363690.2{690_18RS21} | AATCTCAACC TAATAAGAGT GCAGTAAAAA | CTAAatTACAA AGTTTTTAAAT |
| msa363690.2{690_2603} | AATCTCAACC TAATAAGAGT GCAGTAAAAA | CTAAatTACAA AGTTTTTAAAT |

Table 85: Comparative Sequences relating to SAG1361

| | | | | | |
|----------------------------|------------|------------|------------|------------|-------------|
| msa363690.2{690_A909} | AATCTCAACC | TAATAAGAGT | GCAGTAAAAA | CTAAcTACAA | AGTTTTTAAAT |
| msa363690.2{690_JM9130013} | AATCTCAACC | TAATAAGAGT | GCAGTAAAAA | CTAAcTACAA | AGTTTTTAAAT |
| msa363690.2{690_H36B} | AATCTCAACC | TAATAAGAGT | GCAGTAAAAA | CTAAcTACAA | AGTTTTTAAAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | 151 | GAAGTGTTC | GTCCTCAACT | CTTTTGACAG | 200 |
| msa363690.2{690_M732} | GAAGTGTTC | GTCCTCAACT | CTTTTGACAG | GAAAAGCTAA | |
| msa363690.2{690_M781} | GAAGTGTTC | GTCCTCAACT | CTTTTGACAG | GAAAAGCTAA | |
| msa363690.2{690_090} | GAAGTGTTC | GTCCTCAACT | CTTTTGACAG | GAAAAGCTAA | |
| msa363690.2{690_CJB110} | GAAGTGTTC | GTCCTCAACT | CTTTTGACAG | GAAAAGCTAA | |
| msa363690.2{690_1169NT} | GAAGTGTTC | GTCCTCAACT | CTTTTGACAG | GAAAAGCTAA | |
| msa363690.2{690_18RS21} | GAAGTGTTC | GTCCTCAACT | CTTTTGACAG | GAAAAGCTAA | |
| msa363690.2{690_2603} | GAAGTGTTC | GTCCTCAACT | CTTTTGACAG | GAAAAGCTAA | |
| msa363690.2{690_A909} | GAAGTGTTC | GTCCTCAACT | CTTTTGACAG | GAAAAGCTAA | |
| msa363690.2{690_JM9130013} | GAAGTGTTC | GTCCTCAACT | CTTTTGACAG | GAAAAGCTAA | |
| msa363690.2{690_H36B} | GAAGTGTTC | GTCCTCAACT | CTTTTGACAG | GAAAAGCTAA | |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | 201 | GGCTAATCAA | GAACAGTATG | TGTATTTTGA | 250 |
| msa363690.2{690_M732} | GGCTAATCAA | GAACAGTATG | TGTATTTTGA | TGCTAATAAa | GGTAATCGAG |
| msa363690.2{690_M781} | GGCTAATCAA | GAACAGTATG | TGTATTTTGA | TGCTAATAAa | GGTAATCGAG |
| msa363690.2{690_090} | GGCTAATCAA | GAACAGTATG | TGTATTTTGA | TGCTAATAAa | GGTAATCGAG |
| msa363690.2{690_CJB110} | GGCTAATCAA | GAACAGTATG | TGTATTTTGA | TGCTAATAAa | GGTAATCGAG |
| msa363690.2{690_1169NT} | GGCTAATCAA | GAACAGTATG | TGTATTTTGA | TGCTAATAAa | GGTAATCGAG |
| msa363690.2{690_18RS21} | GGCTAATCAA | GAACAGTATG | TGTATTTTGA | TGCTAATAAa | GGTAATCGAG |
| msa363690.2{690_2603} | GGCTAATCAA | GAACAGTATG | TGTATTTTGA | TGCTAATAAa | GGTAATCGAG |
| msa363690.2{690_A909} | GGCTAATCAA | GAACAGTATG | TGTATTTTGA | TGCTAATAAa | GGTAATCGAG |
| msa363690.2{690_JM9130013} | GGCTAATCAA | GAACAGTATG | TGTATTTTGA | TGCTAATAAa | GGTAATCGAG |
| msa363690.2{690_H36B} | GGCTAATCAA | GAACAGTATG | TGTATTTTGA | TGCTAATAAa | GGTAATCGAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | 251 | CAACTGTtAC | AGTTAAAGTG | GGTGATAAAA | 300 |
| msa363690.2{690_M732} | CAACTGTtAC | AGTTAAAGTG | GGTGATAAAA | TCACAGCTGG | TCAGCAGTTA |
| msa363690.2{690_M781} | CAACTGTtAC | AGTTAAAGTG | GGTGATAAAA | TCACAGCTGG | TCAGCAGTTA |
| msa363690.2{690_090} | CAACTGTtAC | AGTTAAAGTG | GGTGATAAAA | TCACAGCTGG | TCAGCAGTTA |
| msa363690.2{690_CJB110} | CAACTGTtAC | AGTTAAAGTG | GGTGATAAAA | TCACAGCTGG | TCAGCAGTTA |
| msa363690.2{690_1169NT} | CAACTGTtAC | AGTTAAAGTG | GGTGATAAAA | TCACAGCTGG | TCAGCAGTTA |
| msa363690.2{690_18RS21} | CAACTGTtAC | AGTTAAAGTG | GGTGATAAAA | TCACAGCTGG | TCAGCAGTTA |
| msa363690.2{690_2603} | CAACTGTtAC | AGTTAAAGTG | GGTGATAAAA | TCACAGCTGG | TCAGCAGTTA |
| msa363690.2{690_A909} | CAACTGTtAC | AGTTAAAGTG | GGTGATAAAA | TCACAGCTGG | TCAGCAGTTA |
| msa363690.2{690_JM9130013} | CAACTGTtAC | AGTTAAAGTG | GGTGATAAAA | TCACAGCTGG | TCAGCAGTTA |
| msa363690.2{690_H36B} | CAACTGTtAC | AGTTAAAGTG | GGTGATAAAA | TCACAGCTGG | TCAGCAGTTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | 301 | GTTCAATATG | ATACAACAAC | TGCACAAGCA | 350 |
| msa363690.2{690_M732} | GTTCAATATG | ATACAACAAC | TGCACAAGCA | GCCTACGACA | CTGCTAATCG |
| msa363690.2{690_M781} | GTTCAATATG | ATACAACAAC | TGCACAAGCA | GCCTACGACA | CTGCTAATCG |
| msa363690.2{690_090} | GTTCAATATG | ATACAACAAC | TGCACAAGCA | GCCTACGACA | CTGCTAATCG |
| msa363690.2{690_CJB110} | GTTCAATATG | ATACAACAAC | TGCACAAGCA | GCCTACGACA | CTGCTAATCG |
| msa363690.2{690_1169NT} | GTTCAATATG | ATACAACAAC | TGCACAAGCA | GCCTACGACA | CTGCTAATCG |
| msa363690.2{690_18RS21} | GTTCAATATG | ATACAACAAC | TGCACAAGCA | GCCTACGACA | CTGCTAATCG |
| msa363690.2{690_2603} | GTTCAATATG | ATACAACAAC | TGCACAAGCA | GCCTACGACA | CTGCTAATCG |
| msa363690.2{690_A909} | GTTCAATATG | ATACAACAAC | TGCACAAGCA | GCCTACGACA | CTGCTAATCG |
| msa363690.2{690_JM9130013} | GTTCAATATG | ATACAACAAC | TGCACAAGCA | GCCTACGACA | CTGCTAATCG |
| msa363690.2{690_H36B} | GTTCAATATG | ATACAACAAC | TGCACAAGCA | GCCTACGACA | CTGCTAATCG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | 351 | TCAATTAAAT | AAAGTAGCGC | GTCAGATTAA | 400 |
| msa363690.2{690_M732} | TCAATTAAAT | AAAGTAGCGC | GTCAGATTAA | TAATCTAAAG | ACAACAGGgA |
| msa363690.2{690_M781} | TCAATTAAAT | AAAGTAGCGC | GTCAGATTAA | TAATCTAAAG | ACAACAGGgA |
| msa363690.2{690_090} | TCAATTAAAT | AAAGTAGCGC | GTCAGATTAA | TAATCTAAAG | ACAACAGGgA |
| msa363690.2{690_CJB110} | TCAATTAAAT | AAAGTAGCGC | GTCAGATTAA | TAATCTAAAG | ACAACAGGgA |
| msa363690.2{690_1169NT} | TCAATTAAAT | AAAGTAGCGC | GTCAGATTAA | TAATCTAAAG | ACAACAGGgA |
| msa363690.2{690_18RS21} | TCAATTAAAT | AAAGTAGCGC | GTCAGATTAA | TAATCTAAAG | ACAACAGGgA |
| msa363690.2{690_2603} | TCAATTAAAT | AAAGTAGCGC | GTCAGATTAA | TAATCTAAAG | ACAACAGGgA |
| msa363690.2{690_A909} | TCAATTAAAT | AAAGTAGCGC | GTCAGATTAA | TAATCTAAAG | ACAACAGGgA |
| msa363690.2{690_JM9130013} | TCAATTAAAT | AAAGTAGCGC | GTCAGATTAA | TAATCTAAAG | ACAACAGGgA |
| msa363690.2{690_H36B} | TCAATTAAAT | AAAGTAGCGC | GTCAGATTAA | TAATCTAAAG | ACAACAGGgA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | 401 | GTtTCCAGC | TATGGAATcA | AGTGATCAAT | 450 |
| msa363690.2{690_M732} | GTtTCCAGC | TATGGAATcA | AGTGATCAAT | CTTcATCATC | ATCACAAGGA |
| msa363690.2{690_M781} | GTtTCCAGC | TATGGAATcA | AGTGATCAAT | CTTcATCATC | ATCACAAGGA |
| msa363690.2{690_090} | GTtTCCAGC | TATGGAATcA | AGTGATCAAT | CTTcATCATC | ATCACAAGGA |
| msa363690.2{690_CJB110} | GTtTCCAGC | TATGGAATcA | AGTGATCAAT | CTTcATCATC | ATCACAAGGA |
| msa363690.2{690_1169NT} | GTtTCCAGC | TATGGAATcA | AGTGATCAAT | CTTcATCATC | ATCACAAGGA |
| msa363690.2{690_18RS21} | GTtTCCAGC | TATGGAATcA | AGTGATCAAT | CTTcATCATC | ATCACAAGGA |

Table 85: Comparative Sequences relating to SAG1361

| | | | | | |
|----------------------------|------------|------------|-------------|-------------|------------|
| msa363690.2{690_2603} | GTcTTCCAGC | TATGGAATcA | AGTGATCAAT | CTTCtTCATC | ATCACAAGGA |
| msa363690.2{690_A909} | GTcTTCCAGC | TATGGAATcA | AGTGATCAAT | CTTCaTCATC | ATCACAAGGA |
| msa363690.2{690_JM9130013} | GTcTTCCAGC | TATGGAATcA | AGTGATCAAT | CTTCaTCATC | ATCACAAGGA |
| msa363690.2{690_H36B} | GTcTTCCAGC | TATGGAATcA | AGTGATCAAT | CTTCaTCATC | ATCACAAGGA |
| Consensus | ***-***** | *****-* | ***** | *****-***** | ***** |
| msa363690.2{690_COH1} | CAAGGGaCTC | AATCGACTAG | TGGTGCGACG | AATCGTCTAC | AGCAAAATTA |
| msa363690.2{690_M732} | CAAGGGaCTC | AATCGACTAG | TGGTGCGACG | AATCGTCTAC | AGCAAAATTA |
| msa363690.2{690_M781} | CAAGGGaCTC | AATCGACTAG | TGGTGCGACG | AATCGTCTAC | AGCAAAATTA |
| msa363690.2{690_090} | CAAGGGaCTC | AATCGACTAG | TGGTGCGACG | AATCGTCTAC | AGCAAAATTA |
| msa363690.2{690_CJB110} | CAAGGGaCTC | AATCGACTAG | TGGTGCGACG | AATCGTCTAC | AGCAAAATTA |
| msa363690.2{690_1169NT} | CAAGGGaCTC | AATCGACTAG | TGGTGCGACG | AATCGTCTAC | AGCAAAATTA |
| msa363690.2{690_18RS21} | CAAGGGaCTC | AATCGACTAG | TGGTGCGACG | AATCGTCTAC | AGCAAAATTA |
| msa363690.2{690_2603} | CAAGGGaCTC | AATCGACTAG | TGGTGCGACG | AATCGTCTAC | AGCAAAATTA |
| msa363690.2{690_A909} | CAAGGGaCTC | AATCGACTAG | TGGTGCGACG | AATCGTCTAC | AGCAAAATTA |
| msa363690.2{690_JM9130013} | CAAGGGaCTC | AATCGACTAG | TGGTGCGACG | AATCGTCTAC | AGCAAAATTA |
| msa363690.2{690_H36B} | CAAGGGaCTC | AATCGACTAG | TGGTGCGACG | AATCGTCTAC | AGCAAAATTA |
| Consensus | *****-*** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | TCAAAGTCAA | GCTAATGCTT | CATACAACCA | ACAACITCAA | GATTTGAATG |
| msa363690.2{690_M732} | TCAAAGTCAA | GCTAATGCTT | CATACAACCA | ACAACITCAA | GATTTGAATG |
| msa363690.2{690_M781} | TCAAAGTCAA | GCTAATGCTT | CATACAACCA | ACAACITCAA | GATTTGAATG |
| msa363690.2{690_090} | TCAAAGTCAA | GCTAATGCTT | CATACAACCA | ACAACITCAA | GATTTGAATG |
| msa363690.2{690_CJB110} | TCAAAGTCAA | GCTAATGCTT | CATACAACCA | ACAACITCAA | GATTTGAATG |
| msa363690.2{690_1169NT} | TCAAAGTCAA | GCTAATGCTT | CATACAACCA | ACAACITCAA | GATTTGAATG |
| msa363690.2{690_18RS21} | TCAAAGTCAA | GCTAATGCTT | CATACAACCA | ACAACITCAA | GATTTGAATG |
| msa363690.2{690_2603} | TCAAAGTCAA | GCTAATGCTT | CATACAACCA | ACAACITCAA | GATTTGAATG |
| msa363690.2{690_A909} | TCAAAGTCAA | GCTAATGCTT | CATACAACCA | ACAACITCAA | GATTTGAATG |
| msa363690.2{690_JM9130013} | TCAAAGTCAA | GCTAATGCTT | CATACAACCA | ACAACITCAA | GATTTGAATG |
| msa363690.2{690_H36B} | TCAAAGTCAA | GCTAATGCTT | CATACAACCA | ACAACITCAA | GATTTGAATG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | ATGCTTATGC | AGATGCACAG | GCAGAAGTAA | ATAAAGCACA | AAAAGCATTG |
| msa363690.2{690_M732} | ATGCTTATGC | AGATGCACAG | GCAGAAGTAA | ATAAAGCACA | AAAAGCATTG |
| msa363690.2{690_M781} | ATGCTTATGC | AGATGCACAG | GCAGAAGTAA | ATAAAGCACA | AAAAGCATTG |
| msa363690.2{690_090} | ATGCTTATGC | AGATGCACAG | GCAGAAGTAA | ATAAAGCACA | AAAAGCATTG |
| msa363690.2{690_CJB110} | ATGCTTATGC | AGATGCACAG | GCAGAAGTAA | ATAAAGCACA | AAAAGCATTG |
| msa363690.2{690_1169NT} | ATGCTTATGC | AGATGCACAG | GCAGAAGTAA | ATAAAGCACA | AAAAGCATTG |
| msa363690.2{690_18RS21} | ATGCTTATGC | AGATGCACAG | GCAGAAGTAA | ATAAAGCACA | AAAAGCATTG |
| msa363690.2{690_2603} | ATGCTTATGC | AGATGCACAG | GCAGAAGTAA | ATAAAGCACA | AAAAGCATTG |
| msa363690.2{690_A909} | ATGCTTATGC | AGATGCACAG | GCAGAAGTAA | ATAAAGCACA | AAAAGCATTG |
| msa363690.2{690_JM9130013} | ATGCTTATGC | AGATGCACAG | GCAGAAGTAA | ATAAAGCACA | AAAAGCATTG |
| msa363690.2{690_H36B} | ATGCTTATGC | AGATGCACAG | GCAGAAGTAA | ATAAAGCACA | AAAAGCATTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | AATGATACTG | TTATTACAAG | TGACGTATCA | GGGACAGTTG | TTGAAGTTAA |
| msa363690.2{690_M732} | AATGATACTG | TTATTACAAG | TGACGTATCA | GGGACAGTTG | TTGAAGTTAA |
| msa363690.2{690_M781} | AATGATACTG | TTATTACAAG | TGACGTATCA | GGGACAGTTG | TTGAAGTTAA |
| msa363690.2{690_090} | AATGATACTG | TTATTACAAG | TGACGTATCA | GGGACAGTTG | TTGAAGTTAA |
| msa363690.2{690_CJB110} | AATGATACTG | TTATTACAAG | TGACGTATCA | GGGACAGTTG | TTGAAGTTAA |
| msa363690.2{690_1169NT} | AATGATACTG | TTATTACAAG | TGACGTATCA | GGGACAGTTG | TTGAAGTTAA |
| msa363690.2{690_18RS21} | AATGATACTG | TTATTACAAG | TGACGTATCA | GGGACAGTTG | TTGAAGTTAA |
| msa363690.2{690_2603} | AATGATACTG | TTATTACAAG | TGACGTATCA | GGGACAGTTG | TTGAAGTTAA |
| msa363690.2{690_A909} | AATGATACTG | TTATTACAAG | TGACGTATCA | GGGACAGTTG | TTGAAGTTAA |
| msa363690.2{690_JM9130013} | AATGATACTG | TTATTACAAG | TGACGTATCA | GGGACAGTTG | TTGAAGTTAA |
| msa363690.2{690_H36B} | AATGATACTG | TTATTACAAG | TGACGTATCA | GGGACAGTTG | TTGAAGTTAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | TAGTGATATT | GATCCAGCTT | CAAAAACCTAG | TCAAGTACTT | GTCCATGTAG |
| msa363690.2{690_M732} | TAGTGATATT | GATCCAGCTT | CAAAAACCTAG | TCAAGTACTT | GTCCATGTAG |
| msa363690.2{690_M781} | TAGTGATATT | GATCCAGCTT | CAAAAACCTAG | TCAAGTACTT | GTCCATGTAG |
| msa363690.2{690_090} | TAGTGATATT | GATCCAGCTT | CAAAAACCTAG | TCAAGTACTT | GTCCATGTAG |
| msa363690.2{690_CJB110} | TAGTGATATT | GATCCAGCTT | CAAAAACCTAG | TCAAGTACTT | GTCCATGTAG |
| msa363690.2{690_1169NT} | TAGTGATATT | GATCCAGCTT | CAAAAACCTAG | TCAAGTACTT | GTCCATGTAG |
| msa363690.2{690_18RS21} | TAGTGATATT | GATCCAGCTT | CAAAAACCTAG | TCAAGTACTT | GTCCATGTAG |
| msa363690.2{690_2603} | TAGTGATATT | GATCCAGCTT | CAAAAACCTAG | TCAAGTACTT | GTCCATGTAG |
| msa363690.2{690_A909} | TAGTGATATT | GATCCAGCTT | CAAAAACCTAG | TCAAGTACTT | GTCCATGTAG |
| msa363690.2{690_JM9130013} | TAGTGATATT | GATCCAGCTT | CAAAAACCTAG | TCAAGTACTT | GTCCATGTAG |
| msa363690.2{690_H36B} | TAGTGATATT | GATCCAGCTT | CAAAAACCTAG | TCAAGTACTT | GTCCATGTAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | CAACTGAaGG | TAAACTCCAA | GTACAAGGAA | CGATGAGTGA | GTATGATTTG |
| msa363690.2{690_M732} | CAACTGAaGG | TAAACTCCAA | GTACAAGGAA | CGATGAGTGA | GTATGATTTG |
| msa363690.2{690_M781} | CAACTGAaGG | TAAACTCCAA | GTACAAGGAA | CGATGAGTGA | GTATGATTTG |
| msa363690.2{690_090} | CAACTGAaGG | TAAACTCCAA | GTACAAGGAA | CGATGAGTGA | GTATGATTTG |
| msa363690.2{690_CJB110} | CAACTGAaGG | TAAACTCCAA | GTACAAGGAA | CGATGAGTGA | GTATGATTTG |
| msa363690.2{690_1169NT} | CAACTGAaGG | TAAACTCCAA | GTACAAGGAA | CGATGAGTGA | GTATGATTTG |

Table 85: Comparative Sequences relating to SAG1361

| | | | | | |
|----------------------------|------------|------------|-------------|-------------|-------------|
| msa363690.2{690_18RS21} | CAACTGAaGG | TAAACTCCAA | GTACAAGGAA | CGATGAGTGA | GTATGATTGG |
| msa363690.2{690_2603} | CAACTGAaGG | TAAACTCCAA | GTACAAGGAA | CGATGAGTGA | GTATGATTGG |
| msa363690.2{690_A909} | CAACTGAaGG | TAAACTCCAA | GTACAAGGAA | CGATGAGTGA | GTATGATTGG |
| msa363690.2{690_JM9130013} | CAACTGAaGG | TAAACTCCAA | GTACAAGGAA | CGATGAGTGA | GTATGATTGG |
| msa363690.2{690_H36B} | CAACTGAaGG | TAAACTCCAA | GTACAAGGAA | CGATGAGTGA | GTATGATTGG |
| Consensus | *****-* | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | 751 | AAAAAGATCA | GgCTGTTAA | ATAAAAATCTA | AGGTCTATCC |
| msa363690.2{690_M732} | GCTAATGTtA | AAAAAGATCA | GgCTGTTAA | ATAAAAATCTA | AGGTCTATCC |
| msa363690.2{690_M781} | GCTAATGTtA | AAAAAGATCA | GgCTGTTAA | ATAAAAATCTA | AGGTCTATCC |
| msa363690.2{690_090} | GCTAATGTtA | AAAAAGATCA | GgCTGTTAA | ATAAAAATCTA | AGGTCTATCC |
| msa363690.2{690_CJB110} | GCTAATGTtA | AAAAAGATCA | GgCTGTTAA | ATAAAAATCTA | AGGTCTATCC |
| msa363690.2{690_1169NT} | GCTAATGTtA | AAAAAGATCA | GgCTGTTAA | ATAAAAATCTA | AGGTCTATCC |
| msa363690.2{690_18RS21} | GCTAATGTtA | AAAAAGATCA | GgCTGTTAA | ATAAAAATCTA | AGGTCTATCC |
| msa363690.2{690_2603} | GCTAATGTtA | AAAAAGATCA | GgCTGTTAA | ATAAAAATCTA | AGGTCTATCC |
| msa363690.2{690_A909} | GCTAATGTtA | AAAAAGATCA | GgCTGTTAA | ATAAAAATCTA | AGGTCTATCC |
| msa363690.2{690_JM9130013} | GCTAATGTtA | AAAAAGATCA | GgCTGTTAA | ATAAAAATCTA | AGGTCTATCC |
| msa363690.2{690_H36B} | GCTAATGTtA | AAAAAGATCA | GgCTGTTAA | ATAAAAATCTA | AGGTCTATCC |
| Consensus | *****-* | ***** | *-***** | ***** | ***** |
| msa363690.2{690_COH1} | 801 | TGACAAGGAA | TGGGAAGGTA | AAATTTTCATA | TATCTCAAAT |
| msa363690.2{690_M732} | TGACAAGGAA | TGGGAAGGTA | AAATTTTCATA | TATCTCAAAT | TATCCAGAAG |
| msa363690.2{690_M781} | TGACAAGGAA | TGGGAAGGTA | AAATTTTCATA | TATCTCAAAT | TATCCAGAAG |
| msa363690.2{690_090} | TGACAAGGAA | TGGGAAGGTA | AAATTTTCATA | TATCTCAAAT | TATCCAGAAG |
| msa363690.2{690_CJB110} | TGACAAGGAA | TGGGAAGGTA | AAATTTTCATA | TATCTCAAAT | TATCCAGAAG |
| msa363690.2{690_1169NT} | TGACAAGGAA | TGGGAAGGTA | AAATTTTCATA | TATCTCAAAT | TATCCAGAAG |
| msa363690.2{690_18RS21} | TGACAAGGAA | TGGGAAGGTA | AAATTTTCATA | TATCTCAAAT | TATCCAGAAG |
| msa363690.2{690_2603} | TGACAAGGAA | TGGGAAGGTA | AAATTTTCATA | TATCTCAAAT | TATCCAGAAG |
| msa363690.2{690_A909} | TGACAAGGAA | TGGGAAGGTA | AAATTTTCATA | TATCTCAAAT | TATCCAGAAG |
| msa363690.2{690_JM9130013} | TGACAAGGAA | TGGGAAGGTA | AAATTTTCATA | TATCTCAAAT | TATCCAGAAG |
| msa363690.2{690_H36B} | TGACAAGGAA | TGGGAAGGTA | AAATTTTCATA | TATCTCAAAT | TATCCAGAAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | 851 | CAGAAGCAAA | CAACAATGAC | TCTAATAACG | GCTCTAGTGC |
| msa363690.2{690_M732} | CAGAAGCAAA | CAACAATGAC | TCTAATAACG | GCTCTAGTGC | TGTAATTTAT |
| msa363690.2{690_M781} | CAGAAGCAAA | CAACAATGAC | TCTAATAACG | GCTCTAGTGC | TGTAATTTAT |
| msa363690.2{690_090} | CAGAAGCAAA | CAACAATGAC | TCTAATAACG | GCTCTAGTGC | TGTAATTTAT |
| msa363690.2{690_CJB110} | CAGAAGCAAA | CAACAATGAC | TCTAATAACG | GCTCTAGTGC | TGTAATTTAT |
| msa363690.2{690_1169NT} | CAGAAGCAAA | CAACAATGAC | TCTAATAACG | GCTCTAGTGC | TGTAATTTAT |
| msa363690.2{690_18RS21} | CAGAAGCAAA | CAACAATGAC | TCTAATAACG | GCTCTAGTGC | TGTAATTTAT |
| msa363690.2{690_2603} | CAGAAGCAAA | CAACAATGAC | TCTAATAACG | GCTCTAGTGC | TGTAATTTAT |
| msa363690.2{690_A909} | CAGAAGCAAA | CAACAATGAC | TCTAATAACG | GCTCTAGTGC | TGTAATTTAT |
| msa363690.2{690_JM9130013} | CAGAAGCAAA | CAACAATGAC | TCTAATAACG | GCTCTAGTGC | TGTAATTTAT |
| msa363690.2{690_H36B} | CAGAAGCAAA | CAACAATGAC | TCTAATAACG | GCTCTAGTGC | TGTAATTTAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | 901 | AAATATAAAG | TAGATATTAC | TAGCCCTCTC | GATGCATTAA |
| msa363690.2{690_M732} | AAATATAAAG | TAGATATTAC | TAGCCCTCTC | GATGCATTAA | AACAAGGTTT |
| msa363690.2{690_M781} | AAATATAAAG | TAGATATTAC | TAGCCCTCTC | GATGCATTAA | AACAAGGTTT |
| msa363690.2{690_090} | AAATATAAAG | TAGATATTAC | TAGCCCTCTC | GATGCATTAA | AACAAGGTTT |
| msa363690.2{690_CJB110} | AAATATAAAG | TAGATATTAC | TAGCCCTCTC | GATGCATTAA | AACAAGGTTT |
| msa363690.2{690_1169NT} | AAATATAAAG | TAGATATTAC | TAGCCCTCTC | GATGCATTAA | AACAAGGTTT |
| msa363690.2{690_18RS21} | AAATATAAAG | TAGATATTAC | TAGCCCTCTC | GATGCATTAA | AACAAGGTTT |
| msa363690.2{690_2603} | AAATATAAAG | TAGATATTAC | TAGCCCTCTC | GATGCATTAA | AACAAGGTTT |
| msa363690.2{690_A909} | AAATATAAAG | TAGATATTAC | TAGCCCTCTC | GATGCATTAA | AACAAGGTTT |
| msa363690.2{690_JM9130013} | AAATATAAAG | TAGATATTAC | TAGCCCTCTC | GATGCATTAA | AACAAGGTTT |
| msa363690.2{690_H36B} | AAATATAAAG | TAGATATTAC | TAGCCCTCTC | GATGCATTAA | AACAAGGTTT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | 951 | TACcGTATCA | GTTGAAGTAG | TTAATGGAGA | TAAGCACCTT |
| msa363690.2{690_M732} | TACcGTATCA | GTTGAAGTAG | TTAATGGAGA | TAAGCACCTT | ATTGTcCCTA |
| msa363690.2{690_M781} | TACcGTATCA | GTTGAAGTAG | TTAATGGAGA | TAAGCACCTT | ATTGTcCCTA |
| msa363690.2{690_090} | TACcGTATCA | GTTGAAGTAG | TTAATGGAGA | TAAGCACCTT | ATTGTcCCTA |
| msa363690.2{690_CJB110} | TACcGTATCA | GTTGAAGTAG | TTAATGGAGA | TAAGCACCTT | ATTGTcCCTA |
| msa363690.2{690_1169NT} | TACcGTATCA | GTTGAAGTAG | TTAATGGAGA | TAAGCACCTT | ATTGTcCCTA |
| msa363690.2{690_18RS21} | TACcGTATCA | GTTGAAGTAG | TTAATGGAGA | TAAGCACCTT | ATTGTcCCTA |
| msa363690.2{690_2603} | TACcGTATCA | GTTGAAGTAG | TTAATGGAGA | TAAGCACCTT | ATTGTcCCTA |
| msa363690.2{690_A909} | TACcGTATCA | GTTGAAGTAG | TTAATGGAGA | TAAGCACCTT | ATTGTcCCTA |
| msa363690.2{690_JM9130013} | TACcGTATCA | GTTGAAGTAG | TTAATGGAGA | TAAGCACCTT | ATTGTcCCTA |
| msa363690.2{690_H36B} | TACcGTATCA | GTTGAAGTAG | TTAATGGAGA | TAAGCACCTT | ATTGTcCCTA |
| Consensus | ***-***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | 1001 | CAAGTTCTGT | GatAAACAAA | GATAATAAAC | ACTTTGTTTG |
| msa363690.2{690_M732} | CAAGTTCTGT | GatAAACAAA | GATAATAAAC | ACTTTGTTTG | GGTATACAAAT |
| msa363690.2{690_M781} | CAAGTTCTGT | GatAAACAAA | GATAATAAAC | ACTTTGTTTG | GGTATACAAAT |
| msa363690.2{690_090} | CAAGTTCTGT | GatAAACAAA | GATAATAAAC | ACTTTGTTTG | GGTATACAAAT |
| msa363690.2{690_CJB110} | CAAGTTCTGT | GatAAACAAA | GATAATAAAC | ACTTTGTTTG | GGTATACAAAT |

Table 85: Comparative Sequences relating to SAG1361

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| msa363690.2{690_1169NT} | CAAGTTCTGT | GATAAACAAA | GATAATAAAC | ACTTTGTTTG | GGTATACAAT |
| msa363690.2{690_18RS21} | CAAGTTCTGT | GATAAACAAA | GATAATAAAC | ACTTTGTTTG | GGTATACAAT |
| msa363690.2{690_2603} | CAAGTTCTGT | GATAAACAAA | GATAATAAAC | ACTTTGTTTG | GGTATACAAT |
| msa363690.2{690_A909} | CAAGTTCTGT | GATAAACAAA | GATAATAAAC | ACTTTGTTTG | GGTATACAAT |
| msa363690.2{690_JM9130013} | CAAGTTCTGT | GATAAACAAA | GATAATAAAC | ACTTTGTTTG | GGTATACAAT |
| msa363690.2{690_H36B} | CAAGTTCTGT | GATAAACAAA | GATAATAAAC | ACTTTGTTTG | GGTATACAAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | GATTCTAATC | GTAAAAATTC | CAAAGTTGAA | GTCAAAATTG | GTAAAGCTGA |
| msa363690.2{690_M732} | GATTCTAATC | GTAAAAATTC | CAAAGTTGAA | GTCAAAATTG | GTAAAGCTGA |
| msa363690.2{690_M781} | GATTCTAATC | GTAAAAATTC | CAAAGTTGAA | GTCAAAATTG | GTAAAGCTGA |
| msa363690.2{690_090} | GATTCTAATC | GTAAAAATTC | CAAAGTTGAA | GTCAAAATTG | GTAAAGCTGA |
| msa363690.2{690_CJB110} | GATTCTAATC | GTAAAAATTC | CAAAGTTGAA | GTCAAAATTG | GTAAAGCTGA |
| msa363690.2{690_1169NT} | GATTCTAATC | GTAAAAATTC | CAAAGTTGAA | GTCAAAATTG | GTAAAGCTGA |
| msa363690.2{690_18RS21} | GATTCTAATC | GTAAAAATTC | CAAAGTTGAA | GTCAAAATTG | GTAAAGCTGA |
| msa363690.2{690_2603} | GATTCTAATC | GTAAAAATTC | CAAAGTTGAA | GTCAAAATTG | GTAAAGCTGA |
| msa363690.2{690_A909} | GATTCTAATC | GTAAAAATTC | CAAAGTTGAA | GTCAAAATTG | GTAAAGCTGA |
| msa363690.2{690_JM9130013} | GATTCTAATC | GTAAAAATTC | CAAAGTTGAA | GTCAAAATTG | GTAAAGCTGA |
| msa363690.2{690_H36B} | GATTCTAATC | GTAAAAATTC | CAAAGTTGAA | GTCAAAATTG | GTAAAGCTGA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa363690.2{690_COH1} | TGCTAAGACA | CAAGAAATTT | TATCAGGTTT | GAAAGCAGGA | CAATCGTgG |
| msa363690.2{690_M732} | TGCTAAGACA | CAAGAAATTT | TATCAGGTTT | GAAAGCAGGA | CAATCGTgG |
| msa363690.2{690_M781} | TGCTAAGACA | CAAGAAATTT | TATCAGGTTT | GAAAGCAGGA | CAATCGTgG |
| msa363690.2{690_090} | TGCTAAGACA | CAAGAAATTT | TATCAGGTTT | GAAAGCAGGA | CAATCGTgG |
| msa363690.2{690_CJB110} | TGCTAAGACA | CAAGAAATTT | TATCAGGTTT | GAAAGCAGGA | CAATCGTgG |
| msa363690.2{690_1169NT} | TGCTAAGACA | CAAGAAATTT | TATCAGGTTT | GAAAGCAGGA | CAATCGTgG |
| msa363690.2{690_18RS21} | TGCTAAGACA | CAAGAAATTT | TATCAGGTTT | GAAAGCAGGA | CAATCGTgG |
| msa363690.2{690_2603} | TGCTAAGACA | CAAGAAATTT | TATCAGGTTT | GAAAGCAGGA | CAATCGTgG |
| msa363690.2{690_A909} | TGCTAAGACA | CAAGAAATTT | TATCAGGTTT | GAAAGCAGGA | CAATCGTgG |
| msa363690.2{690_JM9130013} | TGCTAAGACA | CAAGAAATTT | TATCAGGTTT | GAAAGCAGGA | CAATCGTgG |
| msa363690.2{690_H36B} | TGCTAAGACA | CAAGAAATTT | TATCAGGTTT | GAAAGCAGGA | CAATCGTgG |
| Consensus | ***** | ***** | ***** | ***** | *****_* |
| msa363690.2{690_COH1} | TTACTAATCC | AAGcAAAaCt | TTCAAGGATG | GGCAAAAAAT | TGATAATATT |
| msa363690.2{690_M732} | TTACTAATCC | AAGcAAAaCt | TTCAAGGATG | GGCAAAAAAT | TGATAATATT |
| msa363690.2{690_M781} | TTACTAATCC | AAGcAAAaCt | TTCAAGGATG | GGCAAAAAAT | TGATAATATT |
| msa363690.2{690_090} | TTACTAATCC | AAGtAAAaCc | TTCAAGGATG | GGCAAAAAAT | TGATAATATT |
| msa363690.2{690_CJB110} | TTACTAATCC | AAGtAAAaCc | TTCAAGGATG | GGCAAAAAAT | TGATAATATT |
| msa363690.2{690_1169NT} | TTACTAATCC | AAGtAAAaCc | TTCAAGGATG | GGCAAAAAAT | TGATAATATT |
| msa363690.2{690_18RS21} | TTACTAATCC | AAGtAAAaCc | TTCAAGGATG | GGCAAAAAAT | TGATAATATT |
| msa363690.2{690_2603} | TTACTAATCC | AAGtAAAaCc | TTCAAGGATG | GGCAAAAAAT | TGATAATATT |
| msa363690.2{690_A909} | TTACTAATCC | AAGcAAAaCt | TTCAAGGATG | GGCAAAAAAT | TGATAATATT |
| msa363690.2{690_JM9130013} | TTACTAATCC | AAGcAAAaCt | TTCAAGGATG | GGCAAAAAAT | TGATAATATT |
| msa363690.2{690_H36B} | TTACTAATCC | AAGtAAAaCt | TTCAAGGATG | GGCAAAAAAT | TGATAATATT |
| Consensus | ***** | ***_***_* | ***** | ***** | ***** |
| msa363690.2{690_COH1} | GAATCAATcG | ATCTTAAGTC | TAATAAGAAA | TCAGAGgtga | a- |
| msa363690.2{690_M732} | GAATCAATcG | ATCTTAAGTC | TAATAAGAAA | TCAGAGgtga | a- |
| msa363690.2{690_M781} | GAATCAATcG | ATCTTAAGTC | TAATAAGAAA | TCAGAGgtga | a- |
| msa363690.2{690_090} | GAATCAATcG | ATCTTAAGTC | TAATAAGAAA | TCAGAGgtga | --- |
| msa363690.2{690_CJB110} | GAATCAATcG | ATCTTAAGTC | TAATAAGAAA | TCAGAGgtga | --- |
| msa363690.2{690_1169NT} | GAATCAATcG | ATCTTAAGTC | TAATAAGAAA | TCAGAGgtga | a- |
| msa363690.2{690_18RS21} | GAATCAATcG | ATCTTAAGTC | TAATAAGAAA | TCAGAGgtga | --- |
| msa363690.2{690_2603} | GAATCAATcG | ATCTTAAGTC | TAATAAGAAA | TCAGAGgtga | aA |
| msa363690.2{690_A909} | GAATCAATaG | ATCTTAAGTC | TAATAAGAAA | TCAGAGgtga | aA |
| msa363690.2{690_JM9130013} | GAATCAATaG | ATCTTAAGTC | TAATAAGAAA | TCAGAGgtga | aA |
| msa363690.2{690_H36B} | GAATCAATcG | ATCTTAAGTC | TAATAAGAAA | TCAGAGgtg- | --- |
| Consensus | *****_* | *****_* | ***** | *****_--- | --- |

SEQ ID NO. 8511

STRAIN 2603 frame: 1

MSKRQNLGI SKKGAI ISGLSVALIVVIGFLVWQSQPNKSAVKTNKYVFNVRREGSVSSST
 LLTGKAKANQEYVYFDANKGNRATVTVKVGDKITAGQQLVQYDTTAAQAAAYDTANRQLN
 KVARQINNLKTTGSLPAMESSDQSSSSSQGGTQSTSGATNRLQONYQSQANASYNQQLQ
 DLNDAYADAQAEVNKAQKALNDTVITSDVSGTVVEVNSDIDPASKTSQVLVHVATEGKLQ
 VQGTMSSEYDLANVKKDQAVIKSKVYPDKWEWEGKISYISNYPEAEANNNDNNSSSAVNY
 KYKVDITSPLDALKQGFVTSVEVNGDKHLIVPTSSVINKDNKHFVWVYNDNSNRKISKVE
 VKIGKADAKTQEILSGLKAGQIVVTNPSKTFKDGQKIDNIESIDLNSNKKSEVK

SEQ ID NO. 8512

STRAIN 090 frame: 1

FLWVQSQPNKSAVKTNKYVFNVRREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTAAQAAAYDTANRQLNKLKTTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQONYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVIKSKVYPDK
 EWEGKISYISNYPEAEANNNDNNSSSAVNYKYKVDITSPLDALKQGFVTSVEVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSE

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8513

STRAIN A909 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGAQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVTNKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8514

STRAIN H36B frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVTNKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 AFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8515

STRAIN I8RS21 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSE

SEQ ID NO. 8516

STRAIN M732 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8517

STRAIN COH1 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8518

STRAIN M781 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8519

STRAIN M781 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8520

STRAIN CJB110 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8521

Table 85: Comparative Sequences relating to SAG1361

STRAIN 1169NT frame: 1

```

FLWVQSQPNKSAVKTNKYVFNREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDITTTAAQAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQONQYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDLANVKKDQAVKI KSKVYPPDK
EWEGKISYISNYPEAEANNDNSNGSSAVNYKYKVDITSPLDALKQGTFSVEVNVGDKH
LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

```

SEQ ID NO. 8522

STRAIN JM9130013 frame: 1

```

FLWVQSQPNKSAVKTNKYVFNREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDITTTAAQAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGAQSTSGATNRLQONQYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDLANVKKDQSVKI KSKVYPPDK
EWEGKISYISNYPEAEANNDNSNGSSAVNYKYKVDITSPLDALKQGTFSVEVNVGDKH
LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

```

PRETTY of: /biotmp/msa375805.2{*} April 1, 2003 02:58 ..

| | | |
|----------------------------|--|-----------------------|
| msa375805.2{690_COH1} | 1 | 50 |
| msa375805.2{690_M732} | -----F | LWVQSQPNKS AVKTNKYVFN |
| msa375805.2{690_M781} | -----F | LWVQSQPNKS AVKTNKYVFN |
| msa375805.2{690_090} | -----F | LWVQSQPNKS AVKTNKYVFN |
| msa375805.2{690_CJB110} | -----F | LWVQSQPNKS AVKTNKYVFN |
| msa375805.2{690_1169NT} | -----F | LWVQSQPNKS AVKTNKYVFN |
| msa375805.2{690_18RS21} | -----F | LWVQSQPNKS AVKTNKYVFN |
| msa375805.2{690_2603} | mskrqnlgis kkgaiisgls valivviggf | LWVQSQPNKS AVKTNKYVFN |
| msa375805.2{690_A909} | -----F | LWVQSQPNKS AVKTNKYVFN |
| msa375805.2{690_JM9130013} | -----F | LWVQSQPNKS AVKTNKYVFN |
| msa375805.2{690_H36B} | -----F | LWVQSQPNKS AVKTNKYVFN |
| Consensus | ***** | ***** |
| msa375805.2{690_COH1} | 51 | 100 |
| msa375805.2{690_M732} | VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV | GDKITAGQQL |
| msa375805.2{690_M781} | VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV | GDKITAGQQL |
| msa375805.2{690_090} | VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV | GDKITAGQQL |
| msa375805.2{690_CJB110} | VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV | GDKITAGQQL |
| msa375805.2{690_1169NT} | VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV | GDKITAGQQL |
| msa375805.2{690_18RS21} | VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV | GDKITAGQQL |
| msa375805.2{690_2603} | VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV | GDKITAGQQL |
| msa375805.2{690_A909} | VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV | GDKITAGQQL |
| msa375805.2{690_JM9130013} | VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV | GDKITAGQQL |
| msa375805.2{690_H36B} | VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV | GDKITAGQQL |
| Consensus | ***** | ***** |
| msa375805.2{690_COH1} | 101 | 150 |
| msa375805.2{690_M732} | VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES | SDQSSSSSQ |
| msa375805.2{690_M781} | VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES | SDQSSSSSQ |
| msa375805.2{690_090} | VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES | SDQSSSSSQ |
| msa375805.2{690_CJB110} | VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES | SDQSSSSSQ |
| msa375805.2{690_1169NT} | VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES | SDQSSSSSQ |
| msa375805.2{690_18RS21} | VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES | SDQSSSSSQ |
| msa375805.2{690_2603} | VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES | SDQSSSSSQ |
| msa375805.2{690_A909} | VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES | SDQSSSSSQ |
| msa375805.2{690_JM9130013} | VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES | SDQSSSSSQ |
| msa375805.2{690_H36B} | VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES | SDQSSSSSQ |
| Consensus | ***** | ***** |
| msa375805.2{690_COH1} | 151 | 200 |
| msa375805.2{690_M732} | QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ | AEVNKAQKAL |
| msa375805.2{690_M781} | QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ | AEVNKAQKAL |
| msa375805.2{690_090} | QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ | AEVNKAQKAL |
| msa375805.2{690_CJB110} | QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ | AEVNKAQKAL |
| msa375805.2{690_1169NT} | QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ | AEVNKAQKAL |
| msa375805.2{690_18RS21} | QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ | AEVNKAQKAL |
| msa375805.2{690_2603} | QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ | AEVNKAQKAL |
| msa375805.2{690_A909} | QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ | AEVNKAQKAL |
| msa375805.2{690_JM9130013} | QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ | AEVNKAQKAL |
| msa375805.2{690_H36B} | QGTQSTSGAT NRLQONQYQSQ ANASYNQQLQ DLNDAYADAQ | AEVNKAQKAL |
| Consensus | ***-***** | ***** |
| msa375805.2{690_COH1} | 201 | 250 |
| msa375805.2{690_M732} | NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ | VQGTMSYIDL |
| msa375805.2{690_M781} | NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ | VQGTMSYIDL |
| msa375805.2{690_090} | NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ | VQGTMSYIDL |

Table 85: Comparative Sequences relating to SAG1361

| | | | | | |
|----------------------------|-------------|------------|------------|------------|-------------|
| msa375805.2{690_CJB110} | NDTVITSQVLS | GTVEVNSDI | DPASKTSQVL | VHVATEGKLQ | VQGTMSSEYDL |
| msa375805.2{690_1169NT} | NDTVITSQVLS | GTVEVNSDI | DPASKTSQVL | VHVATEGKLQ | VQGTMSSEYDL |
| msa375805.2{690_18RS21} | NDTVITSQVLS | GTVEVNSDI | DPASKTSQVL | VHVATEGKLQ | VQGTMSSEYDL |
| msa375805.2{690_2603} | NDTVITSQVLS | GTVEVNSDI | DPASKTSQVL | VHVATEGKLQ | VQGTMSSEYDL |
| msa375805.2{690_A909} | NDTVITSQVLS | GTVEVNSDI | DPASKTSQVL | VHVATEGKLQ | VQGTMSSEYDL |
| msa375805.2{690_JM9130013} | NDTVITSQVLS | GTVEVNSDI | DPASKTSQVL | VHVATEGKLQ | VQGTMSSEYDL |
| msa375805.2{690_H36B} | NDTVITSQVLS | GTVEVNSDI | DPASKTSQVL | VHVATEGKLQ | VQGTMSSEYDL |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 251 | | | | 300 |
| msa375805.2{690_COH1} | ANVKKDQaVK | IKSKVYPDK | WEGKISYISN | YPEAEANNND | SNNGSSAVNY |
| msa375805.2{690_M732} | ANVKKDQaVK | IKSKVYPDK | WEGKISYISN | YPEAEANNND | SNNGSSAVNY |
| msa375805.2{690_M781} | ANVKKDQaVK | IKSKVYPDK | WEGKISYISN | YPEAEANNND | SNNGSSAVNY |
| msa375805.2{690_090} | ANVKKDQaVK | IKSKVYPDK | WEGKISYISN | YPEAEANNND | SNNGSSAVNY |
| msa375805.2{690_CJB110} | ANVKKDQaVK | IKSKVYPDK | WEGKISYISN | YPEAEANNND | SNNGSSAVNY |
| msa375805.2{690_1169NT} | ANVKKDQaVK | IKSKVYPDK | WEGKISYISN | YPEAEANNND | SNNGSSAVNY |
| msa375805.2{690_18RS21} | ANVKKDQaVK | IKSKVYPDK | WEGKISYISN | YPEAEANNND | SNNGSSAVNY |
| msa375805.2{690_2603} | ANVKKDQaVK | IKSKVYPDK | WEGKISYISN | YPEAEANNND | SNNGSSAVNY |
| msa375805.2{690_A909} | ANVKKDQaVK | IKSKVYPDK | WEGKISYISN | YPEAEANNND | SNNGSSAVNY |
| msa375805.2{690_JM9130013} | ANVKKDQaVK | IKSKVYPDK | WEGKISYISN | YPEAEANNND | SNNGSSAVNY |
| msa375805.2{690_H36B} | ANVKKDQaVK | IKSKVYPDK | WEGKISYISN | YPEAEANNND | SNNGSSAVNY |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 301 | | | | 350 |
| msa375805.2{690_COH1} | KYKVDITSPL | DALKQGFTVS | VEVVNGDKHL | IVPTSSVINK | DNKHFVWVYN |
| msa375805.2{690_M732} | KYKVDITSPL | DALKQGFTVS | VEVVNGDKHL | IVPTSSVINK | DNKHFVWVYN |
| msa375805.2{690_M781} | KYKVDITSPL | DALKQGFTVS | VEVVNGDKHL | IVPTSSVINK | DNKHFVWVYN |
| msa375805.2{690_090} | KYKVDITSPL | DALKQGFTVS | VEVVNGDKHL | IVPTSSVINK | DNKHFVWVYN |
| msa375805.2{690_CJB110} | KYKVDITSPL | DALKQGFTVS | VEVVNGDKHL | IVPTSSVINK | DNKHFVWVYN |
| msa375805.2{690_1169NT} | KYKVDITSPL | DALKQGFTVS | VEVVNGDKHL | IVPTSSVINK | DNKHFVWVYN |
| msa375805.2{690_18RS21} | KYKVDITSPL | DALKQGFTVS | VEVVNGDKHL | IVPTSSVINK | DNKHFVWVYN |
| msa375805.2{690_2603} | KYKVDITSPL | DALKQGFTVS | VEVVNGDKHL | IVPTSSVINK | DNKHFVWVYN |
| msa375805.2{690_A909} | KYKVDITSPL | DALKQGFTVS | VEVVNGDKHL | IVPTSSVINK | DNKHFVWVYN |
| msa375805.2{690_JM9130013} | KYKVDITSPL | DALKQGFTVS | VEVVNGDKHL | IVPTSSVINK | DNKHFVWVYN |
| msa375805.2{690_H36B} | KYKVDITSPL | DALKQGFTVS | VEVVNGDKHL | IVPTSSVINK | DNKHFVWVYN |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 351 | | | | 400 |
| msa375805.2{690_COH1} | DSNRKISKVE | VKIGKADAKT | QEILSGLKAG | QIVVTNPSKT | FKDGQKIDNI |
| msa375805.2{690_M732} | DSNRKISKVE | VKIGKADAKT | QEILSGLKAG | QIVVTNPSKT | FKDGQKIDNI |
| msa375805.2{690_M781} | DSNRKISKVE | VKIGKADAKT | QEILSGLKAG | QIVVTNPSKT | FKDGQKIDNI |
| msa375805.2{690_090} | DSNRKISKVE | VKIGKADAKT | QEILSGLKAG | QIVVTNPSKT | FKDGQKIDNI |
| msa375805.2{690_CJB110} | DSNRKISKVE | VKIGKADAKT | QEILSGLKAG | QIVVTNPSKT | FKDGQKIDNI |
| msa375805.2{690_1169NT} | DSNRKISKVE | VKIGKADAKT | QEILSGLKAG | QIVVTNPSKT | FKDGQKIDNI |
| msa375805.2{690_18RS21} | DSNRKISKVE | VKIGKADAKT | QEILSGLKAG | QIVVTNPSKT | FKDGQKIDNI |
| msa375805.2{690_2603} | DSNRKISKVE | VKIGKADAKT | QEILSGLKAG | QIVVTNPSKT | FKDGQKIDNI |
| msa375805.2{690_A909} | DSNRKISKVE | VKIGKADAKT | QEILSGLKAG | QIVVTNPSKT | FKDGQKIDNI |
| msa375805.2{690_JM9130013} | DSNRKISKVE | VKIGKADAKT | QEILSGLKAG | QIVVTNPSKT | FKDGQKIDNI |
| msa375805.2{690_H36B} | DSNRKISKVE | VKIGKADAKT | QEILSGLKAG | QIVVTNPSKT | FKDGQKIDNI |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 401 | | | | 414 |
| msa375805.2{690_COH1} | ESIDLKSNKK | SEV~ | | | |
| msa375805.2{690_M732} | ESIDLKSNKK | SEV~ | | | |
| msa375805.2{690_M781} | ESIDLKSNKK | SEV~ | | | |
| msa375805.2{690_090} | ESIDLKSNKK | SEV~ | | | |
| msa375805.2{690_CJB110} | ESIDLKSNKK | SEV~ | | | |
| msa375805.2{690_1169NT} | ESIDLKSNKK | SEV~ | | | |
| msa375805.2{690_18RS21} | ESIDLKSNKK | SEV~ | | | |
| msa375805.2{690_2603} | ESIDLKSNKK | SEV~ | | | |
| msa375805.2{690_A909} | ESIDLKSNKK | SEV~ | | | |
| msa375805.2{690_JM9130013} | ESIDLKSNKK | SEV~ | | | |
| msa375805.2{690_H36B} | ESIDLKSNKK | SEV~ | | | |
| Consensus | ***** | ***~ | | | |

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8601

STRAIN 2603

atgaaaaaattggaattattgtcctcacactactgacctcttttttggtatcttgcgga
 caacaaactaaacaagaaagcactaaaacaactatttctaaaatgctaaaattgaaggc
 ttcacctattatggaaaaattcctgaaaatccgaaaaagtaatttttacatattct
 tacactgggtatttattaaaactaggtgttaattgttcaagttacagtttagacttagaa
 aaagatagcccggttttttggttaaacactgaagaagctaaaaaattaactgctgatgat
 acagaagctattgcccgcacaaaaacctgatttaatacatggttttcgatcaagatccaaac
 atcaatactctgaaaaaaattgacccaactttagttatataatattggtgcacaaaattat
 ttagatatgatgccagccttggggaaagtattcggtaaagaaaaagaagctaatacagtggtg
 gttagccaatggaaaaactaaaactctcgctgtcaaaaaagatttacaccatatcttaag
 cctaacactacttttactattatggatttttatgataaaaaatctattttatggttaatt
 aattttggacgcggtggagaactaatctatgattcactaggttatgctgccccagaaaaa
 gtcaaaaaagatgtcttttaaaaaagggtggtttaccgtttcgcaagaagcaatcggtgat
 tacgttggagattatgcccttgttaataataacaaaacgactaaaaagcagcttcatca
 cttaagaaagtgatgtctggaagaatttaccagctgtcaaaaaagggcacatcatagaa
 agtaactacgagctgttttatttctctgacctctatctttagaagctcaattaaaatca
 tttacaaaggctatcaagaaaaatacaaat

SEQ ID NO. 8602

STRAIN 090

GAAGGCTTCACCTATTATGGAAAAATTCCTGAAAAATCCGAAAAAGTAAT
 TAATTTTACATATTCTTACACTGGGTATTTATTAATACTAGGTGTTAATG
 TTTCAAGTTACAGTTTAGACTTAGAAAAAGATAGCCCCGTTTTTGGTAAAG
 CAACTGAAAGAGCTAAAAAATTAACCTGCTGATGATACAGAAGCTATTGTC
 CGCACAAAAACCTGATTAAATCATGGTTTTTCGATCAAGATCCAAACATCA
 ATACTCTGAAAAAAATGACCAACTTTAGTTATTAATATGGTGCACAA
 AATTATTTAGATATGATGCCAGCCTTGGGAAAGTATTCGGTAAAGAAAA
 AGAAGCTAATCAGTGGTTAGCCAATGGAAAACTAAAACTCTCGCTGCCA
 AAAAAAGATTTACCATATCTTAAAGCCTAACACTACTTTTACTATTATG
 GATTTTATGATAAAAAATATCTATTTATATGGTAATAATTTTGGACGCGG
 TGGAGAACTAATCTATGATTCACTAGGTATGCTGCCCAgAAAAAGTCA
 AAAAAAGATGTCTTTAAAAAAGGGTGGTTTACCCTTTTCgCAAGAAGCAATC
 GGTGATTACGTTGGAGATTATGCCCTTGTAAATATAACAAAACGACTAA
 AAAAGCAGCTTCatcACTTAAAGAAAGTGATGTCTGGAAGAATTTACCAG
 CTGTCAAAAAAGGGCACATCATAGAAAGTAacTACGACGTGTTTTATTTC
 TCTGACCTCTATCTTTTAGAAGCTCAATTAAAAATCATTTACAAA

SEQ ID NO. 8603

STRAIN A909

GAAGGCTTCACCTATTATGGAAAAATTCCTG
 AAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGGATATTTA
 TTAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAAAAGA
 TAgCCCCGTTTTTGGTAAaCAACTGAAAGGAGCTAAAAAATTAACCTGCTG
 ATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAAATCATGGTTTTTT
 GATCAAGATCCAAACATCAATACTCTGAAAAAATGACCAACTTTTAGT
 TATTAAATATGGTGACAAAAATTTTATGATaTgATGCCAGCTTTGGGGA
 AAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTAGCCaTGGAAA
 ACTAAAACTCTCGCTGCCAAAAAAGATTACACCATATCTTAAACCTAA
 CACTACTTTTACCATTATGGATTTTTATGATAAAAAATCTATTTATATG
 GTAATAATTTTGGACGCGGTGAGAACTAATCTATGATTCACTAGGTTAT
 GCTGCCCCAGAAAAAGTCAAAAAAGATGCTCTTAAAAAAGGGTGGTTTAC
 CGTTTCGCAAGAAAGCAATCGGTgATTACGTTGGAGATTATGCCCTTGTTA
 ATATAACAAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAGTGAT
 GTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAAGTAA
 CTACGACGTGTTTTATTCTCTGACCTcTATCTTTAGAAGCTCAATTAA
 AATCATTTACAAA

SEQ ID NO. 8604

STRAIN H36B

GAAGGCTTCACCTATTATGGAAAA
 ATTCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGG
 ATATTTATTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAG
 AAAAAAGATAgCCCCGTTTTTGGTAAgCAACTGAAAGGAGCTAAAAAATTA
 ACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAAATCAT
 GGTTTTTATGATCAAGATCCAAACATCAATACTCTGAAAAAATGACCAAA
 CTTTAGTTATTAAATATGGTGACAAAAATTTTATGATaTgATGCCAGCT
 TTGGGGAaAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTAGCCA
 ATGGA AAACTAAAACTCTCGCTGCCAAAAAAGATTACACCATATCTTAA
 GGCCTaACaCTACTTTTACTATTATAGatTTTATGATAAAAAATATCTAT
 TTTATATGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATcCACT
 AGGTTATGCTGCCCAgAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGT
 GGTTTACCCTTTTCgCAAGAAGCAATCGGTgATTACGTTGGAGATTATGCC
 CTGTGTTAATAAATAACAAAACGACTAAAAAAGCAGCTTCaTCACTTAAAGA
 AAGTGATGTTTGGAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAG
 AAAGTAACACGACGTGTTTTATTCTCTGACCTCTATCTTTAGAAGCT
 CAATTAAATCATTTACAAA

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8605

STRAIN 18RS21

GAAGGCTTCACCTATTATGGA
 AAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
 TGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
 TAGAAAAAGATAGCCCCGTTTTTGGTAAACAACCTGAAAGAAGCTAAAAAA
 TTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAAT
 CATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCAC
 CAACCTTAGTTATTAAATATGGTGACAAAAATTATTTAgATaTGATGCCA
 GCCTTGGGGAAAGTATTTCGGTAAAGAAAAgAAGCTAATCAGTGGGTTAG
 CCAATGGAAAACTAAAACTCTCGCTGTCAAAAAAGATTACACCATATCT
 TAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATATC
 TATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTCT
 ACTAGGTTATGCTGCCCCagAAAAAGTCAAAAAgATGTCTTTAAAAAAG
 GGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
 GCCCTTGTTAATATAAAACAAACgACTAAAAAAGCAGCTTCATCACTTAA
 AGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACATCA
 TAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAGAA
 GCTCAATTAAATCATTTACAAA

SEQ ID NO. 8606

STRAIN M732

GAAGGCTTCACCTATTATGG
 AAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACA
 CTGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
 TTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA
 ATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAA
 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCA
 CCAACCTTAGTTATTAAATATGGTGACAAAAATTATTTAgATaTGATGCC
 AGCCTTGGGGAAAGTATTTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTA
 GCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTACACCATATC
 TTAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATAT
 CTATTTATATGGTAATAATTTTGGACgCGGTGGAGAACTAATCTATGATT
 CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 GGGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTTAATATAAAACAAACGACTAAAAAAGCAGCTTCATCACTTA
 AAGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACATC
 ATAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAGA
 AGCTCAATTAAATCATTTACAAA

SEQ ID NO. 8607

STRAIN COH1

GAAGGCTTCACCTATTATG
 GAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTAC
 ACTGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAgA
 CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAA
 AATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAA
 ATCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGC
 ACCAATTTAGTTATTAAATATGGTGACAAAAATTATTTAgATaTGATGC
 CAGCCTTGGGGAAAGTaTTcGGTAAAGAAAAAGAGCTAATCAGTGGGTT
 AGCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATAT
 CTTAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATA
 TCTATTTATATGGTAATAATTTTGGACGCGGTGGAGAATAATCTATGAT
 TCCTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 AGGGTGGTTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 ATGCCCTTGTTAATATAAAACAAACGACTAAAAAAGCAGCTTCATCACTT
 AAAGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACAT
 CATAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAG
 AAGCTCAATTAAATCATTTACAAA

SEQ ID NO. 8608

STRAIN M781

GAAGGCTTCACCTATTATGG
 AAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACA
 CTGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
 TTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA
 ATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAA
 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCA
 CCAACCTTAGTTATTAAATATGGTGACAAAAATTATTTAgATaTGATGCC
 AGCCTTGGGGAAAGTATTTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTA
 GCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATATC
 TTAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATAT
 CTATTTATATGGTAATAATTTTGGACGCGGTGGAGAATAATCTATGATT
 CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 GGGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTTAATATAAAACAAACGACTAAAAAAGCAGCTTCATCACTTA

Table 86: Comparative Sequences relating to SAG1393

AAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATC
 ATAGAAAGTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAGAA
 AGCTCAATTAATAATCATTACAAA

SEQ ID NO. 8609

STRAIN CJB110

GAAGGCTTCACCTATTATGGA
 AAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
 TGGGTATTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
 TAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAA
 TTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTAAT
 CATGGTTTTCTGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCAC
 CAACTTTAGTTATTAATATGGTGCACAAAATTTTAgATATGATGCCA
 GCCTTGGGGAAGTATTTCGGTAAAGAAAAAGAAAGCTAATCAGTGGGTAG
 CCAATGGAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATATCT
 TAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATC
 TATTTATATGTTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTC
 ACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAGATGCTTTAAAAAAG
 GGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
 GCCCTTGTTAATATAACAAAACGACTAAAAAAGCAGCTTCATCACTTAA
 AGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATCA
 TAGAAAGTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAGAA
 GCTCAATTAATAATCATTACAAA

SEQ ID NO. 8610

STRAIN 1169NT

GAAGGCTTCACCTATTATGGAATAAT
 CCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGGGTA
 TTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAA
 AAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAATTAAC
 GCTGATGATACAGAAGCTATTGCCGcACAAAaACCTGATTTAATCATGGT
 TTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCACCAACTT
 TAGTTATTAATAATATGGTGCACAAAATTTTAgATATGATGCCAGCCTTG
 GGGAAAGTATTTCGGTAAAGAAAAAGAACTAATCAGTGGGTAGCCAAATG
 GAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATATCTTAAAGC
 CTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATCTATTTA
 TATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTCAC TAGG
 TTATGCTGCCCAgAAAAAGTCAAAAAGATGCTTTAAAAAAGGGTGGT
 TTACCGTTTTcGCAAGAAGCAATCGGTGATTACGTTGGAGATTATGCCCTT
 GTTAATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAG
 TGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATCATAGAAA
 GTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAGAAGCTCAA
 TTAAATCATTACAAA

SEQ ID NO. 8611

STRAIN JM9130013

GAAGGCTTCACCTATTATG
 GAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTAC
 ACTGATATTATTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGA
 CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGGAGCTAAAA
 AATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTA
 ATCATGGTTTTTATCAAGATCCAAACATCAATACTCTGAAAAAATTGTC
 ACCAACTTTAGTTATTAATAATGGTGCACAAAATTTTAgATATGATGC
 CAGCTTTGGGGAAGTATTTCGGTAAAGAAAAAGAAAGCTAATCAGTGGGT
 AGCCAAATGGAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATAT
 CTTAAACCTAACACTACTTTTACCATTATGGATTTTTATGATAAAAATA
 TCTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGAT
 TCAC TAGGTTATGCTGCCCAgAAAAAGTCAAAAAGATGCTTTAAAAA
 AGGGTGGTTTTACCGTTTTcGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 ATGCCCTTGTTAATATAACAAAACGACTAAAAAAGCAGCTTCATCACTT
 AAAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACAT
 CATAGAAAGTAACACGACGTGTTTTATTCTCTGACCCCTCTATCTTTAG
 AAGCTCAATTAATAATCATTACAAA

PRETTY of: /biotmp/msa521731.2{*} April 28, 2003 08:07 ..

| | 1 | 50 |
|-------------------------|------------|---|
| msa521731.2{691_090} | ----- | ----- |
| msa521731.2{691_1169NT} | ----- | ----- |
| msa521731.2{691_CJB110} | ----- | ----- |
| msa521731.2{691_COH1} | ----- | ----- |
| msa521731.2{691_M732} | ----- | ----- |
| msa521731.2{691_M781} | ----- | ----- |
| msa521731.2{691_18RS21} | ----- | ----- |
| msa521731.2{691_2603} | atgaaaaaaa | ttggaattat tgtcctcaca ctactgacct tctttttggt |

Table 86: Comparative Sequences relating to SAG1393

| | | | | | |
|----------------------------|------------|------------|------------|------------|-------------|
| msa521731.2{691_A909} | ----- | ----- | ----- | ----- | ----- |
| msa521731.2{691_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa521731.2{691_H36B} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa521731.2{691_090} | 51 | | | | 100 |
| msa521731.2{691_1169NT} | ----- | ----- | ----- | ----- | ----- |
| msa521731.2{691_CJB110} | ----- | ----- | ----- | ----- | ----- |
| msa521731.2{691_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa521731.2{691_M732} | ----- | ----- | ----- | ----- | ----- |
| msa521731.2{691_M781} | ----- | ----- | ----- | ----- | ----- |
| msa521731.2{691_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa521731.2{691_2603} | atcttgcgga | caacaaacta | aacaagaaag | cactaaaaca | actatttcta |
| msa521731.2{691_A909} | ----- | ----- | ----- | ----- | ----- |
| msa521731.2{691_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa521731.2{691_H36B} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa521731.2{691_090} | 101 | | | | 150 |
| msa521731.2{691_1169NT} | ----- | ----GAAGGC | TTCACCTATT | ATGGAAAAAT | TCCTGAAAAAT |
| msa521731.2{691_CJB110} | ----- | ----GAAGGC | TTCACCTATT | ATGGAAAAAT | TCCTGAAAAAT |
| msa521731.2{691_COH1} | ----- | ----GAAGGC | TTCACCTATT | ATGGAAAAAT | TCCTGAAAAAT |
| msa521731.2{691_M732} | ----- | ----GAAGGC | TTCACCTATT | ATGGAAAAAT | TCCTGAAAAAT |
| msa521731.2{691_M781} | ----- | ----GAAGGC | TTCACCTATT | ATGGAAAAAT | TCCTGAAAAAT |
| msa521731.2{691_18RS21} | ----- | ----GAAGGC | TTCACCTATT | ATGGAAAAAT | TCCTGAAAAAT |
| msa521731.2{691_2603} | aaatgcctaa | aattGAAGGC | TTCACCTATT | ATGGAAAAAT | TCCTGAAAAAT |
| msa521731.2{691_A909} | ----- | ----GAAGGC | TTCACCTATT | ATGGAAAAAT | TCCTGAAAAAT |
| msa521731.2{691_JM9130013} | ----- | ----GAAGGC | TTCACCTATT | ATGGAAAAAT | TCCTGAAAAAT |
| msa521731.2{691_H36B} | ----- | ----GAAGGC | TTCACCTATT | ATGGAAAAAT | TCCTGAAAAAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa521731.2{691_090} | 151 | | | | 200 |
| msa521731.2{691_1169NT} | CCGAAAAAAG | TAATTAATTT | TACATATTCT | TACACTGGgT | ATTTATTAAA |
| msa521731.2{691_CJB110} | CCGAAAAAAG | TAATTAATTT | TACATATTCT | TACACTGGgT | ATTTATTAAA |
| msa521731.2{691_COH1} | CCGAAAAAAG | TAATTAATTT | TACATATTCT | TACACTGGgT | ATTTATTAAA |
| msa521731.2{691_M732} | CCGAAAAAAG | TAATTAATTT | TACATATTCT | TACACTGGgT | ATTTATTAAA |
| msa521731.2{691_M781} | CCGAAAAAAG | TAATTAATTT | TACATATTCT | TACACTGGgT | ATTTATTAAA |
| msa521731.2{691_18RS21} | CCGAAAAAAG | TAATTAATTT | TACATATTCT | TACACTGGgT | ATTTATTAAA |
| msa521731.2{691_2603} | CCGAAAAAAG | TAATTAATTT | TACATATTCT | TACACTGGgT | ATTTATTAAA |
| msa521731.2{691_A909} | CCGAAAAAAG | TAATTAATTT | TACATATTCT | TACACTGGgT | ATTTATTAAA |
| msa521731.2{691_JM9130013} | CCGAAAAAAG | TAATTAATTT | TACATATTCT | TACACTGGgT | ATTTATTAAA |
| msa521731.2{691_H36B} | CCGAAAAAAG | TAATTAATTT | TACATATTCT | TACACTGGgT | ATTTATTAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa521731.2{691_090} | 201 | | | | 250 |
| msa521731.2{691_1169NT} | ACTAGGtGTT | AATGTTTCAA | GTTACAGTTT | AGACTTAGAA | AAAGATAGCC |
| msa521731.2{691_CJB110} | ACTAGGtGTT | AATGTTTCAA | GTTACAGTTT | AGACTTAGAA | AAAGATAGCC |
| msa521731.2{691_COH1} | ACTAGGtGTT | AATGTTTCAA | GTTACAGTTT | AGACTTAGAA | AAAGATAGCC |
| msa521731.2{691_M732} | ACTAGGtGTT | AATGTTTCAA | GTTACAGTTT | AGACTTAGAA | AAAGATAGCC |
| msa521731.2{691_M781} | ACTAGGtGTT | AATGTTTCAA | GTTACAGTTT | AGACTTAGAA | AAAGATAGCC |
| msa521731.2{691_18RS21} | ACTAGGtGTT | AATGTTTCAA | GTTACAGTTT | AGACTTAGAA | AAAGATAGCC |
| msa521731.2{691_2603} | ACTAGGtGTT | AATGTTTCAA | GTTACAGTTT | AGACTTAGAA | AAAGATAGCC |
| msa521731.2{691_A909} | ACTAGGgGTT | AATGTTTCAA | GTTACAGTTT | AGACTTAGAA | AAAGATAGCC |
| msa521731.2{691_JM9130013} | ACTAGGgGTT | AATGTTTCAA | GTTACAGTTT | AGACTTAGAA | AAAGATAGCC |
| msa521731.2{691_H36B} | ACTAGGgGTT | AATGTTTCAA | GTTACAGTTT | AGACTTAGAA | AAAGATAGCC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa521731.2{691_090} | 251 | | | | 300 |
| msa521731.2{691_1169NT} | CCGTTTTTGG | TAAgCAACTG | AAAGaAGCTA | AAAAATTAAC | TGCTGATGAT |
| msa521731.2{691_CJB110} | CCGTTTTTGG | TAAgCAACTG | AAAGaAGCTA | AAAAATTAAC | TGCTGATGAT |
| msa521731.2{691_COH1} | CCGTTTTTGG | TAAgCAACTG | AAAGaAGCTA | AAAAATTAAC | TGCTGATGAT |
| msa521731.2{691_M732} | CCGTTTTTGG | TAAgCAACTG | AAAGaAGCTA | AAAAATTAAC | TGCTGATGAT |
| msa521731.2{691_M781} | CCGTTTTTGG | TAAgCAACTG | AAAGaAGCTA | AAAAATTAAC | TGCTGATGAT |
| msa521731.2{691_18RS21} | CCGTTTTTGG | TAAaCAACTG | AAAGaAGCTA | AAAAATTAAC | TGCTGATGAT |
| msa521731.2{691_2603} | CCGTTTTTGG | TAAaCAACTG | AAAGaAGCTA | AAAAATTAAC | TGCTGATGAT |
| msa521731.2{691_A909} | CCGTTTTTGG | TAAaCAACTG | AAAGgAGCTA | AAAAATTAAC | TGCTGATGAT |
| msa521731.2{691_JM9130013} | CCGTTTTTGG | TAAgCAACTG | AAAGgAGCTA | AAAAATTAAC | TGCTGATGAT |
| msa521731.2{691_H36B} | CCGTTTTTGG | TAAgCAACTG | AAAGgAGCTA | AAAAATTAAC | TGCTGATGAT |
| Consensus | ***** | ***-***** | ***** | ***** | ***** |
| msa521731.2{691_090} | 301 | | | | 350 |
| msa521731.2{691_1169NT} | ACAGAAGCTA | TTGCCGCACA | AAAACCTGAT | TTAATCATGG | TTTTcGATCA |
| msa521731.2{691_1169NT} | ACAGAAGCTA | TTGCCGCACA | AAAACCTGAT | TTAATCATGG | TTTTcGATCA |

Table 86: Comparative Sequences relating to SAG1393

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| msa521731.2{691_CJB110} | ACAGAAGCTA | TTGCCGCACA | AAAACCTGAT | TTAATCATGG | TTTTcGATCA |
| msa521731.2{691_COH1} | ACAGAAGCTA | TTGCCGCACA | AAAACCTGAT | TTAATCATGG | TTTTcGATCA |
| msa521731.2{691_M732} | ACAGAAGCTA | TTGCCGCACA | AAAACCTGAT | TTAATCATGG | TTTTcGATCA |
| msa521731.2{691_M781} | ACAGAAGCTA | TTGCCGCACA | AAAACCTGAT | TTAATCATGG | TTTTcGATCA |
| msa521731.2{691_18RS21} | ACAGAAGCTA | TTGCCGCACA | AAAACCTGAT | TTAATCATGG | TTTTcGATCA |
| msa521731.2{691_2603} | ACAGAAGCTA | TTGCCGCACA | AAAACCTGAT | TTAATCATGG | TTTTcGATCA |
| msa521731.2{691_A909} | ACAGAAGCTA | TTGCCGCACA | AAAACCTGAT | TTAATCATGG | TTTTcGATCA |
| msa521731.2{691_JM9130013} | ACAGAAGCTA | TTGCCGCACA | AAAACCTGAT | TTAATCATGG | TTTTcGATCA |
| msa521731.2{691_H36B} | ACAGAAGCTA | TTGCCGCACA | AAAACCTGAT | TTAATCATGG | TTTTcGATCA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa521731.2{691_090} | AGATCCAAAC | ATCAATACTC | TGAAAAAAT | TGCACCAACT | TTAGTTATTA |
| msa521731.2{691_1169NT} | AGATCCAAAC | ATCAATACTC | TGAAAAAAT | TGCACCAACT | TTAGTTATTA |
| msa521731.2{691_CJB110} | AGATCCAAAC | ATCAATACTC | TGAAAAAAT | TGCACCAACT | TTAGTTATTA |
| msa521731.2{691_COH1} | AGATCCAAAC | ATCAATACTC | TGAAAAAAT | TGCACCAACT | TTAGTTATTA |
| msa521731.2{691_M732} | AGATCCAAAC | ATCAATACTC | TGAAAAAAT | TGCACCAACT | TTAGTTATTA |
| msa521731.2{691_M781} | AGATCCAAAC | ATCAATACTC | TGAAAAAAT | TGCACCAACT | TTAGTTATTA |
| msa521731.2{691_18RS21} | AGATCCAAAC | ATCAATACTC | TGAAAAAAT | TGCACCAACT | TTAGTTATTA |
| msa521731.2{691_2603} | AGATCCAAAC | ATCAATACTC | TGAAAAAAT | TGCACCAACT | TTAGTTATTA |
| msa521731.2{691_A909} | AGATCCAAAC | ATCAATACTC | TGAAAAAAT | TGCACCAACT | TTAGTTATTA |
| msa521731.2{691_JM9130013} | AGATCCAAAC | ATCAATACTC | TGAAAAAAT | TGCACCAACT | TTAGTTATTA |
| msa521731.2{691_H36B} | AGATCCAAAC | ATCAATACTC | TGAAAAAAT | TGCACCAACT | TTAGTTATTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa521731.2{691_090} | AATATGGTGC | ACAAAATTAT | TTAGATATGA | TGCCAGCCTT | GGGGAAAGTA |
| msa521731.2{691_1169NT} | AATATGGTGC | ACAAAATTAT | TTAGATATGA | TGCCAGCCTT | GGGGAAAGTA |
| msa521731.2{691_CJB110} | AATATGGTGC | ACAAAATTAT | TTAGATATGA | TGCCAGCCTT | GGGGAAAGTA |
| msa521731.2{691_COH1} | AATATGGTGC | ACAAAATTAT | TTAGATATGA | TGCCAGCCTT | GGGGAAAGTA |
| msa521731.2{691_M732} | AATATGGTGC | ACAAAATTAT | TTAGATATGA | TGCCAGCCTT | GGGGAAAGTA |
| msa521731.2{691_M781} | AATATGGTGC | ACAAAATTAT | TTAGATATGA | TGCCAGCCTT | GGGGAAAGTA |
| msa521731.2{691_18RS21} | AATATGGTGC | ACAAAATTAT | TTAGATATGA | TGCCAGCCTT | GGGGAAAGTA |
| msa521731.2{691_2603} | AATATGGTGC | ACAAAATTAT | TTAGATATGA | TGCCAGCCTT | GGGGAAAGTA |
| msa521731.2{691_A909} | AATATGGTGC | ACAAAATTAT | TTAGATATGA | TGCCAGCCTT | GGGGAAAGTA |
| msa521731.2{691_JM9130013} | AATATGGTGC | ACAAAATTAT | TTAGATATGA | TGCCAGCCTT | GGGGAAAGTA |
| msa521731.2{691_H36B} | AATATGGTGC | ACAAAATTAT | TTAGATATGA | TGCCAGCCTT | GGGGAAAGTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa521731.2{691_090} | TTCCGTAAG | AAAAAGAAGC | TAATCAGTGG | GTTAGCCAAT | GGAAAACTAA |
| msa521731.2{691_1169NT} | TTCCGTAAG | AAAAAGAAGC | TAATCAGTGG | GTTAGCCAAT | GGAAAACTAA |
| msa521731.2{691_CJB110} | TTCCGTAAG | AAAAAGAAGC | TAATCAGTGG | GTTAGCCAAT | GGAAAACTAA |
| msa521731.2{691_COH1} | TTCCGTAAG | AAAAAGAAGC | TAATCAGTGG | GTTAGCCAAT | GGAAAACTAA |
| msa521731.2{691_M732} | TTCCGTAAG | AAAAAGAAGC | TAATCAGTGG | GTTAGCCAAT | GGAAAACTAA |
| msa521731.2{691_M781} | TTCCGTAAG | AAAAAGAAGC | TAATCAGTGG | GTTAGCCAAT | GGAAAACTAA |
| msa521731.2{691_18RS21} | TTCCGTAAG | AAAAAGAAGC | TAATCAGTGG | GTTAGCCAAT | GGAAAACTAA |
| msa521731.2{691_2603} | TTCCGTAAG | AAAAAGAAGC | TAATCAGTGG | GTTAGCCAAT | GGAAAACTAA |
| msa521731.2{691_A909} | TTCCGTAAG | AAAAAGAAGC | TAATCAGTGG | GTTAGCCAAT | GGAAAACTAA |
| msa521731.2{691_JM9130013} | TTCCGTAAG | AAAAAGAAGC | TAATCAGTGG | GTTAGCCAAT | GGAAAACTAA |
| msa521731.2{691_H36B} | TTCCGTAAG | AAAAAGAAGC | TAATCAGTGG | GTTAGCCAAT | GGAAAACTAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa521731.2{691_090} | AACTCTCGCT | GcCAAAAAAG | ATTTACACCA | TATCTTAAag | CCTAACACTA |
| msa521731.2{691_1169NT} | AACTCTCGCT | GcCAAAAAAG | ATTTACACCA | TATCTTAAag | CCTAACACTA |
| msa521731.2{691_CJB110} | AACTCTCGCT | GcCAAAAAAG | ATTTACACCA | TATCTTAAag | CCTAACACTA |
| msa521731.2{691_COH1} | AACTCTCGCT | GcCAAAAAAG | ATTTACACCA | TATCTTAAag | CCTAACACTA |
| msa521731.2{691_M732} | AACTCTCGCT | GcCAAAAAAG | ATTTACACCA | TATCTTAAag | CCTAACACTA |
| msa521731.2{691_M781} | AACTCTCGCT | GcCAAAAAAG | ATTTACACCA | TATCTTAAag | CCTAACACTA |
| msa521731.2{691_18RS21} | AACTCTCGCT | GcCAAAAAAG | ATTTACACCA | TATCTTAAag | CCTAACACTA |
| msa521731.2{691_2603} | AACTCTCGCT | GcCAAAAAAG | ATTTACACCA | TATCTTAAag | CCTAACACTA |
| msa521731.2{691_A909} | AACTCTCGCT | GcCAAAAAAG | ATTTACACCA | TATCTTAAag | CCTAACACTA |
| msa521731.2{691_JM9130013} | AACTCTCGCT | GcCAAAAAAG | ATTTACACCA | TATCTTAAag | CCTAACACTA |
| msa521731.2{691_H36B} | AACTCTCGCT | GcCAAAAAAG | ATTTACACCA | TATCTTAAag | CCTAACACTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa521731.2{691_090} | CTTTTACTAT | TATgGATTTT | TATGATAAAA | ATATCTATTT | ATATGGTAAT |
| msa521731.2{691_1169NT} | CTTTTACTAT | TATgGATTTT | TATGATAAAA | ATATCTATTT | ATATGGTAAT |
| msa521731.2{691_CJB110} | CTTTTACTAT | TATgGATTTT | TATGATAAAA | ATATCTATTT | ATATGGTAAT |
| msa521731.2{691_COH1} | CTTTTACTAT | TATgGATTTT | TATGATAAAA | ATATCTATTT | ATATGGTAAT |
| msa521731.2{691_M732} | CTTTTACTAT | TATgGATTTT | TATGATAAAA | ATATCTATTT | ATATGGTAAT |
| msa521731.2{691_M781} | CTTTTACTAT | TATgGATTTT | TATGATAAAA | ATATCTATTT | ATATGGTAAT |
| msa521731.2{691_18RS21} | CTTTTACTAT | TATgGATTTT | TATGATAAAA | ATATCTATTT | ATATGGTAAT |
| msa521731.2{691_2603} | CTTTTACTAT | TATgGATTTT | TATGATAAAA | ATATCTATTT | ATATGGTAAT |
| msa521731.2{691_A909} | CTTTTACTAT | TATgGATTTT | TATGATAAAA | ATATCTATTT | ATATGGTAAT |
| msa521731.2{691_JM9130013} | CTTTTACTAT | TATgGATTTT | TATGATAAAA | ATATCTATTT | ATATGGTAAT |

Table 86: Comparative Sequences relating to SAG1393

| | | | | | |
|----------------------------|------------|------------|------------|-------------|-------------|
| msa521731.2{691_H36B} | CTTTTACTAT | TATaGATTTT | TATGATAAAA | ATATCTATTT | ATATGGTAAT |
| Consensus | *****_** | ***_***** | ***** | ***** | ***** |
| | 601 | | | | 650 |
| msa521731.2{691_090} | AATTTTGGAC | GCGGTGGAGA | ACTAATCTAT | GATTCAC TAG | GTTATGCTGC |
| msa521731.2{691_1169NT} | AATTTTGGAC | GCGGTGGAGA | ACTAATCTAT | GATTCAC TAG | GTTATGCTGC |
| msa521731.2{691_CJB110} | AATTTTGGAC | GCGGTGGAGA | ACTAATCTAT | GATTCAC TAG | GTTATGCTGC |
| msa521731.2{691_COH1} | AATTTTGGAC | GCGGTGGAGA | ACTAATCTAT | GATTCAC TAG | GTTATGCTGC |
| msa521731.2{691_M732} | AATTTTGGAC | GCGGTGGAGA | ACTAATCTAT | GATTCAC TAG | GTTATGCTGC |
| msa521731.2{691_M781} | AATTTTGGAC | GCGGTGGAGA | ACTAATCTAT | GATTCAC TAG | GTTATGCTGC |
| msa521731.2{691_18RS21} | AATTTTGGAC | GCGGTGGAGA | ACTAATCTAT | GATTCAC TAG | GTTATGCTGC |
| msa521731.2{691_2603} | AATTTTGGAC | GCGGTGGAGA | ACTAATCTAT | GATTCAC TAG | GTTATGCTGC |
| msa521731.2{691_A909} | AATTTTGGAC | GCGGTGGAGA | ACTAATCTAT | GATTCAC TAG | GTTATGCTGC |
| msa521731.2{691_JM9130013} | AATTTTGGAC | GCGGTGGAGA | ACTAATCTAT | GATTCAC TAG | GTTATGCTGC |
| msa521731.2{691_H36B} | AATTTTGGAC | GCGGTGGAGA | ACTAATCTAT | GATTCAC TAG | GTTATGCTGC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 651 | | | | 700 |
| msa521731.2{691_090} | CCCAGAAAAA | GTCAAAAAAG | ATGTCTTTAA | AAAAGGGTGG | TTTACCGTTT |
| msa521731.2{691_1169NT} | CCCAGAAAAA | GTCAAAAAAG | ATGTCTTTAA | AAAAGGGTGG | TTTACCGTTT |
| msa521731.2{691_CJB110} | CCCAGAAAAA | GTCAAAAAAG | ATGTCTTTAA | AAAAGGGTGG | TTTACCGTTT |
| msa521731.2{691_COH1} | CCCAGAAAAA | GTCAAAAAAG | ATGTCTTTAA | AAAAGGGTGG | TTTACCGTTT |
| msa521731.2{691_M732} | CCCAGAAAAA | GTCAAAAAAG | ATGTCTTTAA | AAAAGGGTGG | TTTACCGTTT |
| msa521731.2{691_M781} | CCCAGAAAAA | GTCAAAAAAG | ATGTCTTTAA | AAAAGGGTGG | TTTACCGTTT |
| msa521731.2{691_18RS21} | CCCAGAAAAA | GTCAAAAAAG | ATGTCTTTAA | AAAAGGGTGG | TTTACCGTTT |
| msa521731.2{691_2603} | CCCAGAAAAA | GTCAAAAAAG | ATGTCTTTAA | AAAAGGGTGG | TTTACCGTTT |
| msa521731.2{691_A909} | CCCAGAAAAA | GTCAAAAAAG | ATGTCTTTAA | AAAAGGGTGG | TTTACCGTTT |
| msa521731.2{691_JM9130013} | CCCAGAAAAA | GTCAAAAAAG | ATGTCTTTAA | AAAAGGGTGG | TTTACCGTTT |
| msa521731.2{691_H36B} | CCCAGAAAAA | GTCAAAAAAG | ATGTCTTTAA | AAAAGGGTGG | TTTACCGTTT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 701 | | | | 750 |
| msa521731.2{691_090} | CGCAAGAAGC | AATCGGTGAT | TACGTTGGAG | ATTATGCCCT | TGTTAATATA |
| msa521731.2{691_1169NT} | CGCAAGAAGC | AATCGGTGAT | TACGTTGGAG | ATTATGCCCT | TGTTAATATA |
| msa521731.2{691_CJB110} | CGCAAGAAGC | AATCGGTGAT | TACGTTGGAG | ATTATGCCCT | TGTTAATATA |
| msa521731.2{691_COH1} | CGCAAGAAGC | AATCGGTGAT | TACGTTGGAG | ATTATGCCCT | TGTTAATATA |
| msa521731.2{691_M732} | CGCAAGAAGC | AATCGGTGAT | TACGTTGGAG | ATTATGCCCT | TGTTAATATA |
| msa521731.2{691_M781} | CGCAAGAAGC | AATCGGTGAT | TACGTTGGAG | ATTATGCCCT | TGTTAATATA |
| msa521731.2{691_18RS21} | CGCAAGAAGC | AATCGGTGAT | TACGTTGGAG | ATTATGCCCT | TGTTAATATA |
| msa521731.2{691_2603} | CGCAAGAAGC | AATCGGTGAT | TACGTTGGAG | ATTATGCCCT | TGTTAATATA |
| msa521731.2{691_A909} | CGCAAGAAGC | AATCGGTGAT | TACGTTGGAG | ATTATGCCCT | TGTTAATATA |
| msa521731.2{691_JM9130013} | CGCAAGAAGC | AATCGGTGAT | TACGTTGGAG | ATTATGCCCT | TGTTAATATA |
| msa521731.2{691_H36B} | CGCAAGAAGC | AATCGGTGAT | TACGTTGGAG | ATTATGCCCT | TGTTAATATA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 751 | | | | 800 |
| msa521731.2{691_090} | AACAAAACGA | CTAAAAAAGC | AGCTTCATCA | CTTAAAGAAA | GTGATGTcTG |
| msa521731.2{691_1169NT} | AACAAAACGA | CTAAAAAAGC | AGCTTCATCA | CTTAAAGAAA | GTGATGTcTG |
| msa521731.2{691_CJB110} | AACAAAACGA | CTAAAAAAGC | AGCTTCATCA | CTTAAAGAAA | GTGATGTcTG |
| msa521731.2{691_COH1} | AACAAAACGA | CTAAAAAAGC | AGCTTCATCA | CTTAAAGAAA | GTGATGTcTG |
| msa521731.2{691_M732} | AACAAAACGA | CTAAAAAAGC | AGCTTCATCA | CTTAAAGAAA | GTGATGTcTG |
| msa521731.2{691_M781} | AACAAAACGA | CTAAAAAAGC | AGCTTCATCA | CTTAAAGAAA | GTGATGTcTG |
| msa521731.2{691_18RS21} | AACAAAACGA | CTAAAAAAGC | AGCTTCATCA | CTTAAAGAAA | GTGATGTcTG |
| msa521731.2{691_2603} | AACAAAACGA | CTAAAAAAGC | AGCTTCATCA | CTTAAAGAAA | GTGATGTcTG |
| msa521731.2{691_A909} | AACAAAACGA | CTAAAAAAGC | AGCTTCATCA | CTTAAAGAAA | GTGATGTcTG |
| msa521731.2{691_JM9130013} | AACAAAACGA | CTAAAAAAGC | AGCTTCATCA | CTTAAAGAAA | GTGATGTcTG |
| msa521731.2{691_H36B} | AACAAAACGA | CTAAAAAAGC | AGCTTCATCA | CTTAAAGAAA | GTGATGTcTG |
| Consensus | ***** | ***** | ***** | ***** | *****_** |
| | 801 | | | | 850 |
| msa521731.2{691_090} | GAAGAATTTA | CCAGCTGTCA | AAAAAGGGCA | CATCATAGAA | AGTAAC TACG |
| msa521731.2{691_1169NT} | GAAGAATTTA | CCAGCTGTCA | AAAAAGGGCA | CATCATAGAA | AGTAAC TACG |
| msa521731.2{691_CJB110} | GAAGAATTTA | CCAGCTGTCA | AAAAAGGGCA | CATCATAGAA | AGTAAC TACG |
| msa521731.2{691_COH1} | GAAGAATTTA | CCAGCTGTCA | AAAAAGGGCA | CATCATAGAA | AGTAAC TACG |
| msa521731.2{691_M732} | GAAGAATTTA | CCAGCTGTCA | AAAAAGGGCA | CATCATAGAA | AGTAAC TACG |
| msa521731.2{691_M781} | GAAGAATTTA | CCAGCTGTCA | AAAAAGGGCA | CATCATAGAA | AGTAAC TACG |
| msa521731.2{691_18RS21} | GAAGAATTTA | CCAGCTGTCA | AAAAAGGGCA | CATCATAGAA | AGTAAC TACG |
| msa521731.2{691_2603} | GAAGAATTTA | CCAGCTGTCA | AAAAAGGGCA | CATCATAGAA | AGTAAC TACG |
| msa521731.2{691_A909} | GAAGAATTTA | CCAGCTGTCA | AAAAAGGGCA | CATCATAGAA | AGTAAC TACG |
| msa521731.2{691_JM9130013} | GAAGAATTTA | CCAGCTGTCA | AAAAAGGGCA | CATCATAGAA | AGTAAC TACG |
| msa521731.2{691_H36B} | GAAGAATTTA | CCAGCTGTCA | AAAAAGGGCA | CATCATAGAA | AGTAAC TACG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 851 | | | | 900 |
| msa521731.2{691_090} | ACGTGTTTTA | TTTCTCTGAC | CCTCTATCTT | TAGAAGCTCA | ATTAAATCA |
| msa521731.2{691_1169NT} | ACGTGTTTTA | TTTCTCTGAC | CCTCTATCTT | TAGAAGCTCA | ATTAAATCA |
| msa521731.2{691_CJB110} | ACGTGTTTTA | TTTCTCTGAC | CCTCTATCTT | TAGAAGCTCA | ATTAAATCA |
| msa521731.2{691_COH1} | ACGTGTTTTA | TTTCTCTGAC | CCTCTATCTT | TAGAAGCTCA | ATTAAATCA |

Table 86: Comparative Sequences relating to SAG1393

| | | | | | |
|----------------------------|------------|------------|------------|------------|-----------|
| msa521731.2{691_M732} | ACGTGTTTTA | TTTCTCTGAC | CCTCTATCTT | TAGAAGCTCA | ATTAAATCA |
| msa521731.2{691_M781} | ACGTGTTTTA | TTTCTCTGAC | CCTCTATCTT | TAGAAGCTCA | ATTAAATCA |
| msa521731.2{691_18RS21} | ACGTGTTTTA | TTTCTCTGAC | CCTCTATCTT | TAGAAGCTCA | ATTAAATCA |
| msa521731.2{691_2603} | ACGTGTTTTA | TTTCTCTGAC | CCTCTATCTT | TAGAAGCTCA | ATTAAATCA |
| msa521731.2{691_A909} | ACGTGTTTTA | TTTCTCTGAC | CCTCTATCTT | TAGAAGCTCA | ATTAAATCA |
| msa521731.2{691_JM9130013} | ACGTGTTTTA | TTTCTCTGAC | CCTCTATCTT | TAGAAGCTCA | ATTAAATCA |
| msa521731.2{691_H36B} | ACGTGTTTTA | TTTCTCTGAC | CCTCTATCTT | TAGAAGCTCA | ATTAAATCA |
| Consensus | ***** | ***** | ***** | ***** | ***** |

| | | | |
|----------------------------|------------|------------|------------|
| | 901 | | 930 |
| msa521731.2{691_090} | TTTACAAA-- | ----- | ----- |
| msa521731.2{691_1169NT} | TTTACAAA-- | ----- | ----- |
| msa521731.2{691_CJB110} | TTTACAAA-- | ----- | ----- |
| msa521731.2{691_COH1} | TTTACAAA-- | ----- | ----- |
| msa521731.2{691_M732} | TTTACAAA-- | ----- | ----- |
| msa521731.2{691_M781} | TTTACAAA-- | ----- | ----- |
| msa521731.2{691_18RS21} | TTTACAAA-- | ----- | ----- |
| msa521731.2{691_2603} | TTTACAAAgg | ctatcaaaga | aaatacaaat |
| msa521731.2{691_A909} | TTTACAAA-- | ----- | ----- |
| msa521731.2{691_JM9130013} | TTTACAAA-- | ----- | ----- |
| msa521731.2{691_H36B} | TTTACAAA-- | ----- | ----- |
| Consensus | ***** | ***** | ***** |

SEQ ID NO. 8612

STRAIN 2603 frame: 1

MKKIGIIVLTLLTFFLVSCGQQTKESTKTTISKMPKIEGFTYYGKIPENPKKVINFTYS
 YTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTADDTEAIAAQKPDLMVFDQDPN
 INTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEANQWVSQWKTTLAVKKDLHHILK
 PNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAPEKVKKDVFKKGWFTVSQEAIGD
 YVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHIIESNYDVFFYFSDPLSLEAQLKS
 FTKAIKENTN

SEQ ID NO. 8613

STRAIN 090 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8614

STRAIN A909 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8615

STRAIN H36B frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8616

STRAIN 18RS21 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8617

STRAIN M732 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8618

STRAIN COH1 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN

Table 86: Comparative Sequences relating to SAG1393

QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8619

STRAIN M781 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8620

STRAIN CJB110 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8621

STRAIN 1169NT frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8622

STRAIN JM9130013 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

PRETTY of: /biotmp/msa522124.2{*} April 28, 2003 08:17 ..

| | | | | | |
|----------------------------|------------|------------|-------------|------------|---------------|
| | 1 | | | | 50 |
| msa522124.2{691_090} | ----- | ----- | ----- | ----- | EG FTYYGKIPEN |
| msa522124.2{691_1169NT} | ----- | ----- | ----- | ----- | EG FTYYGKIPEN |
| msa522124.2{691_CJB110} | ----- | ----- | ----- | ----- | EG FTYYGKIPEN |
| msa522124.2{691_COH1} | ----- | ----- | ----- | ----- | EG FTYYGKIPEN |
| msa522124.2{691_M732} | ----- | ----- | ----- | ----- | EG FTYYGKIPEN |
| msa522124.2{691_M781} | ----- | ----- | ----- | ----- | EG FTYYGKIPEN |
| msa522124.2{691_18RS21} | ----- | ----- | ----- | ----- | EG FTYYGKIPEN |
| msa522124.2{691_2603} | mkkigiivlt | lltfflvscg | qqtqgestkt | tiskmpkieg | FTYYGKIPEN |
| msa522124.2{691_A909} | ----- | ----- | ----- | ----- | EG FTYYGKIPEN |
| msa522124.2{691_JM9130013} | ----- | ----- | ----- | ----- | EG FTYYGKIPEN |
| msa522124.2{691_H36B} | ----- | ----- | ----- | ----- | EG FTYYGKIPEN |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 51 | | | | 100 |
| msa522124.2{691_090} | PKKVINFTYS | YTGYYLLKLG | VNVSSYSLDLE | KDSPVFGKQL | KeAKKLTAADD |
| msa522124.2{691_1169NT} | PKKVINFTYS | YTGYYLLKLG | VNVSSYSLDLE | KDSPVFGKQL | KeAKKLTAADD |
| msa522124.2{691_CJB110} | PKKVINFTYS | YTGYYLLKLG | VNVSSYSLDLE | KDSPVFGKQL | KeAKKLTAADD |
| msa522124.2{691_COH1} | PKKVINFTYS | YTGYYLLKLG | VNVSSYSLDLE | KDSPVFGKQL | KeAKKLTAADD |
| msa522124.2{691_M732} | PKKVINFTYS | YTGYYLLKLG | VNVSSYSLDLE | KDSPVFGKQL | KeAKKLTAADD |
| msa522124.2{691_M781} | PKKVINFTYS | YTGYYLLKLG | VNVSSYSLDLE | KDSPVFGKQL | KeAKKLTAADD |
| msa522124.2{691_18RS21} | PKKVINFTYS | YTGYYLLKLG | VNVSSYSLDLE | KDSPVFGKQL | KeAKKLTAADD |
| msa522124.2{691_2603} | PKKVINFTYS | YTGYYLLKLG | VNVSSYSLDLE | KDSPVFGKQL | KeAKKLTAADD |
| msa522124.2{691_A909} | PKKVINFTYS | YTGYYLLKLG | VNVSSYSLDLE | KDSPVFGKQL | KgAKKLTAADD |
| msa522124.2{691_JM9130013} | PKKVINFTYS | YTGYYLLKLG | VNVSSYSLDLE | KDSPVFGKQL | KgAKKLTAADD |
| msa522124.2{691_H36B} | PKKVINFTYS | YTGYYLLKLG | VNVSSYSLDLE | KDSPVFGKQL | KgAKKLTAADD |
| Consensus | ***** | ***** | ***** | ***** | *-***** |
| | 101 | | | | 150 |
| msa522124.2{691_090} | TEAIAAQKPD | LIMVFDQDPN | INTLKKIAPT | LVIKYGAQNY | LDMMPALGKV |
| msa522124.2{691_1169NT} | TEAIAAQKPD | LIMVFDQDPN | INTLKKIAPT | LVIKYGAQNY | LDMMPALGKV |
| msa522124.2{691_CJB110} | TEAIAAQKPD | LIMVFDQDPN | INTLKKIAPT | LVIKYGAQNY | LDMMPALGKV |
| msa522124.2{691_COH1} | TEAIAAQKPD | LIMVFDQDPN | INTLKKIAPT | LVIKYGAQNY | LDMMPALGKV |
| msa522124.2{691_M732} | TEAIAAQKPD | LIMVFDQDPN | INTLKKIAPT | LVIKYGAQNY | LDMMPALGKV |
| msa522124.2{691_M781} | TEAIAAQKPD | LIMVFDQDPN | INTLKKIAPT | LVIKYGAQNY | LDMMPALGKV |
| msa522124.2{691_18RS21} | TEAIAAQKPD | LIMVFDQDPN | INTLKKIAPT | LVIKYGAQNY | LDMMPALGKV |
| msa522124.2{691_2603} | TEAIAAQKPD | LIMVFDQDPN | INTLKKIAPT | LVIKYGAQNY | LDMMPALGKV |
| msa522124.2{691_A909} | TEAIAAQKPD | LIMVFDQDPN | INTLKKIAPT | LVIKYGAQNY | LDMMPALGKV |
| msa522124.2{691_JM9130013} | TEAIAAQKPD | LIMVFDQDPN | INTLKKIAPT | LVIKYGAQNY | LDMMPALGKV |

Table 86: Comparative Sequences relating to SAG1393

| | | | | | |
|----------------------------|------------|-------------|------------|-------------|-------------|
| msa522124.2{691_H36B} | TEAIAAQKPD | LIMVFDQDPN | INTLKKIAPT | LVIKYGAQNY | LDMMPALGKV |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 151 | | | | 200 |
| msa522124.2{691_090} | FGKEKEANQW | VSQWKTKTTLA | aKKDLHHILk | PNTTFTImDF | YDKNIYLYGN |
| msa522124.2{691_1169NT} | FGKEKEANQW | VSQWKTKTTLA | aKKDLHHILk | PNTTFTImDF | YDKNIYLYGN |
| msa522124.2{691_CJB110} | FGKEKEANQW | VSQWKTKTTLA | aKKDLHHILk | PNTTFTImDF | YDKNIYLYGN |
| msa522124.2{691_COH1} | FGKEKEANQW | VSQWKTKTTLA | aKKDLHHILk | PNTTFTImDF | YDKNIYLYGN |
| msa522124.2{691_M732} | FGKEKEANQW | VSQWKTKTTLA | aKKDLHHILk | PNTTFTImDF | YDKNIYLYGN |
| msa522124.2{691_M781} | FGKEKEANQW | VSQWKTKTTLA | aKKDLHHILk | PNTTFTImDF | YDKNIYLYGN |
| msa522124.2{691_18RS21} | FGKEKEANQW | VSQWKTKTTLA | vKKDLHHILk | PNTTFTImDF | YDKNIYLYGN |
| msa522124.2{691_2603} | FGKEKEANQW | VSQWKTKTTLA | vKKDLHHILk | PNTTFTImDF | YDKNIYLYGN |
| msa522124.2{691_A909} | FGKEKEANQW | VSQWKTKTTLA | aKKDLHHILk | PNTTFTImDF | YDKNIYLYGN |
| msa522124.2{691_JM9130013} | FGKEKEANQW | VSQWKTKTTLA | aKKDLHHILk | PNTTFTImDF | YDKNIYLYGN |
| msa522124.2{691_H36B} | FGKEKEANQW | VSQWKTKTTLA | aKKDLHHILk | PNTTFTImDF | YDKNIYLYGN |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 201 | | | | 250 |
| msa522124.2{691_090} | NFGRGGELIY | DSLGYAAPEK | VKKDVFKKGW | FTVSQEAIGD | YVG DYALVNI |
| msa522124.2{691_1169NT} | NFGRGGELIY | DSLGYAAPEK | VKKDVFKKGW | FTVSQEAIGD | YVG DYALVNI |
| msa522124.2{691_CJB110} | NFGRGGELIY | DSLGYAAPEK | VKKDVFKKGW | FTVSQEAIGD | YVG DYALVNI |
| msa522124.2{691_COH1} | NFGRGGELIY | DSLGYAAPEK | VKKDVFKKGW | FTVSQEAIGD | YVG DYALVNI |
| msa522124.2{691_M732} | NFGRGGELIY | DSLGYAAPEK | VKKDVFKKGW | FTVSQEAIGD | YVG DYALVNI |
| msa522124.2{691_M781} | NFGRGGELIY | DSLGYAAPEK | VKKDVFKKGW | FTVSQEAIGD | YVG DYALVNI |
| msa522124.2{691_18RS21} | NFGRGGELIY | DSLGYAAPEK | VKKDVFKKGW | FTVSQEAIGD | YVG DYALVNI |
| msa522124.2{691_2603} | NFGRGGELIY | DSLGYAAPEK | VKKDVFKKGW | FTVSQEAIGD | YVG DYALVNI |
| msa522124.2{691_A909} | NFGRGGELIY | DSLGYAAPEK | VKKDVFKKGW | FTVSQEAIGD | YVG DYALVNI |
| msa522124.2{691_JM9130013} | NFGRGGELIY | DSLGYAAPEK | VKKDVFKKGW | FTVSQEAIGD | YVG DYALVNI |
| msa522124.2{691_H36B} | NFGRGGELIY | DSLGYAAPEK | VKKDVFKKGW | FTVSQEAIGD | YVG DYALVNI |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 251 | | | | 300 |
| msa522124.2{691_090} | NKTTKKAASS | LKESDVWKNL | PAVKKGHIIE | SNYDVFFYFSD | PLSLEAQLKS |
| msa522124.2{691_1169NT} | NKTTKKAASS | LKESDVWKNL | PAVKKGHIIE | SNYDVFFYFSD | PLSLEAQLKS |
| msa522124.2{691_CJB110} | NKTTKKAASS | LKESDVWKNL | PAVKKGHIIE | SNYDVFFYFSD | PLSLEAQLKS |
| msa522124.2{691_COH1} | NKTTKKAASS | LKESDVWKNL | PAVKKGHIIE | SNYDVFFYFSD | PLSLEAQLKS |
| msa522124.2{691_M732} | NKTTKKAASS | LKESDVWKNL | PAVKKGHIIE | SNYDVFFYFSD | PLSLEAQLKS |
| msa522124.2{691_M781} | NKTTKKAASS | LKESDVWKNL | PAVKKGHIIE | SNYDVFFYFSD | PLSLEAQLKS |
| msa522124.2{691_18RS21} | NKTTKKAASS | LKESDVWKNL | PAVKKGHIIE | SNYDVFFYFSD | PLSLEAQLKS |
| msa522124.2{691_2603} | NKTTKKAASS | LKESDVWKNL | PAVKKGHIIE | SNYDVFFYFSD | PLSLEAQLKS |
| msa522124.2{691_A909} | NKTTKKAASS | LKESDVWKNL | PAVKKGHIIE | SNYDVFFYFSD | PLSLEAQLKS |
| msa522124.2{691_JM9130013} | NKTTKKAASS | LKESDVWKNL | PAVKKGHIIE | SNYDVFFYFSD | PLSLEAQLKS |
| msa522124.2{691_H36B} | NKTTKKAASS | LKESDVWKNL | PAVKKGHIIE | SNYDVFFYFSD | PLSLEAQLKS |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 301 | 310 | | | |
| msa522124.2{691_090} | FT----- | | | | |
| msa522124.2{691_1169NT} | FT----- | | | | |
| msa522124.2{691_CJB110} | FT----- | | | | |
| msa522124.2{691_COH1} | FT----- | | | | |
| msa522124.2{691_M732} | FT----- | | | | |
| msa522124.2{691_M781} | FT----- | | | | |
| msa522124.2{691_18RS21} | FT----- | | | | |
| msa522124.2{691_2603} | FTkaikentn | | | | |
| msa522124.2{691_A909} | FT----- | | | | |
| msa522124.2{691_JM9130013} | FT----- | | | | |
| msa522124.2{691_H36B} | FT----- | | | | |
| Consensus | ***** | | | | |

Table 87: Comparative Sequences relating to SAG0645

SEQ ID NO. 8701

STRAIN 2603

ATGAAATATCGAAGAAGTTATTGTTTTTCGGCTGCTGTT
 TTAACAATGGTGGCGGGTCAACTGTTGAACCAAGTAGCTCAGTTTGCAGTGGAAATGAGT
 ATTGTAAGAGCTGCAGAAGTGTCAAGAAGCGCCAGCGAAAAACAACAGTAAATATCTAT
 AAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAATGGTGGTATCGAGAATAAA
 GACGGCGAAGTAATATCTAACTAGCTAACTTGGTGACAATGTAAAAGGTTTGCAAGGT
 GTACAGTTTAAACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTG
 ACAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAGTCTA
 CCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGATTCAAAAAAGTAATGTG
 AGATACCTTGTATGTAGAAGATTTAAAGAATTACCTTCAAACATTACCAAGCTTATGCT
 GTACCGTTTGTGTTGGAATTACCAGTTGCTAACTCTACAGGTACAGGTTTCCCTTCTGAA
 ATTAATATTTACCCTAAAAACGTTGTAAGTGAACCAAAAAACAGATAAAGATGTTAAA
 AAATTAGGTGAGGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTTGAAA
 TCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTGAAATTAAGTATAAATTTGCA
 GATGGCTTGAATATAAATCTGTTGAAAAAATCAAGATTGGTTGAAAAACACTGAATAGA
 GATGAGCACTACACTATTGATGAACCAACAGTTGATAACCAAAATACATTAATAATTACG
 TTTAAACAGAGAAATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCTTGTTTAAA
 AATCAAGATGCTCTTGAATAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAAATT
 CCAAGTTGATCAACTATTATGAAAAAGCAGTTTAGGAAAAAGCAATTGAAAAATCTTTT
 GAACCTTCAATATGACCAATCTCCTGATAAAGCTGACAAATCCAAAAACCTAATCCTCCA
 AGAAAACAGAAAGTTCATCTGGTGGGAAACGATTGTAAGAAAGACTCAACAGAAACA
 CAAACACTAGGTGGTCTGAGTTTGAATTTGTTGGCTTCTGATGGGACAGCAGTAAATGG
 ACAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATGCTGGAGAAGCTGTTACT
 GGGCAACCAATCAAAATTGAAATCACATACAGACGGTACGTTTGAAGTTAAAGGTTTGGCT
 TATGCAAGTTGATGCGAATGCAAGGGTACAGCAGTAACCTACAAATTTAAAGAAACAAAA
 GCACCAGAAGGTTATGTAATCCCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCT
 TATAATACAAAACCACTGACATCACGGTTGATAGTCTGATGCAACCTGATACAATT
 AAAAAACAAACCACTCCTTCAATCCCTAATACTGGTGGTATGTTACGGCTATCTTTGTC
 GCTATCGGTGCTGCGGTGATGGCTTTTGTGTTAAGGGGATGAAGCGTCTACAAAGAT
 AAC

SEQ ID NO. 8702

STRAIN 090

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGA
 TTTCAAAAAGTAAATGTGAGATACCTGTAATGTAGAAGATTTAAAGAATTAC
 CTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTTACCC
 TAAAAACGTTGTAACCTGATGAACCAAAAAACAGATAAAGATGTTAAAAAAT
 TAGGTGAGACGATGCAAGTTTATACGATTGGTGAAGAATTCAAATGGTTCT
 TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAATCA
 AGATTGGTTGAAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAATAAATACGTTTAAACCCAGAGAA
 ATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCTTGTAAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGG
 GAAATTCAGATTGCATCAACTATTAAATGAAAAAGCAGTTTGGGAAAAAGC
 AATTGAAAAATCTTTTGAACCTTCAATATGACCATACCTGATAAAGCTG
 ACAATCCAAAACCATCTAATCCTCCAAAGAAACCAAGAAGTTCACTACTGGT
 GGGAAACGATTGTAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
 TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
 GATTAAAGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGTTACAGCAG
 TAACTTACAAATTTAAAGAAACAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAAC
 AACTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTAATA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8703

STRAIN A909

GCAGAAGTGTCAAGAAGCGCCAGCGAA
 AACCAACAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAA
 TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
 TATGCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAA
 ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
 CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
 GTCAAGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCT
 GGAATCAAAAAGTAAATGTGAGATCTTGTATGTAGAAGATTAAAGAAAT
 CACCTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
 CCAGTTGCTAACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTTA
 CCCTAAaAACGTTGTAACCTGATGAACCAAAAAACAGATAAAGATGTTAAAA
 AATTAGGTGAGGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGG
 TTCTTGAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGA
 AATTACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAA
 TCAAGATTGGTTGAAAAACACTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAAAAATTAAGTTTAAACCGA

Table 87: Comparative Sequences relating to SAG0645

GAAATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCCTTGTAAAA
 ATCAAGATGCTCTTGATAAAGCTACTGCAATACAGATGATGCGGCATTT
 TTGGAAATTCAGTTGTCATCAACTATTAATGAAAAAGCAGTTTATAGGAAA
 AGCAATTGAAAACTCTTTGAACTTCAATATGACCATACTCCTGATAAAG
 CTGACAAATCCAAAACCATCTAATCCTCCAGAAAACCCAGAAAGTTCATACT
 GGTGGGAAACGATTTGTAAGAAAGACTCAACAGAAACACAAACACTAGG
 TGGTGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGGA
 CAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
 GCTGTACTGGGCAACCAATCAAATGAAATCACAATACAGACGGTACGTT
 TGAGATTAAAGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAG
 CAGTAACCTTACAAATTAAAAAGAAAACAAAGCACCAGAGGTTATGTAATC
 CCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAA
 ACCAACTGACATCACGGTTGATAGTCTGATGCAACACCTGATACAAATTA
 AAAACACAA

SEQ ID NO. 8704

STRAIN 18RS21

GCAGAAGTGTCACAAGAACGCCAGCGAAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTCTTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAAACGATCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
 TTCAAAAGTAATGTGAGATACTTGTATGTAGAAGATTAAAGAATTACAC
 CTTCAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCTTCTGAAATTAATATTACCC
 TAAAAACGTTGTAAGTATGAACCAAAAAAGATGTAAGATGTTAAATAAT
 TAGGTACAGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAATCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTTGAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAATCA
 AGATTGGTTGAAAAACCTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAAAAAATTACGTTTAAACCAAGAGAA
 ATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGT
 GAAATTCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTATAGGAAAAGC
 AATTGAAAAATCTTTTGAACCTCAATATGACCACTACTCTGATCAAGCTG
 ACAATCCAAACCATCTAATCCTCCAGAAAACCCAGAAAGTTCATACTGGT
 GGGAAACGATTTGTAAGAAAGACTCAACAGAAAACACAAACACTAGGTGG
 TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
 GATTAAAGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAGCAG
 TAACCTTACAAATTAAAAAGAAACAAAGCACCAGAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAACCC
 AACTGACATCACGGTTGATAGTCTGATGCAACACCTGATACAAATAAAA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8705

STRAIN M732

GCAGAAGTGTCACAAGAACGCCAGCGAAAAACACAGT
 AAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTAATTTCTA
 ATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAA
 CTGTGTGACAATGTAAAGGTTTGCAAGGTGTACAGTTTAAACGTTATAA
 AGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGTGT
 AAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCACTTA
 CCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATTCAAA
 AAGTAATGTGAGATACTTGTATGTAGAAGATTAAAGAATTACCTTCAA
 ACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGTTGCT
 AACTCTACAGGTACAGGTTTCTTCTGAAATTAATATTACCTAAAAA
 CGTTGTAACTGATGAACCAAAAAACAGATAAAGATGTTAAAAAATTAGGTC
 AGGACGATGCAAGTTATACGATTTGGTGAAGAATTCAAATGGTTCTTGAA
 TCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAATTACTGA
 TAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAAATCAAGATTG
 GTTCGAAAACTGAATAGAGATGAGCACTACACTATTGATGAACCAACA
 GTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAAGAGAAATTAA
 AGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATCAAGATG
 CTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGGAAATT
 CCAGTTGCATCAACTATTAATGAAAAAGCAGTTTATAGGAAAAGCAATTGA
 AAATACTTTTGAACCTCAATATGACCATACTCTGATAAAGCTGACAATC
 CAAAACCACTAATCTCCAGAAAACCCAGAAAGTTCATACTGGTGGGAAA
 CGATTGTAAAGAAAGACTCAACAGAAAACACAAACACTAGGTGGTGTGA
 GTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTC
 TTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACT
 GGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAATTA
 AGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAGCAGTAACCT
 ACAATTAAGAAACAAAGCACCAGAGGTTATGTAATCCCTGATAAA
 GAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAACCAACTGA
 CATCACGGTTGATAGTCTGATGCAACACCTGATACAAATAAAAACA
 AACGTCCTTCA

SEQ ID NO. 8706

STRAIN COHI

Table 87: Comparative Sequences relating to SAG0645

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTTnTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
 TTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTAC
 CTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTACCC
 TAAAAACGTTGTAACGTGATGAACCAAAACAGATAAAGATGTTAAAAAAT
 TAGGTGAGGACGATGACAGTTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCA
 AGATTGGTTCGAAAACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAGAA
 ATTTAAAGAAATGTCTGAGCTACTTAAGGAATGACCCCTGTTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAATACAGATGATGCGGCATTTTGTG
 GAAATTCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTTAGGAAAAAGC
 AATTGAAAAATACTTTGAACCTCAATATGACCATACTCCTGATAAAGCTG
 ACAATCCAAACCACTCTAATCCTCCAAGAAAACCAAGAAGTTCACTAGGT
 GGGAAACGATTTGTAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
 TGTGAGTTTGTATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAGCT
 GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
 GATTAAGGTTTGGCTTATGCAAGTTGATGCGAATGACAGGGTACAGCAG
 TAACTTCAAAATTAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCAAAACATCTTATAATACAAAACC
 AACTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTAATA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8707

STRAIN M781

GCAGAAGTGTCAAGAAGCGCCAGCGAAAACAG
 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC
 TAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAAACGTT
 ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACACA
 GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAG
 TCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATT
 CAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTACCT
 TCAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGT
 TGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTACCTTA
 AAAACGTTGTAACTGATGAACCAAAACAGATAAAGATGTTAAAAAATTA
 GGTGAGGACGATGACAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTT
 GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTGAAATTA
 CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCAAG
 ATTGGTTTCGAAAACTGAATAGAGATGAGCACTACACTATTGATGAACC
 AACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAGAAAT
 TTAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATCAA
 GATGCTCTTGATAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGTA
 AATTCCAGTTGCACTCAACTATTAAATGAAAAAGCAGTTTTAGGAAAAAGCAA
 TTGAAAAATCTTTTGAACCTTCAATATGACCATACTCCTGATAAAGCTGAC
 AATCCAAAACCACTAATCCTCCAAGAAAACCAAGAAGTTCACTAGGTGG
 GAAACGATTTGTAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTG
 CTGAGTTTGTATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGAT
 GCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT
 TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAAGA
 TTAAGGTTTGGCTTATGCAAGTTGATGCGAATGACAGGGTACAGCAGTA
 ACTTACAAATTAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGA
 TAAAGAAATCGAGTTTACAGTATCAAAACATCTTATAATACAAAACCAA
 CTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTAATAAC
 AACAAACGT

SEQ ID NO. 8708

STRAIN CJB110

GCAGAAGTGTCAAGAAGCGCCAGCGAA
 AACAGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATGGAAA
 TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
 TATGCTAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAA
 ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
 CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
 GTGAGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCT
 GGATTCAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATT
 CACCTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
 CCAAGTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATT
 CCTTAAAAACGTTGTAATGATGAACCAAAACAGATAAAGATGTTAAAA
 AATTAGGTGAGGACGATGACAGTTTATACGATTGGTGAAGAATTCAAATGG
 TCTTGAAGATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGA
 AATTACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAA
 TCAAGATTGGTTGAAAAACCTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAA
 GAAATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAA

Table 87: Comparative Sequences relating to SAG0645

ATCAAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTT
 TTGGAAATTCAGTTGTCATCAACTATTAATGAAAAAGCAGTTTATAGGAAA
 AGCAATTGAAAACTCTTTGAACTTCAATATGACCATACTCCTGATAAAG
 CTGCAATcCAAAACCATCTAATCCTCCAGAAAACAGAGTTCTACT
 GGTGGGAAACGATTTGTAAAGAAAGACTCAACAGAAAACAAACACTAGG
 TGGTGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGA
 CAGATGCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
 GCTGTTACTGGGCAACCAATCAAAATGAAATCAGATACAGACGGTACGTT
 TGAGATTAAAGGTTTGGCTTATGCGAGTTGATGCGAATGCAGAGGGTACAG
 CAGTAACCTACAAATTAAAGAAAACAAAGCACCAGAGGTTATGTAATC
 CCTGATAAAGAAATCGAGTTTACAGTATCAGAAACATCTTATAATCCAAA
 ACCAATGACATCAGGTTGATAGTGCTGATGCAACCTGATACAATTA
 AAAACAACAAACGCTCCTCA

SEQ ID NO. 8709

STRAIN JM9130013

GCAGAAGTGTCAAGAACGCCAGCGAAAACAGCAGTA
 AATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAA
 TGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAATGCTAAAC
 TTGGTGCAATGTAAAGGTTTGCAGGTTGATCAGTTTAAACGTTATAAA
 GTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATGACAACAGTTGA
 AGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAGTCTAC
 CTCAAAAAATAATGCTCAAGGTTTGGTTCGTCGATGCTCTGGATTCAAAA
 AGTAATGTGAGATACCTGTATGTAGAAGATTAAAGAATTACCTTCAAA
 CATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGTTGCTA
 ACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTACCTAAAAAC
 GTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAAAAATTAGGTCA
 GGACGATGCGAGTTATACGATTGGTGAAGAATTCAAAATGGTTCTTGAAAT
 CTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAATTACTGAT
 AAATTTGAGATGGCTTGACTTATAAATCTGTTGGAATAATCAAGATTGG
 TTGGAACCACTGAATAGAGATGAGCACTACACTATTGATGAACCAACAG
 TTGATAACCAAAATACATTAATAAATTACGTTTAAACAGAGAAATTTAAA
 GAAATTTGCTGAGCTACTTAAAGGAATGACCTTGTATAAATCAAGATGC
 TCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAAATTC
 CAGTTGCTCACTATTAATGAAAAAGCAGTTTATGGAAGAAGCAATTGAA
 AATACTTTTGAACCTCAATATGACCATACTCTGATAAAGCTGACAAATCC
 AAAACCATCTAATcCTcCAAGAAAACAGAAAGTTCATCTGTTGGGAAAC
 GATTTGTAAGAAAGACTCAACAGAAAACAAACACTAGGTTGGTGTCTGAG
 TTTGATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTCT
 TATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACTG
 GGCACCAATCAAATTGAAATCAGATACAGACGGTACGTTTGGATTAA
 GGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAGCAGTAACCTA
 CAAATTAAGAAAACAAAGCACCAGAGGTTATGTAATCCCTGATAAAG
 AAATCGAGTTTACAGTATCAGAAACATCTTATAATACAAAACCACTGAC
 ATCAGGTTGATAGTGCTGATGCAACCTGATACAATTAACAAACAAAC
 ACGTCTCTCA

PRETTY of: /biotmp/msa123961.2{*} April 30, 2003 07:17 ..

| | | | | | |
|----------------------------|------------|------------|-------------|------------|------------|
| | 1 | | | | 50 |
| msa123961.2{80_2603} | atgaaattat | cgaagaagtt | attgtttttcg | gctgctgttt | taacaatggt |
| msa123961.2{80_A909} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_M732} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_090} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_M781} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{801_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80h_CJB110} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ----- | ----- | ----- | ----- | ----- |

| | | | | | |
|----------------------------|-------------|------------|------------|------------|------------|
| | 51 | | | | 100 |
| msa123961.2{80_2603} | ggcgggggtca | actgttgaac | cagtagctca | gtttgcgact | ggaatgagta |
| msa123961.2{80_A909} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_M732} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_090} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_M781} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{801_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80h_CJB110} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ----- | ----- | ----- | ----- | ----- |

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| | 101 | | | | 150 |
| msa123961.2{80_2603} | ttgtaagagc | tGCAGAAGTG | TCACAAGAAC | GCCCAGCGAA | AACAaCAGTA |
| msa123961.2{80_A909} | ----- | -GCAGAAGTG | TCACAAGAAC | GCCCAGCGAA | AACAaCAGTA |
| msa123961.2{80_M732} | ----- | -GCAGAAGTG | TCACAAGAAC | GCCCAGCGAA | AACAaCAGTA |
| msa123961.2{80_090} | ----- | -GCAGAAGTG | TCACAAGAAC | GCCCAGCGAA | AACAaCAGTA |
| msa123961.2{80_COH1} | ----- | -GCAGAAGTG | TCACAAGAAC | GCCCAGCGAA | AACAaCAGTA |
| msa123961.2{80_M781} | ----- | -GCAGAAGTG | TCACAAGAAC | GCCCAGCGAA | AACAaCAGTA |
| msa123961.2{801_JM9130013} | ----- | -GCAGAAGTG | TCACAAGAAC | GCCCAGCGAA | AACAaCAGTA |
| msa123961.2{80_18RS21} | ----- | -GCAGAAGTG | TCACAAGAAC | GCCCAGCGAA | AACAaCAGTA |

Table 87: Comparative Sequences relating to SAG0645

| | | | | | |
|----------------------------|-------|------------|------------|------------|------------|
| msa123961.2{80h_CJB110} | ----- | -GCAGAAGTG | TCACAAGAAC | GCCCAGCGAA | AACAgCAGTA |
| Consensus | ----- | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | 151 | AATATCTATA | AATTACAAGC | TGATAGTTAT | AAATcGGAAA |
| msa123961.2{80_A909} | | AATATCTATA | AATTACAAGC | TGATAGTTAT | AAATcGGAAA |
| msa123961.2{80_M732} | | AATATCTATA | AATTACAAGC | TGATAGTTAT | AAATcGGAAA |
| msa123961.2{80_090} | | AATATCTATA | AATTACAAGC | TGATAGTTAT | AAATcGGAAA |
| msa123961.2{80_COH1} | | AATATCTATA | AATTACAAGC | TGATAGTTAT | AAATcGGAAA |
| msa123961.2{80_M781} | | AATATCTATA | AATTACAAGC | TGATAGTTAT | AAATcGGAAA |
| msa123961.2{801_JM9130013} | | AATATCTATA | AATTACAAGC | TGATAGTTAT | AAATcGGAAA |
| msa123961.2{80_18RS21} | | AATATCTATA | AATTACAAGC | TGATAGTTAT | AAATcGGAAA |
| msa123961.2{80h_CJB110} | | AATATCTATA | AATTACAAGC | TGATAGTTAT | AAATcGGAAA |
| Consensus | | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | 201 | TGGTGGTATC | GAGAATAAAG | ACGGCGAAGT | AATATCTAAC |
| msa123961.2{80_A909} | | TGGTGGTATC | GAGAATAAAG | ACGGCGAAGT | AATATCTAAC |
| msa123961.2{80_M732} | | TGGTGGTATC | GAGAATAAAG | ACGGCGAAGT | AATATCTAAC |
| msa123961.2{80_090} | | TGGTGGTATC | GAGAATAAAG | ACGGCGAAGT | AATATCTAAC |
| msa123961.2{80_COH1} | | TGGTGGTATC | GAGAATAAAG | ACGGCGAAGT | AATATCTAAC |
| msa123961.2{80_M781} | | TGGTGGTATC | GAGAATAAAG | ACGGCGAAGT | AATATCTAAC |
| msa123961.2{801_JM9130013} | | TGGTGGTATC | GAGAATAAAG | ACGGCGAAGT | AATATCTAAC |
| msa123961.2{80_18RS21} | | TGGTGGTATC | GAGAATAAAG | ACGGCGAAGT | AATATCTAAC |
| msa123961.2{80h_CJB110} | | TGGTGGTATC | GAGAATAAAG | ACGGCGAAGT | AATATCTAAC |
| Consensus | | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | 251 | TTGGTGACAA | TGTAAAAGGT | TTGCAAGGTG | TACAGTTTAA |
| msa123961.2{80_A909} | | TTGGTGACAA | TGTAAAAGGT | TTGCAAGGTG | TACAGTTTAA |
| msa123961.2{80_M732} | | TTGGTGACAA | TGTAAAAGGT | TTGCAAGGTG | TACAGTTTAA |
| msa123961.2{80_090} | | TTGGTGACAA | TGTAAAAGGT | TTGCAAGGTG | TACAGTTTAA |
| msa123961.2{80_COH1} | | TTGGTGACAA | TGTAAAAGGT | TTGCAAGGTG | TACAGTTTAA |
| msa123961.2{80_M781} | | TTGGTGACAA | TGTAAAAGGT | TTGCAAGGTG | TACAGTTTAA |
| msa123961.2{801_JM9130013} | | TTGGTGACAA | TGTAAAAGGT | TTGCAAGGTG | TACAGTTTAA |
| msa123961.2{80_18RS21} | | TTGGTGACAA | TGTAAAAGGT | TTGCAAGGTG | TACAGTTTAA |
| msa123961.2{80h_CJB110} | | TTGGTGACAA | TGTAAAAGGT | TTGCAAGGTG | TACAGTTTAA |
| Consensus | | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | 301 | GTCAAGACGG | ATATTTCTGT | TGATGAATTG | AAAAAATTGA |
| msa123961.2{80_A909} | | GTCAAGACGG | ATATTTCTGT | TGATGAATTG | AAAAAATTGA |
| msa123961.2{80_M732} | | GTCAAGACGG | ATATTTCTGT | TGATGAATTG | AAAAAATTGA |
| msa123961.2{80_090} | | GTCAAGACGG | ATATTTCTGT | TGATGAATTG | AAAAAATTGA |
| msa123961.2{80_COH1} | | GTCAAGACGG | ATATTTCTGT | TGATGAATTG | AAAAAATTGA |
| msa123961.2{80_M781} | | GTCAAGACGG | ATATTTCTGT | TGATGAATTG | AAAAAATTGA |
| msa123961.2{801_JM9130013} | | GTCAAGACGG | ATATTTCTGT | TGATGAATTG | AAAAAATTGA |
| msa123961.2{80_18RS21} | | GTCAAGACGG | ATATTTCTGT | TGATGAATTG | AAAAAATTGA |
| msa123961.2{80h_CJB110} | | GTCAAGACGG | ATATTTCTGT | TGATGAATTG | AAAAAATTGA |
| Consensus | | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | 351 | AGCAGCAGAT | GCAAAAGTTG | GAACGATTCT | TGAAGAAGGT |
| msa123961.2{80_A909} | | AGCAGCAGAT | GCAAAAGTTG | GAACGATTCT | TGAAGAAGGT |
| msa123961.2{80_M732} | | AGCAGCAGAT | GCAAAAGTTG | GAACGATTCT | TGAAGAAGGT |
| msa123961.2{80_090} | | AGCAGCAGAT | GCAAAAGTTG | GAACGATTCT | TGAAGAAGGT |
| msa123961.2{80_COH1} | | AGCAGCAGAT | GCAAAAGTTG | GAACGATTCT | TGAAGAAGGT |
| msa123961.2{80_M781} | | AGCAGCAGAT | GCAAAAGTTG | GAACGATTCT | TGAAGAAGGT |
| msa123961.2{801_JM9130013} | | AGCAGCAGAT | GCAAAAGTTG | GAACGATTCT | TGAAGAAGGT |
| msa123961.2{80_18RS21} | | AGCAGCAGAT | GCAAAAGTTG | GAACGATTCT | TGAAGAAGGT |
| msa123961.2{80h_CJB110} | | AGCAGCAGAT | GCAAAAGTTG | GAACGATTCT | TGAAGAAGGT |
| Consensus | | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | 401 | CTCAAAAAAC | TAATGCTCAA | GGTTTGGTCG | TCGATGCTCT |
| msa123961.2{80_A909} | | CTCAAAAAAC | TAATGCTCAA | GGTTTGGTCG | TCGATGCTCT |
| msa123961.2{80_M732} | | CTCAAAAAAC | TAATGCTCAA | GGTTTGGTCG | TCGATGCTCT |
| msa123961.2{80_090} | | CTCAAAAAAC | TAATGCTCAA | GGTTTGGTCG | TCGATGCTCT |
| msa123961.2{80_COH1} | | CTCAAAAAAC | TAATGCTCAA | GGTTTGGTCG | TCGATGCTCT |
| msa123961.2{80_M781} | | CTCAAAAAAC | TAATGCTCAA | GGTTTGGTCG | TCGATGCTCT |
| msa123961.2{801_JM9130013} | | CTCAAAAAAC | TAATGCTCAA | GGTTTGGTCG | TCGATGCTCT |
| msa123961.2{80_18RS21} | | CTCAAAAAAC | TAATGCTCAA | GGTTTGGTCG | TCGATGCTCT |
| msa123961.2{80h_CJB110} | | CTCAAAAAAC | TAATGCTCAA | GGTTTGGTCG | TCGATGCTCT |
| Consensus | | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | 451 | AGTAATGTGA | GATACTTGTA | TGTAGAAGAT | TTAAAGAATT |
| msa123961.2{80_A909} | | AGTAATGTGA | GATACTTGTA | TGTAGAAGAT | TTAAAGAATT |
| msa123961.2{80_M732} | | AGTAATGTGA | GATACTTGTA | TGTAGAAGAT | TTAAAGAATT |
| msa123961.2{80_090} | | AGTAATGTGA | GATACTTGTA | TGTAGAAGAT | TTAAAGAATT |
| msa123961.2{80_COH1} | | AGTAATGTGA | GATACTTGTA | TGTAGAAGAT | TTAAAGAATT |
| msa123961.2{80_M781} | | AGTAATGTGA | GATACTTGTA | TGTAGAAGAT | TTAAAGAATT |
| msa123961.2{801_JM9130013} | | AGTAATGTGA | GATACTTGTA | TGTAGAAGAT | TTAAAGAATT |
| Consensus | | ***** | ***** | ***** | ***** |

Table 87: Comparative Sequences relating to SAG0645

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| msa123961.2{80_18RS21} | AGTAATGTGA | GATACTTGTA | TGTAGAAGAT | TTAAAGAATT | CACCTTCAAA |
| msa123961.2{80h_CJB110} | AGTAATGTGA | GATACTTGTA | TGTAGAAGAT | TTAAAGAATT | CACCTTCAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | CATTACCAAA | GCTTATGCTG | TACCGTTTGT | GTGGAATTA | CCAGTTGCTA |
| msa123961.2{80_A909} | CATTACCAAA | GCTTATGCTG | TACCGTTTGT | GTGGAATTA | CCAGTTGCTA |
| msa123961.2{80_M732} | CATTACCAAA | GCTTATGCTG | TACCGTTTGT | GTGGAATTA | CCAGTTGCTA |
| msa123961.2{80_090} | CATTACCAAA | GCTTATGCTG | TACCGTTTGT | GTGGAATTA | CCAGTTGCTA |
| msa123961.2{80_COH1} | CATTACCAAA | GCTTATGCTG | TACCGTTTGT | GTGGAATTA | CCAGTTGCTA |
| msa123961.2{80_M781} | CATTACCAAA | GCTTATGCTG | TACCGTTTGT | GTGGAATTA | CCAGTTGCTA |
| msa123961.2{801_JM9130013} | CATTACCAAA | GCTTATGCTG | TACCGTTTGT | GTGGAATTA | CCAGTTGCTA |
| msa123961.2{80_18RS21} | CATTACCAAA | GCTTATGCTG | TACCGTTTGT | GTGGAATTA | CCAGTTGCTA |
| msa123961.2{80h_CJB110} | CATTACCAAA | GCTTATGCTG | TACCGTTTGT | GTGGAATTA | CCAGTTGCTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | ACTCTACAGG | TACAGGTTTC | CTTTCTGAAA | TTAATATTTA | CCCTAAAAAC |
| msa123961.2{80_A909} | ACTCTACAGG | TACAGGTTTC | CTTTCTGAAA | TTAATATTTA | CCCTAAAAAC |
| msa123961.2{80_M732} | ACTCTACAGG | TACAGGTTTC | CTTTCTGAAA | TTAATATTTA | CCCTAAAAAC |
| msa123961.2{80_090} | ACTCTACAGG | TACAGGTTTC | CTTTCTGAAA | TTAATATTTA | CCCTAAAAAC |
| msa123961.2{80_COH1} | ACTCTACAGG | TACAGGTTTC | CTTTCTGAAA | TTAATATTTA | CCCTAAAAAC |
| msa123961.2{80_M781} | ACTCTACAGG | TACAGGTTTC | CTTTCTGAAA | TTAATATTTA | CCCTAAAAAC |
| msa123961.2{801_JM9130013} | ACTCTACAGG | TACAGGTTTC | CTTTCTGAAA | TTAATATTTA | CCCTAAAAAC |
| msa123961.2{80_18RS21} | ACTCTACAGG | TACAGGTTTC | CTTTCTGAAA | TTAATATTTA | CCCTAAAAAC |
| msa123961.2{80h_CJB110} | ACTCTACAGG | TACAGGTTTC | CTTTCTGAAA | TTAATATTTA | CCCTAAAAAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | GTGTAACTG | ATGAACCAAA | AACAGATAAA | GATGTTAAa | AATTAGGTCA |
| msa123961.2{80_A909} | GTGTAACTG | ATGAACCAAA | AACAGATAAA | GATGTTAAa | AATTAGGTCA |
| msa123961.2{80_M732} | GTGTAACTG | ATGAACCAAA | AACAGATAAA | GATGTTAAa | AATTAGGTCA |
| msa123961.2{80_090} | GTGTAACTG | ATGAACCAAA | AACAGATAAA | GATGTTAAa | AATTAGGTCA |
| msa123961.2{80_COH1} | GTGTAACTG | ATGAACCAAA | AACAGATAAA | GATGTTAAa | AATTAGGTCA |
| msa123961.2{80_M781} | GTGTAACTG | ATGAACCAAA | AACAGATAAA | GATGTTAAa | AATTAGGTCA |
| msa123961.2{801_JM9130013} | GTGTAACTG | ATGAACCAAA | AACAGATAAA | GATGTTAAa | AATTAGGTCA |
| msa123961.2{80_18RS21} | GTGTAACTG | ATGAACCAAA | AACAGATAAA | GATGTTAAa | AATTAGGTCA |
| msa123961.2{80h_CJB110} | GTGTAACTG | ATGAACCAAA | AACAGATAAA | GATGTTAAa | AATTAGGTCA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | GGACGATGCA | GGTTATACGA | TTGGTGAAGA | ATTCAAATGG | TTCTTGAAAT |
| msa123961.2{80_A909} | GGACGATGCA | GGTTATACGA | TTGGTGAAGA | ATTCAAATGG | TTCTTGAAAT |
| msa123961.2{80_M732} | GGACGATGCA | GGTTATACGA | TTGGTGAAGA | ATTCAAATGG | TTCTTGAAAT |
| msa123961.2{80_090} | GGACGATGCA | GGTTATACGA | TTGGTGAAGA | ATTCAAATGG | TTCTTGAAAT |
| msa123961.2{80_COH1} | GGACGATGCA | GGTTATACGA | TTGGTGAAGA | ATTCAAATGG | TTCTTGAAAT |
| msa123961.2{80_M781} | GGACGATGCA | GGTTATACGA | TTGGTGAAGA | ATTCAAATGG | TTCTTGAAAT |
| msa123961.2{801_JM9130013} | GGACGATGCA | GGTTATACGA | TTGGTGAAGA | ATTCAAATGG | TTCTTGAAAT |
| msa123961.2{80_18RS21} | GGACGATGCA | GGTTATACGA | TTGGTGAAGA | ATTCAAATGG | TTCTTGAAAT |
| msa123961.2{80h_CJB110} | GGACGATGCA | GGTTATACGA | TTGGTGAAGA | ATTCAAATGG | TTCTTGAAAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | CTACAATCCC | TGCCAATTTA | GGTGACTATG | AAAAATTTGA | AATTACTGAT |
| msa123961.2{80_A909} | CTACAATCCC | TGCCAATTTA | GGTGACTATG | AAAAATTTGA | AATTACTGAT |
| msa123961.2{80_M732} | CTACAATCCC | TGCCAATTTA | GGTGACTATG | AAAAATTTGA | AATTACTGAT |
| msa123961.2{80_090} | CTACAATCCC | TGCCAATTTA | GGTGACTATG | AAAAATTTGA | AATTACTGAT |
| msa123961.2{80_COH1} | CTACAATCCC | TGCCAATTTA | GGTGACTATG | AAAAATTTGA | AATTACTGAT |
| msa123961.2{80_M781} | CTACAATCCC | TGCCAATTTA | GGTGACTATG | AAAAATTTGA | AATTACTGAT |
| msa123961.2{801_JM9130013} | CTACAATCCC | TGCCAATTTA | GGTGACTATG | AAAAATTTGA | AATTACTGAT |
| msa123961.2{80_18RS21} | CTACAATCCC | TGCCAATTTA | GGTGACTATG | AAAAATTTGA | AATTACTGAT |
| msa123961.2{80h_CJB110} | CTACAATCCC | TGCCAATTTA | GGTGACTATG | AAAAATTTGA | AATTACTGAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | AAATTTGCAG | ATGGCTTGAC | TTATAAATCT | GTTGGAAAAA | TCAAGATTGG |
| msa123961.2{80_A909} | AAATTTGCAG | ATGGCTTGAC | TTATAAATCT | GTTGGAAAAA | TCAAGATTGG |
| msa123961.2{80_M732} | AAATTTGCAG | ATGGCTTGAC | TTATAAATCT | GTTGGAAAAA | TCAAGATTGG |
| msa123961.2{80_090} | AAATTTGCAG | ATGGCTTGAC | TTATAAATCT | GTTGGAAAAA | TCAAGATTGG |
| msa123961.2{80_COH1} | AAATTTGCAG | ATGGCTTGAC | TTATAAATCT | GTTGGAAAAA | TCAAGATTGG |
| msa123961.2{80_M781} | AAATTTGCAG | ATGGCTTGAC | TTATAAATCT | GTTGGAAAAA | TCAAGATTGG |
| msa123961.2{801_JM9130013} | AAATTTGCAG | ATGGCTTGAC | TTATAAATCT | GTTGGAAAAA | TCAAGATTGG |
| msa123961.2{80_18RS21} | AAATTTGCAG | ATGGCTTGAC | TTATAAATCT | GTTGGAAAAA | TCAAGATTGG |
| msa123961.2{80h_CJB110} | AAATTTGCAG | ATGGCTTGAC | TTATAAATCT | GTTGGAAAAA | TCAAGATTGG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | TTCGAAAACA | CTGAATAGAG | ATGAGCACTA | CACATTGAT | GAACCAACAG |
| msa123961.2{80_A909} | TTCGAAAACA | CTGAATAGAG | ATGAGCACTA | CACATTGAT | GAACCAACAG |
| msa123961.2{80_M732} | TTCGAAAACA | CTGAATAGAG | ATGAGCACTA | CACATTGAT | GAACCAACAG |
| msa123961.2{80_090} | TTCGAAAACA | CTGAATAGAG | ATGAGCACTA | CACATTGAT | GAACCAACAG |
| msa123961.2{80_COH1} | TTCGAAAACA | CTGAATAGAG | ATGAGCACTA | CACATTGAT | GAACCAACAG |
| msa123961.2{80_M781} | TTCGAAAACA | CTGAATAGAG | ATGAGCACTA | CACATTGAT | GAACCAACAG |

Table 87: Comparative Sequences relating to SAG0645

| | | | | | |
|----------------------------|------------|------------|------------|------------|------------|
| msa123961.2{801_JM9130013} | TTGATAACCA | AAATACATTA | AAAATTACGT | TTAAACCAGA | GAAATTTAAA |
| msa123961.2{80_18RS21} | TTGATAACCA | AAATACATTA | AAAATTACGT | TTAAACCAGA | GAAATTTAAA |
| msa123961.2{80h_CJB110} | TTGATAACCA | AAATACATTA | AAAATTACGT | TTAAACCAGA | GAAATTTAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 851 | | | | 900 |
| msa123961.2{80_2603} | TTGATAACCA | AAATACATTA | AAAATTACGT | TTAAACCAGA | GAAATTTAAA |
| msa123961.2{80_A909} | TTGATAACCA | AAATACATTA | AAAATTACGT | TTAAACCAGA | GAAATTTAAA |
| msa123961.2{80_M732} | TTGATAACCA | AAATACATTA | AAAATTACGT | TTAAACCAGA | GAAATTTAAA |
| msa123961.2{80_090} | TTGATAACCA | AAATACATTA | AAAATTACGT | TTAAACCAGA | GAAATTTAAA |
| msa123961.2{80_COH1} | TTGATAACCA | AAATACATTA | AAAATTACGT | TTAAACCAGA | GAAATTTAAA |
| msa123961.2{80_M781} | TTGATAACCA | AAATACATTA | AAAATTACGT | TTAAACCAGA | GAAATTTAAA |
| msa123961.2{801_JM9130013} | TTGATAACCA | AAATACATTA | AAAATTACGT | TTAAACCAGA | GAAATTTAAA |
| msa123961.2{80_18RS21} | TTGATAACCA | AAATACATTA | AAAATTACGT | TTAAACCAGA | GAAATTTAAA |
| msa123961.2{80h_CJB110} | TTGATAACCA | AAATACATTA | AAAATTACGT | TTAAACCAGA | GAAATTTAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 901 | | | | 950 |
| msa123961.2{80_2603} | GAAATTGCTG | AGCTACTTAA | AGGAATGACC | CTTGTAAAA | ATCAAGATGC |
| msa123961.2{80_A909} | GAAATTGCTG | AGCTACTTAA | AGGAATGACC | CTTGTAAAA | ATCAAGATGC |
| msa123961.2{80_M732} | GAAATTGCTG | AGCTACTTAA | AGGAATGACC | CTTGTAAAA | ATCAAGATGC |
| msa123961.2{80_090} | GAAATTGCTG | AGCTACTTAA | AGGAATGACC | CTTGTAAAA | ATCAAGATGC |
| msa123961.2{80_COH1} | GAAATTGCTG | AGCTACTTAA | AGGAATGACC | CTTGTAAAA | ATCAAGATGC |
| msa123961.2{80_M781} | GAAATTGCTG | AGCTACTTAA | AGGAATGACC | CTTGTAAAA | ATCAAGATGC |
| msa123961.2{801_JM9130013} | GAAATTGCTG | AGCTACTTAA | AGGAATGACC | CTTGTAAAA | ATCAAGATGC |
| msa123961.2{80_18RS21} | GAAATTGCTG | AGCTACTTAA | AGGAATGACC | CTTGTAAAA | ATCAAGATGC |
| msa123961.2{80h_CJB110} | GAAATTGCTG | AGCTACTTAA | AGGAATGACC | CTTGTAAAA | ATCAAGATGC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 951 | | | | 1000 |
| msa123961.2{80_2603} | TCCTGATAAA | GCTACTGCAA | ATACAGATGA | TGCGGCATT | TTGGAAATTC |
| msa123961.2{80_A909} | TCCTGATAAA | GCTACTGCAA | ATACAGATGA | TGCGGCATT | TTGGAAATTC |
| msa123961.2{80_M732} | TCCTGATAAA | GCTACTGCAA | ATACAGATGA | TGCGGCATT | TTGGAAATTC |
| msa123961.2{80_090} | TCCTGATAAA | GCTACTGCAA | ATACAGATGA | TGCGGCATT | TTGGAAATTC |
| msa123961.2{80_COH1} | TCCTGATAAA | GCTACTGCAA | ATACAGATGA | TGCGGCATT | TTGGAAATTC |
| msa123961.2{80_M781} | TCCTGATAAA | GCTACTGCAA | ATACAGATGA | TGCGGCATT | TTGGAAATTC |
| msa123961.2{801_JM9130013} | TCCTGATAAA | GCTACTGCAA | ATACAGATGA | TGCGGCATT | TTGGAAATTC |
| msa123961.2{80_18RS21} | TCCTGATAAA | GCTACTGCAA | ATACAGATGA | TGCGGCATT | TTGGAAATTC |
| msa123961.2{80h_CJB110} | TCCTGATAAA | GCTACTGCAA | ATACAGATGA | TGCGGCATT | TTGGAAATTC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 1001 | | | | 1050 |
| msa123961.2{80_2603} | CAGTTGCATC | AACATTAAAT | GAAAAAGCAG | TTTTAGGAAA | AGCAATTGAA |
| msa123961.2{80_A909} | CAGTTGCATC | AACATTAAAT | GAAAAAGCAG | TTTTAGGAAA | AGCAATTGAA |
| msa123961.2{80_M732} | CAGTTGCATC | AACATTAAAT | GAAAAAGCAG | TTTTAGGAAA | AGCAATTGAA |
| msa123961.2{80_090} | CAGTTGCATC | AACATTAAAT | GAAAAAGCAG | TTTTAGGAAA | AGCAATTGAA |
| msa123961.2{80_COH1} | CAGTTGCATC | AACATTAAAT | GAAAAAGCAG | TTTTAGGAAA | AGCAATTGAA |
| msa123961.2{80_M781} | CAGTTGCATC | AACATTAAAT | GAAAAAGCAG | TTTTAGGAAA | AGCAATTGAA |
| msa123961.2{801_JM9130013} | CAGTTGCATC | AACATTAAAT | GAAAAAGCAG | TTTTAGGAAA | AGCAATTGAA |
| msa123961.2{80_18RS21} | CAGTTGCATC | AACATTAAAT | GAAAAAGCAG | TTTTAGGAAA | AGCAATTGAA |
| msa123961.2{80h_CJB110} | CAGTTGCATC | AACATTAAAT | GAAAAAGCAG | TTTTAGGAAA | AGCAATTGAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 1051 | | | | 1100 |
| msa123961.2{80_2603} | AATACITTTG | AACITCAATA | TGACCATACT | CCTGATAAAG | CTGACAATCC |
| msa123961.2{80_A909} | AATACITTTG | AACITCAATA | TGACCATACT | CCTGATAAAG | CTGACAATCC |
| msa123961.2{80_M732} | AATACITTTG | AACITCAATA | TGACCATACT | CCTGATAAAG | CTGACAATCC |
| msa123961.2{80_090} | AATACITTTG | AACITCAATA | TGACCATACT | CCTGATAAAG | CTGACAATCC |
| msa123961.2{80_COH1} | AATACITTTG | AACITCAATA | TGACCATACT | CCTGATAAAG | CTGACAATCC |
| msa123961.2{80_M781} | AATACITTTG | AACITCAATA | TGACCATACT | CCTGATAAAG | CTGACAATCC |
| msa123961.2{801_JM9130013} | AATACITTTG | AACITCAATA | TGACCATACT | CCTGATAAAG | CTGACAATCC |
| msa123961.2{80_18RS21} | AATACITTTG | AACITCAATA | TGACCATACT | CCTGATAAAG | CTGACAATCC |
| msa123961.2{80h_CJB110} | AATACITTTG | AACITCAATA | TGACCATACT | CCTGATAAAG | CTGACAATCC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 1101 | | | | 1150 |
| msa123961.2{80_2603} | AAAACCATCT | AATCCTCCAA | GAAAACCAGA | AGTTCATACT | GGTGGGAAAC |
| msa123961.2{80_A909} | AAAACCATCT | AATCCTCCAA | GAAAACCAGA | AGTTCATACT | GGTGGGAAAC |
| msa123961.2{80_M732} | AAAACCATCT | AATCCTCCAA | GAAAACCAGA | AGTTCATACT | GGTGGGAAAC |
| msa123961.2{80_090} | AAAACCATCT | AATCCTCCAA | GAAAACCAGA | AGTTCATACT | GGTGGGAAAC |
| msa123961.2{80_COH1} | AAAACCATCT | AATCCTCCAA | GAAAACCAGA | AGTTCATACT | GGTGGGAAAC |
| msa123961.2{80_M781} | AAAACCATCT | AATCCTCCAA | GAAAACCAGA | AGTTCATACT | GGTGGGAAAC |
| msa123961.2{801_JM9130013} | AAAACCATCT | AATCCTCCAA | GAAAACCAGA | AGTTCATACT | GGTGGGAAAC |
| msa123961.2{80_18RS21} | AAAACCATCT | AATCCTCCAA | GAAAACCAGA | AGTTCATACT | GGTGGGAAAC |
| msa123961.2{80h_CJB110} | AAAACCATCT | AATCCTCCAA | GAAAACCAGA | AGTTCATACT | GGTGGGAAAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 1151 | | | | 1200 |
| msa123961.2{80_2603} | GATTTGTAAA | GAAAGACTCA | ACAGAAACAC | AAACACTAGG | TGGTGCTGAG |
| msa123961.2{80_A909} | GATTTGTAAA | GAAAGACTCA | ACAGAAACAC | AAACACTAGG | TGGTGCTGAG |
| msa123961.2{80_M732} | GATTTGTAAA | GAAAGACTCA | ACAGAAACAC | AAACACTAGG | TGGTGCTGAG |
| msa123961.2{80_090} | GATTTGTAAA | GAAAGACTCA | ACAGAAACAC | AAACACTAGG | TGGTGCTGAG |
| msa123961.2{80_COH1} | GATTTGTAAA | GAAAGACTCA | ACAGAAACAC | AAACACTAGG | TGGTGCTGAG |

Table 87: Comparative Sequences relating to SAG0645

| | | | | | |
|----------------------------|------------|------------|-------------|------------|-------------|
| msa123961.2{80_M781} | GATTGTGAAA | GAAAGACTCA | ACAGAAACAC | AAACACTAGG | TGGTGCCTGAG |
| msa123961.2{801_JM9130013} | GATTGTGAAA | GAAAGACTCA | ACAGAAACAC | AAACACTAGG | TGGTGCCTGAG |
| msa123961.2{80_18RS21} | GATTGTGAAA | GAAAGACTCA | ACAGAAACAC | AAACACTAGG | TGGTGCCTGAG |
| msa123961.2{80h_CJB110} | GATTGTGAAA | GAAAGACTCA | ACAGAAACAC | AAACACTAGG | TGGTGCCTGAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | TTTGATTTGT | TGGCTTCTGA | TGGGACAGCA | GTAAAATGGA | CAGATGCTCT |
| msa123961.2{80_A909} | TTTGATTTGT | TGGCTTCTGA | TGGGACAGCA | GTAAAATGGA | CAGATGCTCT |
| msa123961.2{80_M732} | TTTGATTTGT | TGGCTTCTGA | TGGGACAGCA | GTAAAATGGA | CAGATGCTCT |
| msa123961.2{80_090} | TTTGATTTGT | TGGCTTCTGA | TGGGACAGCA | GTAAAATGGA | CAGATGCTCT |
| msa123961.2{80_COH1} | TTTGATTTGT | TGGCTTCTGA | TGGGACAGCA | GTAAAATGGA | CAGATGCTCT |
| msa123961.2{80_M781} | TTTGATTTGT | TGGCTTCTGA | TGGGACAGCA | GTAAAATGGA | CAGATGCTCT |
| msa123961.2{801_JM9130013} | TTTGATTTGT | TGGCTTCTGA | TGGGACAGCA | GTAAAATGGA | CAGATGCTCT |
| msa123961.2{80_18RS21} | TTTGATTTGT | TGGCTTCTGA | TGGGACAGCA | GTAAAATGGA | CAGATGCTCT |
| msa123961.2{80h_CJB110} | TTTGATTTGT | TGGCTTCTGA | TGGGACAGCA | GTAAAATGGA | CAGATGCTCT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | TATTAAAGCG | AATACTAATA | AAAACATATAT | TGCTGGAGAA | GCTGTTACTG |
| msa123961.2{80_A909} | TATTAAAGCG | AATACTAATA | AAAACATATAT | TGCTGGAGAA | GCTGTTACTG |
| msa123961.2{80_M732} | TATTAAAGCG | AATACTAATA | AAAACATATAT | TGCTGGAGAA | GCTGTTACTG |
| msa123961.2{80_090} | TATTAAAGCG | AATACTAATA | AAAACATATAT | TGCTGGAGAA | GCTGTTACTG |
| msa123961.2{80_COH1} | TATTAAAGCG | AATACTAATA | AAAACATATAT | TGCTGGAGAA | GCTGTTACTG |
| msa123961.2{80_M781} | TATTAAAGCG | AATACTAATA | AAAACATATAT | TGCTGGAGAA | GCTGTTACTG |
| msa123961.2{801_JM9130013} | TATTAAAGCG | AATACTAATA | AAAACATATAT | TGCTGGAGAA | GCTGTTACTG |
| msa123961.2{80_18RS21} | TATTAAAGCG | AATACTAATA | AAAACATATAT | TGCTGGAGAA | GCTGTTACTG |
| msa123961.2{80h_CJB110} | TATTAAAGCG | AATACTAATA | AAAACATATAT | TGCTGGAGAA | GCTGTTACTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | GGCAACCAAT | CAAATTGAAA | TCACATACAG | ACGGTACGTT | TGAGATTAAA |
| msa123961.2{80_A909} | GGCAACCAAT | CAAATTGAAA | TCACATACAG | ACGGTACGTT | TGAGATTAAA |
| msa123961.2{80_M732} | GGCAACCAAT | CAAATTGAAA | TCACATACAG | ACGGTACGTT | TGAGATTAAA |
| msa123961.2{80_090} | GGCAACCAAT | CAAATTGAAA | TCACATACAG | ACGGTACGTT | TGAGATTAAA |
| msa123961.2{80_COH1} | GGCAACCAAT | CAAATTGAAA | TCACATACAG | ACGGTACGTT | TGAGATTAAA |
| msa123961.2{80_M781} | GGCAACCAAT | CAAATTGAAA | TCACATACAG | ACGGTACGTT | TGAGATTAAA |
| msa123961.2{801_JM9130013} | GGCAACCAAT | CAAATTGAAA | TCACATACAG | ACGGTACGTT | TGAGATTAAA |
| msa123961.2{80_18RS21} | GGCAACCAAT | CAAATTGAAA | TCACATACAG | ACGGTACGTT | TGAGATTAAA |
| msa123961.2{80h_CJB110} | GGCAACCAAT | CAAATTGAAA | TCACATACAG | ACGGTACGTT | TGAGATTAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | GGTTTGGCTT | ATGCAGTTGA | TGCGAATGCA | GAGGGTACAG | CAGTAACCTA |
| msa123961.2{80_A909} | GGTTTGGCTT | ATGCAGTTGA | TGCGAATGCA | GAGGGTACAG | CAGTAACCTA |
| msa123961.2{80_M732} | GGTTTGGCTT | ATGCAGTTGA | TGCGAATGCA | GAGGGTACAG | CAGTAACCTA |
| msa123961.2{80_090} | GGTTTGGCTT | ATGCAGTTGA | TGCGAATGCA | GAGGGTACAG | CAGTAACCTA |
| msa123961.2{80_COH1} | GGTTTGGCTT | ATGCAGTTGA | TGCGAATGCA | GAGGGTACAG | CAGTAACCTA |
| msa123961.2{80_M781} | GGTTTGGCTT | ATGCAGTTGA | TGCGAATGCA | GAGGGTACAG | CAGTAACCTA |
| msa123961.2{801_JM9130013} | GGTTTGGCTT | ATGCAGTTGA | TGCGAATGCA | GAGGGTACAG | CAGTAACCTA |
| msa123961.2{80_18RS21} | GGTTTGGCTT | ATGCAGTTGA | TGCGAATGCA | GAGGGTACAG | CAGTAACCTA |
| msa123961.2{80h_CJB110} | GGTTTGGCTT | ATGCAGTTGA | TGCGAATGCA | GAGGGTACAG | CAGTAACCTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | CAAATTAAAA | GAAACAAAAG | CACCAGAAGG | TTATGTAATC | CCTGATAAAG |
| msa123961.2{80_A909} | CAAATTAAAA | GAAACAAAAG | CACCAGAAGG | TTATGTAATC | CCTGATAAAG |
| msa123961.2{80_M732} | CAAATTAAAA | GAAACAAAAG | CACCAGAAGG | TTATGTAATC | CCTGATAAAG |
| msa123961.2{80_090} | CAAATTAAAA | GAAACAAAAG | CACCAGAAGG | TTATGTAATC | CCTGATAAAG |
| msa123961.2{80_COH1} | CAAATTAAAA | GAAACAAAAG | CACCAGAAGG | TTATGTAATC | CCTGATAAAG |
| msa123961.2{80_M781} | CAAATTAAAA | GAAACAAAAG | CACCAGAAGG | TTATGTAATC | CCTGATAAAG |
| msa123961.2{801_JM9130013} | CAAATTAAAA | GAAACAAAAG | CACCAGAAGG | TTATGTAATC | CCTGATAAAG |
| msa123961.2{80_18RS21} | CAAATTAAAA | GAAACAAAAG | CACCAGAAGG | TTATGTAATC | CCTGATAAAG |
| msa123961.2{80h_CJB110} | CAAATTAAAA | GAAACAAAAG | CACCAGAAGG | TTATGTAATC | CCTGATAAAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | AAATCGAGTT | TACAGTATCA | CAAACATCTT | ATAATaCAAA | ACCAACTGAC |
| msa123961.2{80_A909} | AAATCGAGTT | TACAGTATCA | CAAACATCTT | ATAATaCAAA | ACCAACTGAC |
| msa123961.2{80_M732} | AAATCGAGTT | TACAGTATCA | CAAACATCTT | ATAATaCAAA | ACCAACTGAC |
| msa123961.2{80_090} | AAATCGAGTT | TACAGTATCA | CAAACATCTT | ATAATaCAAA | ACCAACTGAC |
| msa123961.2{80_COH1} | AAATCGAGTT | TACAGTATCA | CAAACATCTT | ATAATaCAAA | ACCAACTGAC |
| msa123961.2{80_M781} | AAATCGAGTT | TACAGTATCA | CAAACATCTT | ATAATaCAAA | ACCAACTGAC |
| msa123961.2{801_JM9130013} | AAATCGAGTT | TACAGTATCA | CAAACATCTT | ATAATaCAAA | ACCAACTGAC |
| msa123961.2{80_18RS21} | AAATCGAGTT | TACAGTATCA | CAAACATCTT | ATAATaCAAA | ACCAACTGAC |
| msa123961.2{80h_CJB110} | AAATCGAGTT | TACAGTATCA | CAAACATCTT | ATAATaCAAA | ACCAACTGAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | ATCACGGTTG | ATAGTGCTGA | TGCAACACCT | GATACAATTA | AAAACAACAA |
| msa123961.2{80_A909} | ATCACGGTTG | ATAGTGCTGA | TGCAACACCT | GATACAATTA | AAAACAACAA |
| msa123961.2{80_M732} | ATCACGGTTG | ATAGTGCTGA | TGCAACACCT | GATACAATTA | AAAACAACAA |
| msa123961.2{80_090} | ATCACGGTTG | ATAGTGCTGA | TGCAACACCT | GATACAATTA | AAAACAACAA |

Table 87: Comparative Sequences relating to SAG0645

| | | | | | |
|----------------------------|------------|-------------|-------------|------------|------------|
| msa123961.2{80_COH1} | ATCACGGTTG | ATAGTGCTGA | TGCAACACCT | GATACAATTA | AAAACAACAA |
| msa123961.2{80_M781} | ATCACGGTTG | ATAGTGCTGA | TGCAACACCT | GATACAATTA | AAAACAACAA |
| msa123961.2{801_JM9130013} | ATCACGGTTG | ATAGTGCTGA | TGCAACACCT | GATACAATTA | AAAACAACAA |
| msa123961.2{80_18RS21} | ATCACGGTTG | ATAGTGCTGA | TGCAACACCT | GATACAATTA | AAAACAACAA |
| msa123961.2{80h_CJB110} | ATCACGGTTG | ATAGTGCTGA | TGCAACACCT | GATACAATTA | AAAACAACAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa123961.2{80_2603} | acgtccttca | atccctaata | ctgggtggtat | tggtacggct | atctttgtcg |
| msa123961.2{80_A909} | acgtccttca | ----- | ----- | ----- | ----- |
| msa123961.2{80_M732} | acgtccttca | ----- | ----- | ----- | ----- |
| msa123961.2{80_090} | acgtccttca | ----- | ----- | ----- | ----- |
| msa123961.2{80_COH1} | acgtccttca | ----- | ----- | ----- | ----- |
| msa123961.2{80_M781} | acgtccttca | ----- | ----- | ----- | ----- |
| msa123961.2{801_JM9130013} | acgtccttca | ----- | ----- | ----- | ----- |
| msa123961.2{80_18RS21} | acgtccttca | ----- | ----- | ----- | ----- |
| msa123961.2{80h_CJB110} | acgtccttca | ----- | ----- | ----- | ----- |
| Consensus | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_2603} | ctatcggtgc | tgccggtgatg | gcttttgcgtg | ttaaggggat | gaagcgtcgt |
| msa123961.2{80_A909} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_M732} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_090} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_COH1} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_M781} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{801_JM9130013} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_18RS21} | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80h_CJB110} | ----- | ----- | ----- | ----- | ----- |
| Consensus | ----- | ----- | ----- | ----- | ----- |
| msa123961.2{80_2603} | acaaaagata | ac | | | |
| msa123961.2{80_A909} | ----- | -- | | | |
| msa123961.2{80_M732} | ----- | -- | | | |
| msa123961.2{80_090} | ----- | -- | | | |
| msa123961.2{80_COH1} | ----- | -- | | | |
| msa123961.2{80_M781} | ----- | -- | | | |
| msa123961.2{801_JM9130013} | ----- | -- | | | |
| msa123961.2{80_18RS21} | ----- | -- | | | |
| msa123961.2{80h_CJB110} | ----- | -- | | | |
| Consensus | ----- | -- | | | |

SEQ ID NO. 8710

STRAIN 2603 frame: 1

MKLSKKLFLSAAVLTVMAGSTVEPVAQFATGMSIVRAAEVSQERPAKTTVNIYKLQADSY
 KSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFKRYKVKTDISVDELKKLTVEAAD
 AKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLYVEDLKNSPSNITKAYAVPFVLEL
 PVANSTGTGFLSEINIYPKNVVTDEPKTDKDKVKKLGQDDAGYTI GEEFKWFLKSTIPANL
 GDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNQTLLKITFKPEKFK
 EIAELLKGMTLVKNQDALDKATANTDDAAFLIPVASTINEKAVLGKAIENTFELQYDHT
 PDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLGGAEFDLLASDGTAVKWTDALIKA
 NTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVDANAEGTAVTYKLKETKAPEGYVI
 PDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNKRPSIPTGGIGTAIFVAIGAAMV
 AFAVKGMRRTKDN

SEQ ID NO. 8711

STRAIN 090 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLEL PVANSTGTGFLSEINIYPKNVVTDEPKTDKDKVKKLGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQTLLKITFKPEKFK EIAELLKGMTLVKNQDALDKATANTDDAAFLIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8712

STRAIN 18RS21 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLEL PVANSTGTGFLSEINIYPKNVVTDEPKTDKDKVKKLGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQTLLKITFKPEKFK EIAELLKGMTLVKNQDALDKATANTDDAAFLIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8713

STRAIN M732 frame: 1

AEVSQERPAKTTVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK

Table 87: Comparative Sequences relating to SAG0645

RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLETKAPEGYVIPDKEIEFTVSQTSYNTKPTDIITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8714

STRAIN M781 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLETKAPEGYVIPDKEIEFTVSQTSYNTKPTDIITVDSADATPDTIKNNK
R

SEQ ID NO. 8715

STRAIN COH1 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLETKAPEGYVIPDKEIEFTVSQTSYNTKPTDIITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8716

STRAIN CJB110 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLETKAPEGYVIPDKEIEFTVSQTSYNTKPTDIITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8717

STRAIN JM9130013 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLETKAPEGYVIPDKEIEFTVSQTSYNTKPTDIITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8718

STRAIN A909 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLETKAPEGYVIPDKEIEFTVSQTSYNTKPTDIITVDSADATPDTIKNNK

PRETTY of: /biotmp/msa124060.2{*} April 30, 2003 07:19 ..

| | | | |
|----------------------------|--|------------|------------|
| | 1 | | 50 |
| msa124060.2{80_2603} | mklskklifs aavltmvags tvepvafat gmsivraAEV | SQERPAKTTv | |
| msa124060.2{80_M732} | ----- | -----AEV | SQERPAKTTv |
| msa124060.2{80_A909} | ----- | -----AEV | SQERPAKTTv |
| msa124060.2{80_090} | ----- | -----AEV | SQERPAKTTv |
| msa124060.2{80_M781} | ----- | -----AEV | SQERPAKTTv |
| msa124060.2{80_COH1} | ----- | -----AEV | SQERPAKTTv |
| msa124060.2{801_JM9130013} | ----- | -----AEV | SQERPAKTTv |
| msa124060.2{80_18RS21} | ----- | -----AEV | SQERPAKTTv |
| msa124060.2{80h_CJB110} | ----- | -----AEV | SQERPAKTTv |
| Consensus | ----- | -----*** | ***** |

Table 87: Comparative Sequences relating to SAG0645

| | | | |
|----------------------------|---|--|-----|
| | 51 | | 100 |
| msa124060.2{80_2603} | NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK | | |
| msa124060.2{80_M732} | NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK | | |
| msa124060.2{80_A909} | NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK | | |
| msa124060.2{80_090} | NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK | | |
| msa124060.2{80_M781} | NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK | | |
| msa124060.2{80_COH1} | NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK | | |
| msa124060.2{801_JM9130013} | NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK | | |
| msa124060.2{80_18RS21} | NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK | | |
| msa124060.2{80h_CJB110} | NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK | | |
| Consensus | ***** *--*--*--* ***** ***** ***** ***** | | |
| | 101 | | 150 |
| msa124060.2{80_2603} | VKTDISVDEL/ KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK | | |
| msa124060.2{80_M732} | VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK | | |
| msa124060.2{80_A909} | VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK | | |
| msa124060.2{80_090} | VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK | | |
| msa124060.2{80_M781} | VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK | | |
| msa124060.2{80_COH1} | VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK | | |
| msa124060.2{801_JM9130013} | VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK | | |
| msa124060.2{80_18RS21} | VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK | | |
| msa124060.2{80h_CJB110} | VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK | | |
| Consensus | ***** ***** ***** ***** ***** ***** | | |
| | 151 | | 200 |
| msa124060.2{80_2603} | SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN | | |
| msa124060.2{80_M732} | SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN | | |
| msa124060.2{80_A909} | SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN | | |
| msa124060.2{80_090} | SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN | | |
| msa124060.2{80_M781} | SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN | | |
| msa124060.2{80_COH1} | SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN | | |
| msa124060.2{801_JM9130013} | SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN | | |
| msa124060.2{80_18RS21} | SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN | | |
| msa124060.2{80h_CJB110} | SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN | | |
| Consensus | ***** ***** ***** ***** ***** ***** | | |
| | 201 | | 250 |
| msa124060.2{80_2603} | VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD | | |
| msa124060.2{80_M732} | VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD | | |
| msa124060.2{80_A909} | VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD | | |
| msa124060.2{80_090} | VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD | | |
| msa124060.2{80_M781} | VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD | | |
| msa124060.2{80_COH1} | VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD | | |
| msa124060.2{801_JM9130013} | VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD | | |
| msa124060.2{80_18RS21} | VVTDEPKTDK DVK.LGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD | | |
| msa124060.2{80h_CJB110} | VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD | | |
| Consensus | ***** ***-***** ***** ***** ***** ***** | | |
| | 251 | | 300 |
| msa124060.2{80_2603} | KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK | | |
| msa124060.2{80_M732} | KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK | | |
| msa124060.2{80_A909} | KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK | | |
| msa124060.2{80_090} | KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK | | |
| msa124060.2{80_M781} | KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK | | |
| msa124060.2{80_COH1} | KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK | | |
| msa124060.2{801_JM9130013} | KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK | | |
| msa124060.2{80_18RS21} | KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK | | |
| msa124060.2{80h_CJB110} | KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK | | |
| Consensus | ***** ***** ***** ***** ***** ***** | | |
| | 301 | | 350 |
| msa124060.2{80_2603} | EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE | | |
| msa124060.2{80_M732} | EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE | | |
| msa124060.2{80_A909} | EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE | | |
| msa124060.2{80_090} | EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE | | |
| msa124060.2{80_M781} | EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE | | |
| msa124060.2{80_COH1} | EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE | | |
| msa124060.2{801_JM9130013} | EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE | | |
| msa124060.2{80_18RS21} | EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE | | |
| msa124060.2{80h_CJB110} | EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE | | |
| Consensus | ***** ***** ***** ***** ***** ***** | | |
| | 351 | | 400 |
| msa124060.2{80_2603} | NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE | | |
| msa124060.2{80_M732} | NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE | | |
| msa124060.2{80_A909} | NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE | | |
| msa124060.2{80_090} | NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE | | |
| msa124060.2{80_M781} | NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE | | |
| msa124060.2{80_COH1} | NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE | | |
| msa124060.2{801_JM9130013} | NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE | | |
| msa124060.2{80_18RS21} | NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE | | |
| msa124060.2{80h_CJB110} | NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE | | |
| Consensus | ***** ***** ***** ***** ***** ***** | | |

Table 87: Comparative Sequences relating to SAG0645

| | | | | |
|----------------------------|------------|-------------|------------|------------------------|
| | 401 | | | 450 |
| msa124060.2{80_2603} | FDLLASDGTA | VKWTDALIKA | NTNKNYIAGE | AVTGQPIKLLK SHTDGTFEIK |
| msa124060.2{80_M732} | FDLLASDGTA | VKWTDALIKA | NTNKNYIAGE | AVTGQPIKLLK SHTDGTFEIK |
| msa124060.2{80_A909} | FDLLASDGTA | VKWTDALIKA | NTNKNYIAGE | AVTGQPIKLLK SHTDGTFEIK |
| msa124060.2{80_090} | FDLLASDGTA | VKWTDALIKA | NTNKNYIAGE | AVTGQPIKLLK SHTDGTFEIK |
| msa124060.2{80_M781} | FDLLASDGTA | VKWTDALIKA | NTNKNYIAGE | AVTGQPIKLLK SHTDGTFEIK |
| msa124060.2{80_COH1} | FDLLASDGTA | VKWTDALIKA | NTNKNYIAGE | AVTGQPIKLLK SHTDGTFEIK |
| msa124060.2{801_JM9130013} | FDLLASDGTA | VKWTDALIKA | NTNKNYIAGE | AVTGQPIKLLK SHTDGTFEIK |
| msa124060.2{80_18RS21} | FDLLASDGTA | VKWTDALIKA | NTNKNYIAGE | AVTGQPIKLLK SHTDGTFEIK |
| msa124060.2{80h_CJB110} | FDLLASDGTA | VKWTDALIKA | NTNKNYIAGE | AVTGQPIKLLK SHTDGTFEIK |
| Consensus | ***** | ***** | ***** | ***** |
| | 451 | | | 500 |
| msa124060.2{80_2603} | GLAYAVDANA | EGTAVTYKLLK | ETKAPEGYVI | PDKEIEFTVS QTSYNtKPTD |
| msa124060.2{80_M732} | GLAYAVDANA | EGTAVTYKLLK | ETKAPEGYVI | PDKEIEFTVS QTSYNtKPTD |
| msa124060.2{80_A909} | GLAYAVDANA | EGTAVTYKLLK | ETKAPEGYVI | PDKEIEFTVS QTSYNtKPTD |
| msa124060.2{80_090} | GLAYAVDANA | EGTAVTYKLLK | ETKAPEGYVI | PDKEIEFTVS QTSYNtKPTD |
| msa124060.2{80_M781} | GLAYAVDANA | EGTAVTYKLLK | ETKAPEGYVI | PDKEIEFTVS QTSYNtKPTD |
| msa124060.2{80_COH1} | GLAYAVDANA | EGTAVTYKLLK | ETKAPEGYVI | PDKEIEFTVS QTSYNtKPTD |
| msa124060.2{801_JM9130013} | GLAYAVDANA | EGTAVTYKLLK | ETKAPEGYVI | PDKEIEFTVS QTSYNtKPTD |
| msa124060.2{80_18RS21} | GLAYAVDANA | EGTAVTYKLLK | ETKAPEGYVI | PDKEIEFTVS QTSYNtKPTD |
| msa124060.2{80h_CJB110} | GLAYAVDANA | EGTAVTYKLLK | ETKAPEGYVI | PDKEIEFTVS QTSYNpKPTD |
| Consensus | ***** | ***** | ***** | ***** |
| | 501 | | | 550 |
| msa124060.2{80_2603} | ITVDSADATP | DTIKNNkrps | ipntggigta | ifvaigaavm afavkgmkrr |
| msa124060.2{80_M732} | ITVDSADATP | DTIKNNkrps | ----- | ----- |
| msa124060.2{80_A909} | ITVDSADATP | DTIKNN---- | ----- | ----- |
| msa124060.2{80_090} | ITVDSADATP | DTIKNNkrps | ----- | ----- |
| msa124060.2{80_M781} | ITVDSADATP | DTIKNNkr-- | ----- | ----- |
| msa124060.2{80_COH1} | ITVDSADATP | DTIKNNkrps | ----- | ----- |
| msa124060.2{801_JM9130013} | ITVDSADATP | DTIKNNkrps | ----- | ----- |
| msa124060.2{80_18RS21} | ITVDSADATP | DTIKNNkrps | ----- | ----- |
| msa124060.2{80h_CJB110} | ITVDSADATP | DTIKNNkrps | ----- | ----- |
| Consensus | ***** | ***** | ----- | ----- |
| | 551 | | | |
| msa124060.2{80_2603} | tkdn | | | |
| msa124060.2{80_M732} | ---- | | | |
| msa124060.2{80_A909} | ---- | | | |
| msa124060.2{80_090} | ---- | | | |
| msa124060.2{80_M781} | ---- | | | |
| msa124060.2{80_COH1} | ---- | | | |
| msa124060.2{801_JM9130013} | ---- | | | |
| msa124060.2{80_18RS21} | ---- | | | |
| msa124060.2{80h_CJB110} | ---- | | | |
| Consensus | ---- | | | |

Table 88: Comparative Sequences relating to SAG0477

SEQ ID NO. 8801

STRAIN 2603

ATGCCCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATTGTCTTAACGGAATGGCAA
 AAGCGTAACCTTGAATTTTAAAAAACGCAAGAGATGAAGAAGAACAAAAACGTATT
 AACGAAAAATTACGCTTAGATAAAAAGAGTAAATTAATATTCTCTCCTGAAGAACCT
 CAAATACTACTAAAATTAAGAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAACTAATCGCATTAGAACT
 GCACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTCCGTTTTCCTACTAATCCT
 TTTAGTAAGCAAAAAACAAATACAGTTAGTGGAAATCAGCATACCTGATGATATTTTG
 ATAGAGAAAAACGAAATATTCAAAAAACGATTAATTTCTTTCTTTAATTTTAAACATAAA
 GCTATTGAACAACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATGTCATATGCACAT
 ACAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAGGCTGATCCTGTAAATAGT
 TCAGAGCTACCAAGCACTTCTTAACAATTAACCTTGATAAGGAAGATAGATTAAAGCTA
 TTAATTAAAGATTAAAGGCTTTAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGT
 TTAGCTGATTCTAAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGT
 ATTAGAATACCAATTCTAAATTTAAAGAAAGACTTCTCTTTTACAAACAATTAAGAAG
 AACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAAATACC
 ATTGAATCAACCCCTGTAAAGCAGAAGATACAAAAATAAATCAACTGATAAAACACAA
 ACACAAATGGTCAGGTTGCGGAAATAGTCAAGGACAAACAAATAACTCAAACTAAT
 CAACAAGGACACAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8802

STRAIN H36B

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTCTCTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAGACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAACTAATCGCA
 TTAGAAGCTGACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTTCC
 GTTTTCTCTACTAATCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTGTAGAGAAAAACGAATATTCAAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAG
 GCTGATCCTGTAAATAGTTTCAAGCTACCAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAATAACCATTTGAATCAACCCCTGTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAAACACAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAATAACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8803

STRAIN 18RS21

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTCTCTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAGACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAACTAATCGCA
 TTAGAAGCTGACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTTCC
 GTTTTCTCTACTAATCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTGTAGAGAAAAACGAATATTCAAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAG
 GCTGATCCTGTAAATAGTTTCAAGCTACCAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAATAACCATTTGAATCAACCCCTGTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAAACACAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAATAACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8804

STRAIN M732

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAG
 TTGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAAGAGTAAATTAATATTCTCTCTCCTGAAGAACCTCAAAATACTA
 CTAAAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAACTAATCG
 CATTAGAAGTGCACCTATATTGTAGTAGCATTCCTAGTCATTTAGTTT

Table 88: Comparative Sequences relating to SAG0477

CCGTTTTCCTACTAAGTCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC
 ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAA
 AGGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATT
 CTAAAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTCTTTTACAAACA
 AATTAAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAATAAATAAATACTGATAAAACACAAACACAAATGGTCAGGTTGC
 GGAAATAGTCAAGGACAAACAATAAATCAATACTAATACTAATAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8805

STRAIN COH1

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAGTT
 GTCTTAACCGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTTCTTCTCTCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCAATTTCCAAAGATTTCAAAACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACATAATCGCA
 TTAGAACTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTTCC
 GTTTTCTCTACTAAGTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCAAA
 AAAACGATTATTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAAAG
 GCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATAC
 AAAAAATAAATAAATACTGATAAAACACAAACACAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAATAAATCAATACTAATACTAATAAGGACAA
 CAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8806

STRAIN M781

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAG
 TTGTCTTAACCGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTTCTTCTCTCTGAAGAACCTCAAAATACTA
 CTAAATTAAGAAGCTTCAATTTCCAAAGATTTCAAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACATAATCG
 CATTAGAAGTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTT
 CCGTTTTCCTACTAAGTCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC
 ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAA
 AGGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATT
 CTAAAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTACAAACA
 AATTAAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAATAAATAAATACTGATAAAACACAAACACAAATGGTCAGGTTGC
 GGAAATAGTCAAGGACAAACAATAAATCAATACTAATACTAATAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8807

STRAIN CJB110

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAG
 TTGTCTTAACCGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTTCTTCTCTCTGAAGAACCTCAAAATACTA
 CTAAATTAAGAAGCTTCAATTTCCAAAGATTTCAAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACATAATCG
 CATTAGAAGTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTT
 CCGTTTTCCTACTAAGTCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC

Table 88: Comparative Sequences relating to SAG0477

ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAA
 AGGCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCTGATTTAATAAGTGAGATTAGGTTAGCTGATT
 CTAACACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGT
 ATTAGAATACCATTATCTAAATTTAAAGAAAGACTTCTTTTACAAACA
 AATTAAAGAAAGCCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 AAAAAAATAAATCAACTGATAAAAACAACAACAAAATGGTCAGGTTGC
 GAAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCCAACCTCAAAATGTTAAT

SEQ ID NO. 8808

STRAIN 1169NT

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAAGT
 TGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCA
 AAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGAT
 AAAAGAAGTAAATTAATATTCTTCTCCTGAAGAACCTCAAAATACTAC
 TAAATTAAGAAGCTTCATTTTCCAAAGATTCAAAACCTAAGATTGAAA
 AGAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGC
 ATTAGAAGCTGCACCTATATTTAGTAGCATTCTAGTCATTTAGTTTC
 CGTTTTCTACTAAGCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTG
 GAAATCAGCATACACCTGATGATATTTGATAGAGAAAAAGCAATATTCAA
 AAAACGATTATTCTTTCTTTAATTTTAAACATAAAGCTATTGAACA
 ACCTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATC
 AATTTCCCAACAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCA
 TATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAA
 GGCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTA
 ACCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGCT
 TTAGACCTGATTAAATAAGTGAGATTAGGTTGATAAGTTTAGCTGATT
 TAAAAAGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTA
 TTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAA
 ATTAAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGT
 TTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATA
 CAAAAAATAAATCAACTGATAAAAACAACCCAAAATGGTCAGGTTGCG
 GAAAAATAGTCAAGGACAAACAAATACTCAAATACTAATCAACAAGGACA
 ACAACAGATAGCAACGAGCAGGCACCCCAACCTCAAAATGTTAAT

SEQ ID NO. 8809

STRAIN JM9130013

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAAGT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCA
 AAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAAGAAGTAAATTAATATTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGCA
 TTAGAAGCTGCACCTATATTGTTAGTAGCATTCTAGTCATTTAGTTTCC
 GTTTTCTACTAAGCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTGATAGAGAAAAAGCAATATTCAA
 AAAACGATTATTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAAG
 CCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTA
 CCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTAGGTTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGT
 TACACAACAACAATAACCTTGAATCAACCCCTGTTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATAAAAACAACAACAAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATACTCAAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8810

STRAIN A909

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAAGTGTCT
 TTAACGGAATGGCAAAAGCGTAACCTTGAATTTTaaAAAAACGCAAGA
 AGATGAAGAAGAAaCAAAAAACGTATTACGAAAAATTACGCTTAGATAAAA
 GAAGTAAATTAATATTCTTCTCCTGAAGAACCTCAAAATACTACTAA
 ATTAAGAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAAAAGAA
 ACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGCATTA
 GAAGTGCACCTATATTGTTAGTAGCATTCTAGTCATTTTAGTTTCCGTT
 TTCTCTAAGCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGGAAA
 TCAGCATACACCTGATGATATTTGATAGAGAAAAAGCAATATTCAAAAA
 ACGATTATTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAACGT
 TTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATT
 TCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCATATG
 CACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAAGGCT
 GATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTAACCT
 TGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGCTTTAG
 ACCTGATTAAATAAGTGAGATTAGGTTGATAAGTTTAGCTGATTCTAAA
 ACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTATTAA

Table 88: Comparative Sequences relating to SAG0477

AATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAATTA
 AGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTAC
 ACAACAACAAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATACAAA
 AAATAAATCAACTGATAAAACAAACCAAAATGGTCAGGTTGCGGAAA
 ATAGTCAAGGACAAACAAATAACTCAATACTAATCAACAAGGACAACAG
 ATAGCAACAGAGCAGGCACCTAACCTCAAATGTTAAT

SEQ ID NO. 8811

STRAIN 090

TAAGAAGAAATCAGATACCCAGAAAAAGAAGTTGTCTTAACGGAAT
 GGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAAGAAGATGAAGAA
 GAACAAAAACGTATTAAACGAAAAATTACGCTTAGATAAAAGAAGTaaATT
 AAATATTCTCTCTCTGAAGAACCTCAAAATACTACTAAAATTAGAAGC
 TTCATTTTCCAAAGATTTCAAACCTAAGATTGAAAAGAAACGAAAAAA
 GAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGCATTAGAAGTGCACC
 TATATTGTTAGTAGCATTCTTAGTCAATTTAGTTTCCGTTTCTCTACTAA
 CTCTTTTAGTAAGCAAAAACATAACAGTTAGTGGAAATCAGCATACA
 CCTGATGATATTTTATAGAAAAAACGAATATTCAAAAAACGATTATTT
 CTCTTTCTTAATTTTAAACATAAAGCTATTGAACAACGTTTAGCTGCAG
 AAGATGTATGGGTAACAGCTCAGATGACTTATCAATTTCCCAATAAG
 TTTCAATTTCAAGTTCAAGAAAAATAAGATTATTGCATATGCACATACAAA
 GCAAGGATATCAGCCTGTCTTGGAACTGGAAGAAAGGCTGATCCTGTAA
 ATAGTTTCAAGCTACCAAGCACTTCTTAACAATTAACCTTGATAAGGAA
 GATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTTAGACCTGATTT
 AATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATTTAAAACGACACCTG
 ACCTCCTGCTGTTAGATATGCATGATGGAATAGTATTAGAATACCATTA
 TCTAAATTTAAAGAAAGACTTCTCTTTTACAAACAAATTAAGAAGAACTT
 TAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAA
 GTACTATTGAATCAACCCCTGTGAAGCGGAAGATACAAAAATAAATCA
 ACTGATATAACACAAACCAAAATGGTCAGGTTGCGGAAAATAGTCAAGG
 ACAACAAATAACTCAATACTAATCAACAAGGACAACAGATGCAACAG
 AGCAGGCACCAACCTCAAATGTTAAT

PRETTY of: /biotmp/msa24691.2{*} August 5, 2002 05:14 ..

| | | |
|---------------------------|---|-------|
| | 1 | 50 |
| msa252409.2{85_090.con} | ~TAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA | |
| msa252409.2{85_CJB110} | CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA | |
| msa252409.2{85_COH1} | CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA | |
| msa252409.2{85_M732} | CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA | |
| msa252409.2{85_M781} | CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA | |
| msa252409.2{85_18RS21} | CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA | |
| msa252409.2{85_2603} | CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA | |
| msa252409.2{85_A909} | CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA | |
| msa252409.2{85_H36B} | CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA | |
| msa252409.2{85_JM9130013} | CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA | |
| msa252409.2{85_1169NT} | CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA | |
| Consensus | ***** | ***** |
| | 51 | 100 |
| msa252409.2{85_090.con} | ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG | |
| msa252409.2{85_CJB110} | ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG | |
| msa252409.2{85_COH1} | ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG | |
| msa252409.2{85_M732} | ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG | |
| msa252409.2{85_M781} | ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG | |
| msa252409.2{85_18RS21} | ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG | |
| msa252409.2{85_2603} | ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG | |
| msa252409.2{85_A909} | ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG | |
| msa252409.2{85_H36B} | ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG | |
| msa252409.2{85_JM9130013} | ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG | |
| msa252409.2{85_1169NT} | ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG | |
| Consensus | ***** | ***** |
| | 101 | 150 |
| msa252409.2{85_090.con} | AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA | |
| msa252409.2{85_CJB110} | AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA | |
| msa252409.2{85_COH1} | AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA | |
| msa252409.2{85_M732} | AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA | |
| msa252409.2{85_M781} | AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA | |
| msa252409.2{85_18RS21} | AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA | |
| msa252409.2{85_2603} | AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA | |
| msa252409.2{85_A909} | AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA | |
| msa252409.2{85_H36B} | AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA | |
| msa252409.2{85_JM9130013} | AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA | |
| msa252409.2{85_1169NT} | AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA | |
| Consensus | ***** | ***** |
| | 151 | 200 |
| msa252409.2{85_090.con} | TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA | |
| msa252409.2{85_CJB110} | TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA | |
| msa252409.2{85_COH1} | TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA | |
| msa252409.2{85_M732} | TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA | |

Table 88: Comparative Sequences relating to SAG0477

| | | | | | |
|---------------------------|-------------|------------|------------|------------|------------|
| msa252409.2{85_M781} | TTAAATATTT | CTTCTCCTGA | AGAACCTCAA | AATACTACTA | AAATTAAGAA |
| msa252409.2{85_18RS21} | TTAAATATTT | CTTCTCCTGA | AGAACCTCAA | AATACTACTA | AAATTAAGAA |
| msa252409.2{85_2603} | TTAAATATTT | CTTCTCCTGA | AGAACCTCAA | AATACTACTA | AAATTAAGAA |
| msa252409.2{85_A909} | TTAAATATTT | CTTCTCCTGA | AGAACCTCAA | AATACTACTA | AAATTAAGAA |
| msa252409.2{85_H36B} | TTAAATATTT | CTTCTCCTGA | AGAACCTCAA | AATACTACTA | AAATTAAGAA |
| msa252409.2{85_JM9130013} | TTAAATATTT | CTTCTCCTGA | AGAACCTCAA | AATACTACTA | AAATTAAGAA |
| msa252409.2{85_1169NT} | TTAAATATTT | CTTCTCCTGA | AGAACCTCAA | AATACTACTA | AAATTAAGAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 201 | | | | | |
| msa252409.2{85_090.con} | GCTTCATTTT | CCAAAGATTT | CAAaACCTAA | GATTGAAAAG | AAACAGAAAA |
| msa252409.2{85_CJB110} | GCTTCATTTT | CCAAAGATTT | CAAaACCTAA | GATTGAAAAG | AAACAGAAAA |
| msa252409.2{85_COH1} | GCTTCATTTT | CCAAAGATTT | CAAaACCTAA | GATTGAAAAG | AAACAGAAAA |
| msa252409.2{85_M732} | GCTTCATTTT | CCAAAGATTT | CAAaACCTAA | GATTGAAAAG | AAACAGAAAA |
| msa252409.2{85_M781} | GCTTCATTTT | CCAAAGATTT | CAAaACCTAA | GATTGAAAAG | AAACAGAAAA |
| msa252409.2{85_18RS21} | GCTTCATTTT | CCAAAGATTT | CAAaACCTAA | GATTGAAAAG | AAACAGAAAA |
| msa252409.2{85_2603} | GCTTCATTTT | CCAAAGATTT | CAAaACCTAA | GATTGAAAAG | AAACAGAAAA |
| msa252409.2{85_A909} | GCTTCATTTT | CCAAAGATTT | CAAaACCTAA | GATTGAAAAG | AAACAGAAAA |
| msa252409.2{85_H36B} | GCTTCATTTT | CCAAAGATTT | CAAaACCTAA | GATTGAAAAG | AAACAGAAAA |
| msa252409.2{85_JM9130013} | GCTTCATTTT | CCAAAGATTT | CAAaACCTAA | GATTGAAAAG | AAACAGAAAA |
| msa252409.2{85_1169NT} | GCTTCATTTT | CCAAAGATTT | CAAaACCTAA | GATTGAAAAG | AAACAGAAAA |
| Consensus | ***** | ***** | ***-***** | ***** | ***** |
| 251 | | | | | |
| msa252409.2{85_090.con} | AAGAAAAAAT | AGTCAACAGC | TTAGCCAAAA | CTAATCGCAT | TAGAACTGCA |
| msa252409.2{85_CJB110} | AAGAAAAAAT | AGTCAACAGC | TTAGCCAAAA | CTAATCGCAT | TAGAACTGCA |
| msa252409.2{85_COH1} | AAGAAAAAAT | AGTCAACAGC | TTAGCCAAAA | CTAATCGCAT | TAGAACTGCA |
| msa252409.2{85_M732} | AAGAAAAAAT | AGTCAACAGC | TTAGCCAAAA | CTAATCGCAT | TAGAACTGCA |
| msa252409.2{85_M781} | AAGAAAAAAT | AGTCAACAGC | TTAGCCAAAA | CTAATCGCAT | TAGAACTGCA |
| msa252409.2{85_18RS21} | AAGAAAAAAT | AGTCAACAGC | TTAGCCAAAA | CTAATCGCAT | TAGAACTGCA |
| msa252409.2{85_2603} | AAGAAAAAAT | AGTCAACAGC | TTAGCCAAAA | CTAATCGCAT | TAGAACTGCA |
| msa252409.2{85_A909} | AAGAAAAAAT | AGTCAACAGC | TTAGCCAAAA | CTAATCGCAT | TAGAACTGCA |
| msa252409.2{85_H36B} | AAGAAAAAAT | AGTCAACAGC | TTAGCCAAAA | CTAATCGCAT | TAGAACTGCA |
| msa252409.2{85_JM9130013} | AAGAAAAAAT | AGTCAACAGC | TTAGCCAAAA | CTAATCGCAT | TAGAACTGCA |
| msa252409.2{85_1169NT} | AAGAAAAAAT | AGTCAACAGC | TTAGCCAAAA | CTAATCGCAT | TAGAACTGCA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 301 | | | | | |
| msa252409.2{85_090.con} | CCTATATTTg | TAGTAGCATT | CCTAGTCATT | TTAGTTTCCG | TTTTCTTACT |
| msa252409.2{85_CJB110} | CCTATATTTg | TAGTAGCATT | CCTAGTCATT | TTAGTTTCCG | TTTTCTTACT |
| msa252409.2{85_COH1} | CCTATATTTg | TAGTAGCATT | CCTAGTCATT | TTAGTTTCCG | TTTTCTTACT |
| msa252409.2{85_M732} | CCTATATTTg | TAGTAGCATT | CCTAGTCATT | TTAGTTTCCG | TTTTCTTACT |
| msa252409.2{85_M781} | CCTATATTTg | TAGTAGCATT | CCTAGTCATT | TTAGTTTCCG | TTTTCTTACT |
| msa252409.2{85_18RS21} | CCTATATTTg | TAGTAGCATT | CCTAGTCATT | TTAGTTTCCG | TTTTCTTACT |
| msa252409.2{85_2603} | CCTATATTTg | TAGTAGCATT | CCTAGTCATT | TTAGTTTCCG | TTTTCTTACT |
| msa252409.2{85_A909} | CCTATATTTg | TAGTAGCATT | CCTAGTCATT | TTAGTTTCCG | TTTTCTTACT |
| msa252409.2{85_H36B} | CCTATATTTg | TAGTAGCATT | CCTAGTCATT | TTAGTTTCCG | TTTTCTTACT |
| msa252409.2{85_JM9130013} | CCTATATTTg | TAGTAGCATT | CCTAGTCATT | TTAGTTTCCG | TTTTCTTACT |
| msa252409.2{85_1169NT} | CCTATATTTa | TAGTAGCATT | CCTAGTCATT | TTAGTTTCCG | TTTTCTTACT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 351 | | | | | |
| msa252409.2{85_090.con} | AACCTCCTTTT | AGTAAGCAAA | AAACAATAAC | AGTTAGTGGA | AATCAGCATA |
| msa252409.2{85_CJB110} | AACCTCCTTTT | AGTAAGCAAA | AAACAATAAC | AGTTAGTGGA | AATCAGCATA |
| msa252409.2{85_COH1} | AACCTCCTTTT | AGTAAGCAAA | AAACAATAAC | AGTTAGTGGA | AATCAGCATA |
| msa252409.2{85_M732} | AACCTCCTTTT | AGTAAGCAAA | AAACAATAAC | AGTTAGTGGA | AATCAGCATA |
| msa252409.2{85_M781} | AACCTCCTTTT | AGTAAGCAAA | AAACAATAAC | AGTTAGTGGA | AATCAGCATA |
| msa252409.2{85_18RS21} | AACCTCCTTTT | AGTAAGCAAA | AAACAATAAC | AGTTAGTGGA | AATCAGCATA |
| msa252409.2{85_2603} | AACCTCCTTTT | AGTAAGCAAA | AAACAATAAC | AGTTAGTGGA | AATCAGCATA |
| msa252409.2{85_A909} | AACCTCCTTTT | AGTAAGCAAA | AAACAATAAC | AGTTAGTGGA | AATCAGCATA |
| msa252409.2{85_H36B} | AACCTCCTTTT | AGTAAGCAAA | AAACAATAAC | AGTTAGTGGA | AATCAGCATA |
| msa252409.2{85_JM9130013} | AACCTCCTTTT | AGTAAGCAAA | AAACAATAAC | AGTTAGTGGA | AATCAGCATA |
| msa252409.2{85_1169NT} | AACCTCCTTTT | AGTAAGCAAA | AAACAATAAC | AGTTAGTGGA | AATCAGCATA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 401 | | | | | |
| msa252409.2{85_090.con} | CACCTGATGA | TATTTTGATA | GaAAAAACGA | ATATTCAAAA | AAACGATTAT |
| msa252409.2{85_CJB110} | CACCTGATGA | TATTTTGATA | GaAAAAACGA | ATATTCAAAA | AAACGATTAT |
| msa252409.2{85_COH1} | CACCTGATGA | TATTTTGATA | GaAAAAACGA | ATATTCAAAA | AAACGATTAT |
| msa252409.2{85_M732} | CACCTGATGA | TATTTTGATA | GaAAAAACGA | ATATTCAAAA | AAACGATTAT |
| msa252409.2{85_M781} | CACCTGATGA | TATTTTGATA | GaAAAAACGA | ATATTCAAAA | AAACGATTAT |
| msa252409.2{85_18RS21} | CACCTGATGA | TATTTTGATA | GaAAAAACGA | ATATTCAAAA | AAACGATTAT |
| msa252409.2{85_2603} | CACCTGATGA | TATTTTGATA | GaAAAAACGA | ATATTCAAAA | AAACGATTAT |
| msa252409.2{85_A909} | CACCTGATGA | TATTTTGATA | GaAAAAACGA | ATATTCAAAA | AAACGATTAT |
| msa252409.2{85_H36B} | CACCTGATGA | TATTTTGATA | GaAAAAACGA | ATATTCAAAA | AAACGATTAT |
| msa252409.2{85_JM9130013} | CACCTGATGA | TATTTTGATA | GaAAAAACGA | ATATTCAAAA | AAACGATTAT |
| msa252409.2{85_1169NT} | CACCTGATGA | TATTTTGATA | GaAAAAACGA | ATATTCAAAA | AAACGATTAT |
| Consensus | ***** | ***** | ***-***** | ***** | ***** |
| 451 | | | | | |
| msa252409.2{85_090.con} | TTCTTTTCTT | TAATTTTAA | ACATAAAGCT | ATTGAACAAC | GTTTAGCTGC |
| msa252409.2{85_CJB110} | TTCTTTTCTT | TAATTTTAA | ACATAAAGCT | ATTGAACAAC | GTTTAGCTGC |
| msa252409.2{85_COH1} | TTCTTTTCTT | TAATTTTAA | ACATAAAGCT | ATTGAACAAC | GTTTAGCTGC |

Table 88: Comparative Sequences relating to SAG0477

| | | | | | | | |
|---------------------------|------------|-------------|------------|------------|-------------|-------------|-----|
| msa252409.2{85_M732} | TTCTTTTCTT | TAATTTTAA | ACATAAAGCT | ATTGAACAAC | GTTTAGCTGC | | |
| msa252409.2{85_M781} | TTCTTTTCTT | TAATTTTAA | ACATAAAGCT | ATTGAACAAC | GTTTAGCTGC | | |
| msa252409.2{85_18RS21} | TTCTTTTCTT | TAATTTTAA | ACATAAAGCT | ATTGAACAAC | GTTTAGCTGC | | |
| msa252409.2{85_2603} | TTCTTTTCTT | TAATTTTAA | ACATAAAGCT | ATTGAACAAC | GTTTAGCTGC | | |
| msa252409.2{85_A909} | TTCTTTTCTT | TAATTTTAA | ACATAAAGCT | ATTGAACAAC | GTTTAGCTGC | | |
| msa252409.2{85_H36B} | TTCTTTTCTT | TAATTTTAA | ACATAAAGCT | ATTGAACAAC | GTTTAGCTGC | | |
| msa252409.2{85_JM9130013} | TTCTTTTCTT | TAATTTTAA | ACATAAAGCT | ATTGAACAAC | GTTTAGCTGC | | |
| msa252409.2{85_1169NT} | TTCTTTTCTT | TAATTTTAA | ACATAAAGCT | ATTGAACAAC | GTTTAGCTGC | | |
| Consensus | ***** | ***** | ***** | ***** | ***** | | |
| msa252409.2{85_090.con} | 501 | AGAAGATGTA | TGGGTAAAAA | CAGCTCAGAT | GACTTATCAA | TTTCCCAATa | 550 |
| msa252409.2{85_CJB110} | AGAAGATGTA | TGGGTAAAAA | CAGCTCAGAT | GACTTATCAA | TTTCCCAATa | TTTCCCAATa | |
| msa252409.2{85_COH1} | AGAAGATGTA | TGGGTAAAAA | CAGCTCAGAT | GACTTATCAA | TTTCCCAATa | TTTCCCAATa | |
| msa252409.2{85_M732} | AGAAGATGTA | TGGGTAAAAA | CAGCTCAGAT | GACTTATCAA | TTTCCCAATa | TTTCCCAATa | |
| msa252409.2{85_M781} | AGAAGATGTA | TGGGTAAAAA | CAGCTCAGAT | GACTTATCAA | TTTCCCAATa | TTTCCCAATa | |
| msa252409.2{85_18RS21} | AGAAGATGTA | TGGGTAAAAA | CAGCTCAGAT | GACTTATCAA | TTTCCCAATa | TTTCCCAATa | |
| msa252409.2{85_2603} | AGAAGATGTA | TGGGTAAAAA | CAGCTCAGAT | GACTTATCAA | TTTCCCAATa | TTTCCCAATa | |
| msa252409.2{85_A909} | AGAAGATGTA | TGGGTAAAAA | CAGCTCAGAT | GACTTATCAA | TTTCCCAATa | TTTCCCAATa | |
| msa252409.2{85_H36B} | AGAAGATGTA | TGGGTAAAAA | CAGCTCAGAT | GACTTATCAA | TTTCCCAATa | TTTCCCAATa | |
| msa252409.2{85_JM9130013} | AGAAGATGTA | TGGGTAAAAA | CAGCTCAGAT | GACTTATCAA | TTTCCCAATa | TTTCCCAATa | |
| msa252409.2{85_1169NT} | AGAAGATGTA | TGGGTAAAAA | CAGCTCAGAT | GACTTATCAA | TTTCCCAATa | TTTCCCAATa | |
| Consensus | ***** | ***** | ***** | ***** | ***** | *****_* | |
| msa252409.2{85_090.con} | 551 | AGTTTCATAT | TCAAGTTCAA | GAAAATAAGA | TTATTGCATA | TGCACATACA | 600 |
| msa252409.2{85_CJB110} | AGTTTCATAT | TCAAGTTCAA | GAAAATAAGA | TTATTGCATA | TGCACATACA | TGCACATACA | |
| msa252409.2{85_COH1} | AGTTTCATAT | TCAAGTTCAA | GAAAATAAGA | TTATTGCATA | TGCACATACA | TGCACATACA | |
| msa252409.2{85_M732} | AGTTTCATAT | TCAAGTTCAA | GAAAATAAGA | TTATTGCATA | TGCACATACA | TGCACATACA | |
| msa252409.2{85_M781} | AGTTTCATAT | TCAAGTTCAA | GAAAATAAGA | TTATTGCATA | TGCACATACA | TGCACATACA | |
| msa252409.2{85_18RS21} | AGTTTCATAT | TCAAGTTCAA | GAAAATAAGA | TTATTGCATA | TGCACATACA | TGCACATACA | |
| msa252409.2{85_2603} | AGTTTCATAT | TCAAGTTCAA | GAAAATAAGA | TTATTGCATA | TGCACATACA | TGCACATACA | |
| msa252409.2{85_A909} | AGTTTCATAT | TCAAGTTCAA | GAAAATAAGA | TTATTGCATA | TGCACATACA | TGCACATACA | |
| msa252409.2{85_H36B} | AGTTTCATAT | TCAAGTTCAA | GAAAATAAGA | TTATTGCATA | TGCACATACA | TGCACATACA | |
| msa252409.2{85_JM9130013} | AGTTTCATAT | TCAAGTTCAA | GAAAATAAGA | TTATTGCATA | TGCACATACA | TGCACATACA | |
| msa252409.2{85_1169NT} | AGTTTCATAT | TCAAGTTCAA | GAAAATAAGA | TTATTGCATA | TGCACATACA | TGCACATACA | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | |
| msa252409.2{85_090.con} | 601 | AAGCAAGGAT | ATCAgCCTGT | CTTGGAAACT | GGAAAAAAGG | CTGATCCTGT | 650 |
| msa252409.2{85_CJB110} | AAGCAAGGAT | ATCAgCCTGT | CTTGGAAACT | GGAAAAAAGG | CTGATCCTGT | CTGATCCTGT | |
| msa252409.2{85_COH1} | AAGCAAGGAT | ATCAgCCTGT | CTTGGAAACT | GGAAAAAAGG | CTGATCCTGT | CTGATCCTGT | |
| msa252409.2{85_M732} | AAGCAAGGAT | ATCAgCCTGT | CTTGGAAACT | GGAAAAAAGG | CTGATCCTGT | CTGATCCTGT | |
| msa252409.2{85_M781} | AAGCAAGGAT | ATCAgCCTGT | CTTGGAAACT | GGAAAAAAGG | CTGATCCTGT | CTGATCCTGT | |
| msa252409.2{85_18RS21} | AAGCAAGGAT | ATCAaCCTGT | CTTGGAAACT | GGAAAAAAGG | CTGATCCTGT | CTGATCCTGT | |
| msa252409.2{85_2603} | AAGCAAGGAT | ATCAaCCTGT | CTTGGAAACT | GGAAAAAAGG | CTGATCCTGT | CTGATCCTGT | |
| msa252409.2{85_A909} | AAGCAAGGAT | ATCAaCCTGT | CTTGGAAACT | GGAAAAAAGG | CTGATCCTGT | CTGATCCTGT | |
| msa252409.2{85_H36B} | AAGCAAGGAT | ATCAaCCTGT | CTTGGAAACT | GGAAAAAAGG | CTGATCCTGT | CTGATCCTGT | |
| msa252409.2{85_JM9130013} | AAGCAAGGAT | ATCAaCCTGT | CTTGGAAACT | GGAAAAAAGG | CTGATCCTGT | CTGATCCTGT | |
| msa252409.2{85_1169NT} | AAGCAAGGAT | ATCAgCCTGT | CTTGGAAACT | GGAAAAAAGG | CTGATCCTGT | CTGATCCTGT | |
| Consensus | ***** | *****_***** | ***** | ***** | ***** | ***** | |
| msa252409.2{85_090.con} | 651 | AAATAGTTCA | GAGCTACCAA | AGCACTTCTT | AACAATTAAC | CTTGATAAGG | 700 |
| msa252409.2{85_CJB110} | AAATAGTTCA | GAGCTACCAA | AGCACTTCTT | AACAATTAAC | CTTGATAAGG | CTTGATAAGG | |
| msa252409.2{85_COH1} | AAATAGTTCA | GAGCTACCAA | AGCACTTCTT | AACAATTAAC | CTTGATAAGG | CTTGATAAGG | |
| msa252409.2{85_M732} | AAATAGTTCA | GAGCTACCAA | AGCACTTCTT | AACAATTAAC | CTTGATAAGG | CTTGATAAGG | |
| msa252409.2{85_M781} | AAATAGTTCA | GAGCTACCAA | AGCACTTCTT | AACAATTAAC | CTTGATAAGG | CTTGATAAGG | |
| msa252409.2{85_18RS21} | AAATAGTTCA | GAGCTACCAA | AGCACTTCTT | AACAATTAAC | CTTGATAAGG | CTTGATAAGG | |
| msa252409.2{85_2603} | AAATAGTTCA | GAGCTACCAA | AGCACTTCTT | AACAATTAAC | CTTGATAAGG | CTTGATAAGG | |
| msa252409.2{85_A909} | AAATAGTTCA | GAGCTACCAA | AGCACTTCTT | AACAATTAAC | CTTGATAAGG | CTTGATAAGG | |
| msa252409.2{85_H36B} | AAATAGTTCA | GAGCTACCAA | AGCACTTCTT | AACAATTAAC | CTTGATAAGG | CTTGATAAGG | |
| msa252409.2{85_JM9130013} | AAATAGTTCA | GAGCTACCAA | AGCACTTCTT | AACAATTAAC | CTTGATAAGG | CTTGATAAGG | |
| msa252409.2{85_1169NT} | AAATAGTTCA | GAGCTACCAA | AGCACTTCTT | AACAATTAAC | CTTGATAAGG | CTTGATAAGG | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | |
| msa252409.2{85_090.con} | 701 | AAGATAGTAT | TAAGCTATTA | ATTAAAGATT | TAAAGGCTTT | AGACCCCTGAT | 750 |
| msa252409.2{85_CJB110} | AAGATAGTAT | TAAGCTATTA | ATTAAAGATT | TAAAGGCTTT | AGACCCCTGAT | AGACCCCTGAT | |
| msa252409.2{85_COH1} | AAGATAGTAT | TAAGCTATTA | ATTAAAGATT | TAAAGGCTTT | AGACCCCTGAT | AGACCCCTGAT | |
| msa252409.2{85_M732} | AAGATAGTAT | TAAGCTATTA | ATTAAAGATT | TAAAGGCTTT | AGACCCCTGAT | AGACCCCTGAT | |
| msa252409.2{85_M781} | AAGATAGTAT | TAAGCTATTA | ATTAAAGATT | TAAAGGCTTT | AGACCCCTGAT | AGACCCCTGAT | |
| msa252409.2{85_18RS21} | AAGATAGTAT | TAAGCTATTA | ATTAAAGATT | TAAAGGCTTT | AGACCCCTGAT | AGACCCCTGAT | |
| msa252409.2{85_2603} | AAGATAGTAT | TAAGCTATTA | ATTAAAGATT | TAAAGGCTTT | AGACCCCTGAT | AGACCCCTGAT | |
| msa252409.2{85_A909} | AAGATAGTAT | TAAGCTATTA | ATTAAAGATT | TAAAGGCTTT | AGACCCCTGAT | AGACCCCTGAT | |
| msa252409.2{85_H36B} | AAGATAGTAT | TAAGCTATTA | ATTAAAGATT | TAAAGGCTTT | AGACCCCTGAT | AGACCCCTGAT | |
| msa252409.2{85_JM9130013} | AAGATAGTAT | TAAGCTATTA | ATTAAAGATT | TAAAGGCTTT | AGACCCCTGAT | AGACCCCTGAT | |
| msa252409.2{85_1169NT} | AAGATAGTAT | TAAGCTATTA | ATTAAAGATT | TAAAGGCTTT | AGACCCCTGAT | AGACCCCTGAT | |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** | |
| msa252409.2{85_090.con} | 751 | TTAATAAGTG | AGATTCAGGT | GATAAGTTTA | GCTGATTCTA | AAACGACACC | 800 |
| msa252409.2{85_CJB110} | TTAATAAGTG | AGATTCAGGT | GATAAGTTTA | GCTGATTCTA | AAACGACACC | AAACGACACC | |

Table 88: Comparative Sequences relating to SAG0477

| | | | | | |
|---------------------------|--------------|------------|------------|------------|-------------|
| msa252409.2{85_COH1} | TTAATAAGTG | AGATTCAGGT | GATAAGTTTA | GCTGATTCTA | AAACGACACC |
| msa252409.2{85_M732} | TTAATAAGTG | AGATTCAGGT | GATAAGTTTA | GCTGATTCTA | AAACGACACC |
| msa252409.2{85_M781} | TTAATAAGTG | AGATTCAGGT | GATAAGTTTA | GCTGATTCTA | AAACGACACC |
| msa252409.2{85_18RS21} | TTAATAAGTG | AGATTCAGGT | GATAAGTTTA | GCTGATTCTA | AAACGACACC |
| msa252409.2{85_2603} | TTAATAAGTG | AGATTCAGGT | GATAAGTTTA | GCTGATTCTA | AAACGACACC |
| msa252409.2{85_A909} | TTAATAAGTG | AGATTCAGGT | GATAAGTTTA | GCTGATTCTA | AAACGACACC |
| msa252409.2{85_H36B} | TTAATAAGTG | AGATTCAGGT | GATAAGTTTA | GCTGATTCTA | AAACGACACC |
| msa252409.2{85_JM9130013} | TTAATAAGTG | AGATTCAGGT | GATAAGTTTA | GCTGATTCTA | AAACGACACC |
| msa252409.2{85_1169NT} | TTAATAAGTG | AGATTCAGGT | GATAAGTTTA | GCTGATTCTA | AAACGACACC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa252409.2{85_090.con} | TGACCTCCTG | CTGTTAGATA | TGCATGATGG | AAATAGTATT | AgaATACCAT |
| msa252409.2{85_CJB110} | TGACCTCCTG | CTGTTAGATA | TGCATGATGG | AAATAGTATT | AgaATACCAT |
| msa252409.2{85_COH1} | TGACCTCCTG | CTGTTAGATA | TGCATGATGG | AAATAGTATT | AgaATACCAT |
| msa252409.2{85_M732} | TGACCTCCTG | CTGTTAGATA | TGCATGATGG | AAATAGTATT | AgaATACCAT |
| msa252409.2{85_M781} | TGACCTCCTG | CTGTTAGATA | TGCATGATGG | AAATAGTATT | AgaATACCAT |
| msa252409.2{85_18RS21} | TGACCTCCTG | CTGTTAGATA | TGCATGATGG | AAATAGTATT | AgaATACCAT |
| msa252409.2{85_2603} | TGACCTCCTG | CTGTTAGATA | TGCATGATGG | AAATAGTATT | AgaATACCAT |
| msa252409.2{85_A909} | TGACCTCCTG | CTGTTAGATA | TGCATGATGG | AAATAGTATT | AgaATACCAT |
| msa252409.2{85_H36B} | TGACCTCCTG | CTGTTAGATA | TGCATGATGG | AAATAGTATT | AgaATACCAT |
| msa252409.2{85_JM9130013} | TGACCTCCTG | CTGTTAGATA | TGCATGATGG | AAATAGTATT | AgaATACCAT |
| msa252409.2{85_1169NT} | TGACCTCCTG | CTGTTAGATA | TGCATGATGG | AAATAGTATT | AgaATACCAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa252409.2{85_090.con} | TATCTAAATT | TAAAGAAAGA | CTTCCTTTT | ACAAACAAAT | TAAGAAGAAC |
| msa252409.2{85_CJB110} | TATCTAAATT | TAAAGAAAGA | CTTCCTTTT | ACAAACAAAT | TAAGAAGAAC |
| msa252409.2{85_COH1} | TATCTAAATT | TAAAGAAAGA | CTTCCTTTT | ACAAACAAAT | TAAGAAGAAC |
| msa252409.2{85_M732} | TATCTAAATT | TAAAGAAAGA | CTTCCTTTT | ACAAACAAAT | TAAGAAGAAC |
| msa252409.2{85_M781} | TATCTAAATT | TAAAGAAAGA | CTTCCTTTT | ACAAACAAAT | TAAGAAGAAC |
| msa252409.2{85_18RS21} | TATCTAAATT | TAAAGAAAGA | CTTCCTTTT | ACAAACAAAT | TAAGAAGAAC |
| msa252409.2{85_2603} | TATCTAAATT | TAAAGAAAGA | CTTCCTTTT | ACAAACAAAT | TAAGAAGAAC |
| msa252409.2{85_A909} | TATCTAAATT | TAAAGAAAGA | CTTCCTTTT | ACAAACAAAT | TAAGAAGAAC |
| msa252409.2{85_H36B} | TATCTAAATT | TAAAGAAAGA | CTTCCTTTT | ACAAACAAAT | TAAGAAGAAC |
| msa252409.2{85_JM9130013} | TATCTAAATT | TAAAGAAAGA | CTTCCTTTT | ACAAACAAAT | TAAGAAGAAC |
| msa252409.2{85_1169NT} | TATCTAAATT | TAAAGAAAGA | CTTCCTTTT | ACAAACAAAT | TAAGAAGAAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa252409.2{85_090.con} | CTTAAGGAAC | CTTCTATTGT | TGATATGGAA | GTGGGAGTTT | ACACAACAAAC |
| msa252409.2{85_CJB110} | CTTAAGGAAC | CTTCTATTGT | TGATATGGAA | GTGGGAGTTT | ACACAACAAAC |
| msa252409.2{85_COH1} | CTTAAGGAAC | CTTCTATTGT | TGATATGGAA | GTGGGAGTTT | ACACAACAAAC |
| msa252409.2{85_M732} | CTTAAGGAAC | CTTCTATTGT | TGATATGGAA | GTGGGAGTTT | ACACAACAAAC |
| msa252409.2{85_M781} | CTTAAGGAAC | CTTCTATTGT | TGATATGGAA | GTGGGAGTTT | ACACAACAAAC |
| msa252409.2{85_18RS21} | CTTAAGGAAC | CTTCTATTGT | TGATATGGAA | GTGGGAGTTT | ACACAACAAAC |
| msa252409.2{85_2603} | CTTAAGGAAC | CTTCTATTGT | TGATATGGAA | GTGGGAGTTT | ACACAACAAAC |
| msa252409.2{85_A909} | CTTAAGGAAC | CTTCTATTGT | TGATATGGAA | GTGGGAGTTT | ACACAACAAAC |
| msa252409.2{85_H36B} | CTTAAGGAAC | CTTCTATTGT | TGATATGGAA | GTGGGAGTTT | ACACAACAAAC |
| msa252409.2{85_JM9130013} | CTTAAGGAAC | CTTCTATTGT | TGATATGGAA | GTGGGAGTTT | ACACAACAAAC |
| msa252409.2{85_1169NT} | CTTAAGGAAC | CTTCTATTGT | TGATATGGAA | GTGGGAGTTT | ACACAACAAAC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa252409.2{85_090.con} | AAgTACTATT | GAATCAACCC | CTGTgAAAGC | gGAAGATACA | AAAAATAAAT |
| msa252409.2{85_CJB110} | AAgTACTATT | GAATCAACCC | CTGTgAAAGC | gGAAGATACA | AAAAATAAAT |
| msa252409.2{85_COH1} | AAgTACTATT | GAATCAACCC | CTGTgAAAGC | gGAAGATACA | AAAAATAAAT |
| msa252409.2{85_M732} | AAgTACTATT | GAATCAACCC | CTGTgAAAGC | gGAAGATACA | AAAAATAAAT |
| msa252409.2{85_M781} | AAgTACTATT | GAATCAACCC | CTGTgAAAGC | gGAAGATACA | AAAAATAAAT |
| msa252409.2{85_18RS21} | AAaTACcATT | GAATCAACCC | CTGTtAAAGC | aGAAGATACA | AAAAATAAAT |
| msa252409.2{85_2603} | AAaTACcATT | GAATCAACCC | CTGTtAAAGC | aGAAGATACA | AAAAATAAAT |
| msa252409.2{85_A909} | AAaTACcATT | GAATCAACCC | CTGTtAAAGC | aGAAGATACA | AAAAATAAAT |
| msa252409.2{85_H36B} | AAaTACcATT | GAATCAACCC | CTGTtAAAGC | aGAAGATACA | AAAAATAAAT |
| msa252409.2{85_JM9130013} | AAaTACcATT | GAATCAACCC | CTGTtAAAGC | aGAAGATACA | AAAAATAAAT |
| msa252409.2{85_1169NT} | AAgTACTATT | GAATCAACCC | CTGTgAAAGC | gGAAGATACA | AAAAATAAAT |
| Consensus | **--***--*** | ***** | ****--**** | ***** | ***** |
| msa252409.2{85_090.con} | CAACTGATAA | AACACAAaCa | CAAAATGGTC | AGGTTGCGGA | AAATAGTCAA |
| msa252409.2{85_CJB110} | CAACTGATAA | AACACAAaCa | CAAAATGGTC | AGGTTGCGGA | AAATAGTCAA |
| msa252409.2{85_COH1} | CAACTGATAA | AACACAAaCa | CAAAATGGTC | AGGTTGCGGA | AAATAGTCAA |
| msa252409.2{85_M732} | CAACTGATAA | AACACAAaCa | CAAAATGGTC | AGGTTGCGGA | AAATAGTCAA |
| msa252409.2{85_M781} | CAACTGATAA | AACACAAaCa | CAAAATGGTC | AGGTTGCGGA | AAATAGTCAA |
| msa252409.2{85_18RS21} | CAACTGATAA | AACACAAaCa | CAAAATGGTC | AGGTTGCGGA | AAATAGTCAA |
| msa252409.2{85_2603} | CAACTGATAA | AACACAAaCa | CAAAATGGTC | AGGTTGCGGA | AAATAGTCAA |
| msa252409.2{85_A909} | CAACTGATAA | AACACAAaCa | CAAAATGGTC | AGGTTGCGGA | AAATAGTCAA |
| msa252409.2{85_H36B} | CAACTGATAA | AACACAAaCa | CAAAATGGTC | AGGTTGCGGA | AAATAGTCAA |
| msa252409.2{85_JM9130013} | CAACTGATAA | AACACAAaCa | CAAAATGGTC | AGGTTGCGGA | AAATAGTCAA |
| msa252409.2{85_1169NT} | CAACTGATAA | AACACAAaCc | CAAAATGGTC | AGGTTGCGGA | AAATAGTCAA |
| Consensus | ***** | *****-- | ***** | ***** | ***** |
| msa252409.2{85_090.con} | GGACAAACAA | ATAACTCAA | TACTAATCAA | CAAGG...AC | AACAGATAGC |

Table 88: Comparative Sequences relating to SAG0477

| | | | | | |
|---------------------------|------------|------------|------------|------------|------------|
| msa252409.2{85_CJB110} | GGACAAACAA | ATAACTCAA | TACTAATCAA | CAAGG...AC | AACAGATAGC |
| msa252409.2{85_COH1} | GGACAAACAA | ATAACTCAA | TACTAATCAA | CAAGG...AC | AACAGATAGC |
| msa252409.2{85_M732} | GGACAAACAA | ATAACTCAA | TACTAATCAA | CAAGG...AC | AACAGATAGC |
| msa252409.2{85_M781} | GGACAAACAA | ATAACTCAA | TACTAATCAA | CAAGG...AC | AACAGATAGC |
| msa252409.2{85_18RS21} | GGACAAACAA | ATAACTCAA | TACTAATCAA | CAAGG...AC | AACAGATAGC |
| msa252409.2{85_2603} | GGACAAACAA | ATAACTCAA | TACTAATCAA | CAAGG...AC | AACAGATAGC |
| msa252409.2{85_A909} | GGACAAACAA | ATAACTCAA | TACTAATCAA | CAAGG...AC | AACAGATAGC |
| msa252409.2{85_H36B} | GGACAAACAA | ATAACTCAA | TACTAATCAA | CAAGG...AC | AACAGATAGC |
| msa252409.2{85_JM9130013} | GGACAAACAA | ATAACTCAA | TACTAATCAA | CAAGG...AC | AACAGATAGC |
| msa252409.2{85_1169NT} | GGACAAACAA | ATAACTCAA | TACTAATCAA | CAAGGacaAC | AACAGATAGC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa252409.2{85_090.con} | 1101 | | | | 1134 |
| msa252409.2{85_CJB110} | AACaGAGCAG | GCACCcAACC | CTCAAAATGT | TAAT | |
| msa252409.2{85_COH1} | AACaGAGCAG | GCACCcAACC | CTCAAAATGT | TAAT | |
| msa252409.2{85_M732} | AACaGAGCAG | GCACCcAACC | CTCAAAATGT | TAAT | |
| msa252409.2{85_M781} | AACaGAGCAG | GCACCcAACC | CTCAAAATGT | TAAT | |
| msa252409.2{85_18RS21} | AACaGAGCAG | GCACCcAACC | CTCAAAATGT | TAAT | |
| msa252409.2{85_2603} | AACaGAGCAG | GCACCcAACC | CTCAAAATGT | TAAT | |
| msa252409.2{85_A909} | AACaGAGCAG | GCACCcAACC | CTCAAAATGT | TAAT | |
| msa252409.2{85_H36B} | AACaGAGCAG | GCACCcAACC | CTCAAAATGT | TAAT | |
| msa252409.2{85_JM9130013} | AACaGAGCAG | GCACCcAACC | CTCAAAATGT | TAAT | |
| msa252409.2{85_1169NT} | AACaGAGCAG | GCACCcAACC | CTCAAAATGT | TAAT | |
| Consensus | ***-***** | *****-**** | ***** | **** | |

SEQ ID NO. 8812

STRAIN 2603 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPI FVVAFLVILVSVFLLTPF
 SKQKTIITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSI KLL
 IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPHYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8813

STRAIN H36B frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPI FVVAFLVILVSVFLLTPF
 SKQKTIITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSI KLL
 IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPHYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8814

STRAIN 18RS21 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPI FVVAFLVILVSVFLLTPF
 SKQKTIITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSI KLL
 IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPHYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8815

STRAIN M732 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPI FVVAFLVILVSVFLLTPF
 SKQKTIITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSI KLL
 IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPHYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8816

STRAIN COH1 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPI FVVAFLVILVSVFLLTPF
 SKQKTIITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSI KLL
 IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPHYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNSTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8817

STRAIN M781 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEPQ

Table 88: Comparative Sequences relating to SAG0477

NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8818

STRAIN CJB110 frame: 1

PKKKS DTPKEKEEVLTEWQKRNLEFLKRRKEDEEEQKRINEKLRLDKRSKLNISSEPEEQ
 NTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8819

STRAIN 1169NT frame: 1

PKKKS DTPKEKEEVLTEWQKRNLEFLKRRKEDEEEQKRINEKLRLDKRSKLNISSEPEEQ
 NTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8820

STRAIN JM9130013 frame: 1

PKKKS DTPKEKEEVLTEWQKRNLEFLKRRKEDEEEQKRINEKLRLDKRSKLNISSEPEEQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8821

STRAIN A909 frame: 1

PKKKS DTPKEKEEVLTEWQKRNLEFLKRRKEDEEEQKRINEKLRLDKRSKLNISSEPEEQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIXIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8822

STRAIN 090 frame: 2

KKKS DTPKEKEEVLTEWQKRNLEFLKRRKEDEEEQKRINEKLRLDKRSKLNISSEPEEQ
 TTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 KQKTI TVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAEDVWVKTAQMTYQ
 PNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLLI
 KDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKNL
 KEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

PRETTY of: /biotmp/msa252337.2{*} January 31, 2003 03:32 ..

| | | |
|---------------------------|--------------|--|
| | 1 | 50 |
| msa252337.2{85_090} | -KKKS DTPKEK | EEVVLTEWQK RNLEFLKRRK EDEEEQKRIN EKLRLDKRSK |
| msa252337.2{85_18RS21} | PKKKS DTPKEK | EEVVLTEWQK RNLEFLKRRK EDEEEQKRIN EKLRLDKRSK |
| msa252337.2{85_2603} | PKKKS DTPKEK | EEVVLTEWQK RNLEFLKRRK EDEEEQKRIN EKLRLDKRSK |
| msa252337.2{85_A909} | PKKKS DTPKEK | EEVVLTEWQK RNLEFLKRRK EDEEEQKRIN EKLRLDKRSK |
| msa252337.2{85_CJB110} | PKKKS DTPKEK | EEVVLTEWQK RNLEFLKRRK EDEEEQKRIN EKLRLDKRSK |
| msa252337.2{85_COH1} | PKKKS DTPKEK | EEVVLTEWQK RNLEFLKRRK EDEEEQKRIN EKLRLDKRSK |
| msa252337.2{85_H36B} | PKKKS DTPKEK | EEVVLTEWQK RNLEFLKRRK EDEEEQKRIN EKLRLDKRSK |
| msa252337.2{85_JM9130013} | PKKKS DTPKEK | EEVVLTEWQK RNLEFLKRRK EDEEEQKRIN EKLRLDKRSK |
| msa252337.2{85_M732} | PKKKS DTPKEK | EEVVLTEWQK RNLEFLKRRK EDEEEQKRIN EKLRLDKRSK |
| msa252337.2{85_M781} | PKKKS DTPKEK | EEVVLTEWQK RNLEFLKRRK EDEEEQKRIN EKLRLDKRSK |
| msa252337.2{85_1169NT} | PKKKS DTPKEK | EEVVLTEWQK RNLEFLKRRK EDEEEQKRIN EKLRLDKRSK |
| Consensus | ***** | ***** |
| | 51 | 100 |
| msa252337.2{85_090} | LNISSEPEEQ | NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRI RTA |
| msa252337.2{85_18RS21} | LNISSEPEEQ | NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRI RTA |
| msa252337.2{85_2603} | LNISSEPEEQ | NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRI RTA |
| msa252337.2{85_A909} | LNISSEPEEQ | NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRI RTA |
| msa252337.2{85_CJB110} | LNISSEPEEQ | NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRI RTA |

Table 88: Comparative Sequences relating to SAG0477

| | | | | | |
|---------------------------|-------------|------------|------------|------------|-------------|
| msa252337.2{85_COH1} | LNISSPPEEPQ | NTTKIKKLHF | PKISkPKIEK | KQKKEKIVNS | LAKTNRIRTA |
| msa252337.2{85_H36B} | LNISSPPEEPQ | NTTKIKKLHF | PKISrPKIEK | KQKKEKIVNS | LAKTNRIRTA |
| msa252337.2{85_JM9130013} | LNISSPPEEPQ | NTTKIKKLHF | PKISrPKIEK | KQKKEKIVNS | LAKTNRIRTA |
| msa252337.2{85_M732} | LNISSPPEEPQ | NTTKIKKLHF | PKISkPKIEK | KQKKEKIVNS | LAKTNRIRTA |
| msa252337.2{85_M781} | LNISSPPEEPQ | NTTKIKKLHF | PKISkPKIEK | KQKKEKIVNS | LAKTNRIRTA |
| msa252337.2{85_1169NT} | LNISSPPEEPQ | NTTKIKKLHF | PKISkPKIEK | KQKKEKIVNS | LAKTNRIRTA |
| Consensus | ***** | ***** | ****_**** | ***** | ***** |
| msa252337.2{85_090} | PIFvVAFVLVI | LVSFVLLTPF | SKQKTITVSG | NQHTPDDILI | EKTNIQKNDY |
| msa252337.2{85_18RS21} | PIFvVAFVLVI | LVSFVLLTPF | SKQKTITVSG | NQHTPDDILI | EKTNIQKNDY |
| msa252337.2{85_2603} | PIFvVAFVLVI | LVSFVLLTPF | SKQKTITVSG | NQHTPDDILI | EKTNIQKNDY |
| msa252337.2{85_A909} | PIFvVAFVLVI | LVSFVLLTPF | SKQKTITVSG | NQHTPDDILI | EKTNIQKNDY |
| msa252337.2{85_CJB110} | PIFvVAFVLVI | LVSFVLLTPF | SKQKTITVSG | NQHTPDDILI | EKTNIQKNDY |
| msa252337.2{85_COH1} | PIFvVAFVLVI | LVSFVLLTPF | SKQKTITVSG | NQHTPDDILI | EKTNIQKNDY |
| msa252337.2{85_H36B} | PIFvVAFVLVI | LVSFVLLTPF | SKQKTITVSG | NQHTPDDILI | EKTNIQKNDY |
| msa252337.2{85_JM9130013} | PIFvVAFVLVI | LVSFVLLTPF | SKQKTITVSG | NQHTPDDILI | EKTNIQKNDY |
| msa252337.2{85_M732} | PIFvVAFVLVI | LVSFVLLTPF | SKQKTITVSG | NQHTPDDILI | EKTNIQKNDY |
| msa252337.2{85_M781} | PIFvVAFVLVI | LVSFVLLTPF | SKQKTITVSG | NQHTPDDILI | EKTNIQKNDY |
| msa252337.2{85_1169NT} | PIFvVAFVLVI | LVSFVLLTPF | SKQKTITVSG | NQHTPDDILI | EKTNIQKNDY |
| Consensus | ***_***** | ***** | ***** | ***** | ***** |
| msa252337.2{85_090} | FFSLIFKHKA | IEORLAAEDV | WVKTAQMTYQ | FPNKFHIVQV | ENKI IAYAHT |
| msa252337.2{85_18RS21} | FFSLIFKHKA | IEORLAAEDV | WVKTAQMTYQ | FPNKFHIVQV | ENKI IAYAHT |
| msa252337.2{85_2603} | FFSLIFKHKA | IEORLAAEDV | WVKTAQMTYQ | FPNKFHIVQV | ENKI IAYAHT |
| msa252337.2{85_A909} | FFSLIFKHKA | IEORLAAEDV | WVKTAQMTYQ | FPNKFHIVQV | ENKI IAYAHT |
| msa252337.2{85_CJB110} | FFSLIFKHKA | IEORLAAEDV | WVKTAQMTYQ | FPNKFHIVQV | ENKI IAYAHT |
| msa252337.2{85_COH1} | FFSLIFKHKA | IEORLAAEDV | WVKTAQMTYQ | FPNKFHIVQV | ENKI IAYAHT |
| msa252337.2{85_H36B} | FFSLIFKHKA | IEORLAAEDV | WVKTAQMTYQ | FPNKFHIVQV | ENKI IAYAHT |
| msa252337.2{85_JM9130013} | FFSLIFKHKA | IEORLAAEDV | WVKTAQMTYQ | FPNKFHIVQV | ENKI IAYAHT |
| msa252337.2{85_M732} | FFSLIFKHKA | IEORLAAEDV | WVKTAQMTYQ | FPNKFHIVQV | ENKI IAYAHT |
| msa252337.2{85_M781} | FFSLIFKHKA | IEORLAAEDV | WVKTAQMTYQ | FPNKFHIVQV | ENKI IAYAHT |
| msa252337.2{85_1169NT} | FFSLIFKHKA | IEORLAAEDV | WVKTAQMTYQ | FPNKFHIVQV | ENKI IAYAHT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa252337.2{85_090} | KQGYQPVLET | GKKADPVNSS | ELPKHFLTIN | LDKEDSIKLL | IKDLKALDPD |
| msa252337.2{85_18RS21} | KQGYQPVLET | GKKADPVNSS | ELPKHFLTIN | LDKEDSIKLL | IKDLKALDPD |
| msa252337.2{85_2603} | KQGYQPVLET | GKKADPVNSS | ELPKHFLTIN | LDKEDSIKLL | IKDLKALDPD |
| msa252337.2{85_A909} | KQGYQPVLET | GKKADPVNSS | ELPKHFLTIN | LDKEDSIKLL | IKDLKALDPD |
| msa252337.2{85_CJB110} | KQGYQPVLET | GKKADPVNSS | ELPKHFLTIN | LDKEDSIKLL | IKDLKALDPD |
| msa252337.2{85_COH1} | KQGYQPVLET | GKKADPVNSS | ELPKHFLTIN | LDKEDSIKLL | IKDLKALDPD |
| msa252337.2{85_H36B} | KQGYQPVLET | GKKADPVNSS | ELPKHFLTIN | LDKEDSIKLL | IKDLKALDPD |
| msa252337.2{85_JM9130013} | KQGYQPVLET | GKKADPVNSS | ELPKHFLTIN | LDKEDSIKLL | IKDLKALDPD |
| msa252337.2{85_M732} | KQGYQPVLET | GKKADPVNSS | ELPKHFLTIN | LDKEDSIKLL | IKDLKALDPD |
| msa252337.2{85_M781} | KQGYQPVLET | GKKADPVNSS | ELPKHFLTIN | LDKEDSIKLL | IKDLKALDPD |
| msa252337.2{85_1169NT} | KQGYQPVLET | GKKADPVNSS | ELPKHFLTIN | LDKEDSIKLL | IKDLKALDPD |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa252337.2{85_090} | LISEIQVISL | ADSKITPDLL | LLDMHDGNSI | rIPLSKFKER | LPFFYKQIKKN |
| msa252337.2{85_18RS21} | LISEIQVISL | ADSKITPDLL | LLDMHDGNSI | rIPLSKFKER | LPFFYKQIKKN |
| msa252337.2{85_2603} | LISEIQVISL | ADSKITPDLL | LLDMHDGNSI | rIPLSKFKER | LPFFYKQIKKN |
| msa252337.2{85_A909} | LISEIQVISL | ADSKITPDLL | LLDMHDGNSI | xIPLSKFKER | LPFFYKQIKKN |
| msa252337.2{85_CJB110} | LISEIQVISL | ADSKITPDLL | LLDMHDGNSI | rIPLSKFKER | LPFFYKQIKKN |
| msa252337.2{85_COH1} | LISEIQVISL | ADSKITPDLL | LLDMHDGNSI | rIPLSKFKER | LPFFYKQIKKN |
| msa252337.2{85_H36B} | LISEIQVISL | ADSKITPDLL | LLDMHDGNSI | rIPLSKFKER | LPFFYKQIKKN |
| msa252337.2{85_JM9130013} | LISEIQVISL | ADSKITPDLL | LLDMHDGNSI | rIPLSKFKER | LPFFYKQIKKN |
| msa252337.2{85_M732} | LISEIQVISL | ADSKITPDLL | LLDMHDGNSI | rIPLSKFKER | LPFFYKQIKKN |
| msa252337.2{85_M781} | LISEIQVISL | ADSKITPDLL | LLDMHDGNSI | rIPLSKFKER | LPFFYKQIKKN |
| msa252337.2{85_1169NT} | LISEIQVISL | ADSKITPDLL | LLDMHDGNSI | rIPLSKFKER | LPFFYKQIKKN |
| Consensus | ***** | ***** | ***** | -***** | ***** |
| msa252337.2{85_090} | LKEPSIVDME | GVVYTTTtTI | ESTPVKAEDT | KNKSTDKTQc | QNGQVAENSQ |
| msa252337.2{85_18RS21} | LKEPSIVDME | GVVYTTTnTI | ESTPVKAEDT | KNKSTDKTQc | QNGQVAENSQ |
| msa252337.2{85_2603} | LKEPSIVDME | GVVYTTTnTI | ESTPVKAEDT | KNKSTDKTQc | QNGQVAENSQ |
| msa252337.2{85_A909} | LKEPSIVDME | GVVYTTTnTI | ESTPVKAEDT | KNKSTDKTQx | QNGQVAENSQ |
| msa252337.2{85_CJB110} | LKEPSIVDME | GVVYTTTtTI | ESTPVKAEDT | KNKSTDKTQc | QNGQVAENSQ |
| msa252337.2{85_COH1} | LKEPSIVDME | GVVYTTTtTI | ESTPVKAEDT | KNKSTDKTQc | QNGQVAENSQ |
| msa252337.2{85_H36B} | LKEPSIVDME | GVVYTTTnTI | ESTPVKAEDT | KNKSTDKTQc | QNGQVAENSQ |
| msa252337.2{85_JM9130013} | LKEPSIVDME | GVVYTTTnTI | ESTPVKAEDT | KNKSTDKTQc | QNGQVAENSQ |
| msa252337.2{85_M732} | LKEPSIVDME | GVVYTTTtTI | ESTPVKAEDT | KNKSTDKTQc | QNGQVAENSQ |
| msa252337.2{85_M781} | LKEPSIVDME | GVVYTTTtTI | ESTPVKAEDT | KNKSTDKTQc | QNGQVAENSQ |
| msa252337.2{85_1169NT} | LKEPSIVDME | GVVYTTTtTI | ESTPVKAEDT | KNKSTDKTQc | QNGQVAENSQ |
| Consensus | ***** | *****-* | ***** | ***** | ***** |
| msa252337.2{85_090} | GQTNNNSNTNQ | QGQQiatega | pnpqnv- | | |
| msa252337.2{85_18RS21} | GQTNNNSNTNQ | QGQQiatega | pnpqnv- | | |
| msa252337.2{85_2603} | GQTNNNSNTNQ | QGQQiatega | pnpqnv- | | |
| msa252337.2{85_A909} | GQTNNNSNTNQ | QGQQiatega | pnpqnv- | | |

Table 88: Comparative Sequences relating to SAG0477

| | | | |
|---------------------------|-------------|------------|----------|
| msa252337.2{85_CJB110} | GQTNNSENTNQ | QGQQiateqa | pnpgnvn- |
| msa252337.2{85_COH1} | GQTNNSENTNQ | QGQQiateqa | pnpgnvn- |
| msa252337.2{85_H36B} | GQTNNSENTNQ | QGQQiateqa | pnpgnvn- |
| msa252337.2{85_JM9130013} | GQTNNSENTNQ | QGQQiateqa | pnpgnvn- |
| msa252337.2{85_M732} | GQTNNSENTNQ | QGQQiateqa | pnpgnvn- |
| msa252337.2{85_M781} | GQTNNSENTNQ | QGQQiateqa | pnpgnvn- |
| msa252337.2{85_1169NT} | GQTNNSENTNQ | QGQQiateq | apnpgnvn |
| Consensus | ***** | ****- | -----* |

Table 89: Comparative Sequences relating to SAG1350

SEQ ID NO. 8901

STRAIN 2603

ATGAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTCTCTACGTAAA
 TATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTACATAATGGTCACAACTCCTGTT
 TTTGCGGATCAAACATACATCGGTTCAAGTTAATAATCAGACAGGCCTAGTGTGGATGCT
 AATAATTCCTCCAATGAGACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGT
 CAAGCGTCTGATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
 TTAGTAGAGACAAAGCCATGGTGGAAAAACATTACCTGAACAAGGGAATTATGTTTAT
 AGCAAGAAACCGAGGTGAAAAATACACCTTCAAATCAGCCCCAGTAGCTTTCTATGCA
 AAGAAAGGTGATAAAGTTTCTATGACCAAGTATTTAATAAAGATAATGTGAAATGGATT
 TCATATAAGTCTTTTGTGGCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCA
 GGAGGTTCAAGAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTATACATTTTCACATAAAGTAGAAGTAAAAAATGAAGCT
 AAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGACAGAATTTTTTACGACCAA
 ATACTAACTATTGAAGGAAATCAGTGGTTATCTTATAAATCAITCAATGGTGTTCGTCGT
 TTTGTTTGTCTAGGTAAAGCATCTTCAAGTAGAAAAAATGAAGATAAAGAAAAAGTGTCT
 CCTCAACCAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACT
 ACAGGTTTTGATATTTTAAATTACGAATATTAAAGATGATAACGGTATCGTGTCTTAAAG
 GTACCGGTTTGGACTGAACAAGGCGCAAGATGATATTAAATGGGTATACAGCTGTAAT
 ACTGGGGATGGCACTACAAAGTAGCTGTATCATTTGCTGACCATAAAGATGAGAAGGGT
 CTTTATAATATTCTTTTACTACCAAGAGCTAGTGGGACACTTGTAGGTGTAAACAGGA
 ACTAAAGTGACAGTACCTGGAACTAATTTCTCTCAAGAACCTATTGAAAAAGGTTTAGCA
 AAGACTGGTGTTTTAAATATTATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAAATATCA
 AGTCAGACCCAAATTTACTTTAGAAAAAGGTGACAAAAATAATATGATCAAGTATTGACA
 GCAGATGGTTACCAAGTGGATTCTTACAAATCTTATAGTGGTGTTCGTGCTATATTCTCT
 GTGAAAAAGCTAACTACAGTAGTGAAGAAAGCGAAGATGAGGCGACTAAACCGACTAGT
 TATCCCAACTTACCTTAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAGAAATACATTAT
 GATCAAGTGTTAGTAGTAGATGGTTCATCAGTGGATTTTATACAAAGAGTTATTCCGGTATT
 CGTCGCTATATTGAAAT

SEQ ID NO. 8902

STRAIN 090

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACT
 CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
 ATAATGGTCACAAGTCTGTTTGTGCGGATCAAACATACATCGGTTCAAGT
 TAATAATCAGACAGGCCTAGTGTGGATGCTAATAATCTTCCAATGAGA
 CAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 GATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
 TTTAGTAGAGACAAAGCCAAATGGTGGAAAAACATTACCTGAACAAGGGA
 ATTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAATCA
 GCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGACCA
 AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGTG
 GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
 GAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGA
 GAAAAATAGCAACGCAAGGAAATATACATTTTACATAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGA
 GACAGAAATTTTACGACCAAAATACTAACTATTGAAGGAAATCAGTGGTT
 ATCTTATAAATCAITCAATGGTGTTCGTGTTTGTCTAGGTAAAG
 CATCTTCAGTAGAAAAAATGAAGATAAAGAAAAAGTGTCTCCTCAACCA
 CAAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAACT
 TACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCG
 CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATT
 AAATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGT
 ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCAITTAT
 ACTACCAAGAGCTAGTGGGACACTTGTAGGTGTAAACAGGAACATAAGTG
 ACAGTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAAAAGGTTTAGC
 AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAATGAAG
 CTAAAAATATCAAGTCAAGTCAAGCCCAATTTACTTTAGAAAAAGGTGACAAAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAA
 ATCTTATAGTGGTGTTCGTGCTATATTCCTGTGAAAAAGCTAACTACAA
 GTAGTGAAGAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
 TTACCTAAAAAGGTACCTATACATTTACTAAAACTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTCAAAGGGTGAAG
 AAATACATTATGATCAAGTGTAGTAGTAGATGGTTCATCAGTGGATTTCA
 TACAAGAGTTATTCGGTATTCGTGCTATATTGAAAT

SEQ ID NO. 8903

STRAIN A909

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTAC
 TCCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
 CATAAATGGTCACAAGTCTGTTTGTGCGGATCAAACATACATCGGTTCAAG
 TTAATAATCAGACAGGCCTAGTGTGGATGCTAATAATCTTCCAATGAG
 ACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 TGATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTC
 CTTTAGTAGAGACAAAGCCATGGTGGAAAAACATTACCTGAACAAGGG
 AATTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAATC
 AGCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACC
 AAGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGT
 GCGGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTT
 AGAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAG
 AGAAAAATAGCAACGCAAGGAAATTTATACATTTTACATAAAGTAGAAGTA
 AAAAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGG

Table 89: Comparative Sequences relating to SAG1350

AGACAGAAATTTTTACGACCAAATACTAATCTATTGAAGGAAATCAGTGGT
TATCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAA
GCATCTTCAGTAGAAAAAAGCTGAAGATAAAGAAAAAGTGTCTCTCAACC
ACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAA
CTACAGGTTTTGATATTTAATTACGAATATTAAGATGATAACGGTATC
GCTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATAT
TAAATGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTG
TATCATTTGCTGACCATAAGATGAGAAGGGTCTTTATAATATTCATTTA
TACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGT
GACAGTAGCTGGAATAATCTTCTCAAGAACCATTGAAATGGTTTAG
CAAAGACTGGTGTATTATAATATTATCGGAAGTACTGAAGTAAAAATGAA
GCTAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAAT
AAATTTATGATCAAGTATTGACAGCAGATGGTTACAGTGGATTCTTACA
AATCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACA
AGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAA
CTTACCTAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGA
GTCACCTAAAAGTATCAAGTCCAGTGGAAATTAATTTTCAAAGGGTGAA
AAAAATACATTATGATCAAGTGTAGTAGATGGTCATCAGTGGATTTC
ATACAAGAGTTATTCCGGTATTCTGTCGTATATTGAAATT

SEQ ID NO. 8904

STRAIN H36B

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTTC
ATAATGGTCAACAAGTCTGTGTTTTGCGGATCAAACTACATCGGTTCAAGT
TAATAATCAGACAGGCACTAGTGTGGATGATAAATTTCTTCCAATGAGA
CAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCT
GATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
TTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAGGGA
ATTATGTTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCA
GCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCA
AGTATTTAATAAAGATAAATGTGAAATGGATTTCATATAAGTCTTTTTGTG
GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
GAGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATATCAAGA
GAAAAATAGCAACGCAAGGAAATATACATTTTACATAAAGTAGAAGTAA
AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGA
GACAGAATTTTTTACGACCAAACTAATACTATTGAAGGAAATCAGTGGTT
ATCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAAG
CATCTTCAGTAGAAAAAAGCTGAAGATAAAGAAAAAGTGTCTCTCAACCA
CAAGCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAAAC
TACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCG
CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
AAATGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTGT
ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCAATTAT
ACTACCAAGAGCTAGTGGGACACTTGTAGGTGTAACAGCACTAAAGTG
ACAGTAGCTGGAACTAATTTCTTCTCAAGAACCTATTGAAAATGGTTTAGC
AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAATGAAG
CTAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATA
AATTATGATCAAGTATTGACAGCAGATGGTTACAGTGGATTTCTTACAA
ATCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAA
GTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
TTACCTTAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGAG
TCAACCTTAAAGTATCAAGTCCAGTGGAAATTAATTTTCAAAGGGTGAAA
AAATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTC
TACAAGAGTTATTCCGGTATTCTGTCGTATATTGAAATT

SEQ ID NO. 8905

STRAIN 18RS21

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTC
TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCA
TAATGGTCAACAAGTCTGTGTTTTGCGGATCAAACTACATCGGTTCAAGTT
AATAATCAGACAGGCACTAGTGTGGATGCTAATAATTTCTTCCAATGAGAC
AAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTG
ATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCT
TTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAGGGAA
TTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAG
CCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCAA
GTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTGG
CGTAGCTGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTGAG
AGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
AAAATAGCAACGCAAGGAAATATACATTTTACATAAAGTAGAAGTAAA
AAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGCAAAAGGAG
ACAGAATTTTTACGACCAAACTAATACTATTGAAGGAAATCAGTGGTTA
TCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAAGC
ATCTTCAGTAGAAAAAAGCTGAAGATAAAGAAAAAGTGTCTCTCAACCAC
AAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACT
ACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCGC
TGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTA
AATGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTGTA
TCATTTGCTGACCATAAAGATGAGAAGGGTCTTTATAATATTCAATTTATA
CTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTGA
CAGTAGCTGGAACATAATTTCTTCAAGAACCTATTGAAAAAGTTTAGCA
AAGACTGGTGTATTATAATATTATCGGAAGTACTGAAGTAAAAATGAAGC

Table 89: Comparative Sequences relating to SAG1350

TAAATATCAAGTCAGACCCCAATTTACTTTAGAAAAAGGTGACAAAATAA
 ATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAAA
 TCTTATAGTGGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAAG
 TAGTGA AAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACT
 TACCTAAAACAGGTACCTATACATTTACTAAAACGTAGATGTGAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAAGGGTGAAAA
 AATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTTCAT
 ACAAGAGTTATTCCGGTATTTCGTGCTATATTGAAATT

SEQ ID NO. 8906

STRAIN M732

CAAGTAAATGATaCTAAGCAATCTTACTCTCTACGTAAATATAAATTGCG
 TTTAGCATCAGTAATTTTAGGGTCATTCTATAATGGTCACAAGTCCGTGTTT
 TTGCGGATCAAACTACATCGGTTCAAGTTAATAATCAGACAGGCACTAGT
 GTGGATGCTAATAATTCTTCCAATGAGACAAGTCCGTCAAGTGTGATTAC
 TTCCAATATGATAGTGTTCAGCGCTCGATAAAGTTGTAAATAGTCAAA
 ATACGGCAACAAAGGACATTACTACTCCTTTAGTAGAGACAAAGCCAATG
 GTGGA AAAACATTTACCTGAACAAGGGAATTTATGTTTATAGCAAGA AAC
 CGAGGTGAAAAATACACCTTCAAAATCAGCCCAAGTACGTTTCTATGCAA
 AGAAAGGTGATAAAGTTTCTATGACCAAGTATTTAATAAAGATAATGTG
 AAATGGATTTTATATAAGTCTTTTGGTGGCGTACGTGATACGCAGCTAT
 TGAGTCACTAGATCCATCAGGAGGTTTCAAGAGACTAAAGCACCTACTCCTG
 TAACAAATTCAGGAAGCAATAATCAAGAGAAAAATAGCAACGCAAGGAAT
 TATACATTTTACATAAAGTAGAAGTAAAAATGAAGCTAAGGTAGCGAG
 TCCAATCAATTTTACATTTGGACAAAGGAGACAGAATTTTACGACCAAA
 TACTAACTatTGAAGGAATCAGTGGTTATCTTATAAATCATTCATGGT
 GTTCGTGCTTTTGTtTtGtTAGGTAAGCATCTTCAGTAGAAAAAACTGA
 AGATAAAGAAAAAGTGTCTCTCAACCACAAGCCGTATTACTAAAACCTG
 GTAGACTGACTATTTCTAACGAAACCAACTACAGGTTTGTATATTTAATT
 ACGAATATTAAGATGATAACGGTATCGCTGCTGTTAAGGTACCGGTTTG
 GACTGAACAGGAGGCGCAAGATGATTTAAATGGTATACAGCTGTAACATA
 CTGGGGATGGCAACTACAAAGTAGCTGTATCATTTGCTGACCATAGAAT
 GAGAAGGGTCTTTATAAATTTTATTATATCTACCAAGAAGCTAGTGGGAC
 ACTTGTAGGTGTAACAGGAACATAAGTGACAGTAGCTGGAACATAATCTT
 CTCAAGAACCTATTGAAAATGGTTTACCAAGACTGGTGTTTATAATATT
 ATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAAATATCAAGTCAGACCCA
 ATTTACTTTAGAAAAAGGTGACAAAAATAAATTATGATCAAGTATTGACAG
 CAGATGGTTTACCAGTGGATTTCTTACAAATCTTATAGTGGTGTTCGTGCG
 TATATTCTGTGAAAAAGCTAACTACAAGTAGTAAAAAGCGAAAGATGA
 GGCGACTAAACCGACTAGTTATCCCAACTTACCTAAACAGGTACCTATA
 CATTTACTAAAACGTAGATGTGAAAAGTCAACCTAAAGTATCAAGTCCA
 GTGGAATTTAATTTTCAAAAGGGTGAAAAATACATTATGATCAAGTGT
 AGTAGTAGATGGTATCAGTGGATTTTATACAAAGATTATTCCGGTATTC
 GTCGCTATATTGAAATT

SEQ ID NO. 8907

STRAIN COH1

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTCTCT
 ACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCTATAA
 TGGTCACAAGTCCGTGTTTTCGCGGATCAAACTACATCGGTTCAAGTTAAT
 AATCAGACAGGCACTAGTGTGGATGCTAATAATTTCTTCCAATGAGACAAG
 TGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTGATA
 AAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCTTTA
 GTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAAGGAATTA
 TGTTTATAGCAAAAGAACCGAGGTGAAAAATACACCTTCAAAATCAGCCC
 CAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGACCAAGTA
 TTTAATAAAGATAATGTTAAATGGATTTTATATAAGTCTTTTGGTGGCGT
 ACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAGAGA
 CTAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGAGAAA
 ATAGCAACGCAAGGAAATTTATACATTTTACATAAAGTAGAAGTAaaaaa
 TGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGACA
 GAATTTTTTACGACCAATACTAATCTATTGAAGGAAATCAGTGGTTATCT
 TATAAATCATTTCAATGGTGTTCGTGCTTTTGTtTGCTAGGTAAAGCATC
 TTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCTCAACCACAAG
 CCCGTTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACTACA
 GGTTTTGTATTTTAAATACGAATATTAAAGATGATAACGGTATCGCTGC
 TGTTAAGGTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATTAAAT
 GGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGTATCA
 TTTGCTGACCATAGAATGAGAAGGGTCTTTATAAATTTTCAATTTACTA
 CCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTGACAG
 TAGCTGGAACATAATCTTCTCAAGAACCTATTGAAAAAGGTTTACCAAG
 ACTGGTGTTTATAAATATATCGAAGTACTGAAGTAAAAAATGAAGCTAA
 AATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATAAAT
 ATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTCTTACAAATCT
 TATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAAGTAG
 TGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTAC
 CTAAAAACAGGTACCTATACATTTACTAAAACGTAGATGTGAAAAAGTCAA
 CCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAAGGGTGAAAAAT
 ACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTTATACA
 AGAGTTATTCCGGTATTTCGTGCTATATTGAAATT

SEQ ID NO. 8908

STRAIN M781

Table 89: Comparative Sequences relating to SAG1350

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTT
 ACTCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCA
 TTCATAATGGTCAACAAGTCCTGTTTTTGGGATCAAACCTACATCGGTTCA
 AGTTAATAATCAGACAGGCACTAGTGTGGATGCTAATAATTTCTCCAATG
 AGACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCG
 TCTGATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTAC
 TCCTTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAAG
 GGAATATGTTTTATAGCAAAAGAAACCGAGGTGAAAAATACACCTTCAAAA
 TCAGCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGA
 CCAAGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTG
 GTGGCGTACGTGATACGACGCTATTGAGTCACTAGATCCATCAGGAGGT
 TCAGAGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCA
 AGAGAAAATAGCAACGCAAGGAAATATACATTTTCACATAAAGTAGAAG
 TAAAAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAA
 GGAGACAGAAATTTTACGACCAAACTACTAATTTGAAGGAAATCAGTG
 GTTATCTTATAAATCATTTCAATGGTGTTCGTCGTTTTGTTTGTCTAGGTA
 AAGCATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAA
 CCACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAAC
 AACTACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTA
 TCGCTGCTGTTAAGGTACCGGTTTGGACTGAACAGGAGGGCAAGATGAT
 ATTAATGGTATACAGCTGTAACTACTGGGGATGGCACTACAAAGTAGC
 TGTATCATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCAAT
 TATACACCAAGAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAA
 GTGACAGTAGCTGGAACTAATTTCTCTCAAGAACCTATTGAAATGGTTT
 ACCAAAGACTGGTGTATATAATATTATCGGAAGTACTGAAGTAAAAATG
 AAGCTAAAAATATCAAGTCAAGCCAAATTTACTTTAGAAAAAGGTGACAAA
 ATAAATTTAGTCAAGTATTTGACAGCAGATGGTTACCAAGTGGATTTCTTA
 CAAATCTTATAGTGGTGTTCGTCGTATATTTCTGTGAAAAAGCTAACTA
 CAAGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCC
 AACTTACCTAAAAACAGGTACCTATACATTTTACTAAAACTGTAGATGTGAA
 AAGTCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTG
 AAAAAATACATTATGATCAAGTGTAGTAGTAGATGGTCACTAGTGGATT
 TCATACAAGAGTTATTCGGGTATTCGTCGTATATTGAAATT

SEQ ID NO. 8909

STRAIN CJB110

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTCTC
 TACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTATA
 ATGGTCAACAAGTCCTGTTTTTGGGATCAAACCTACATCGGTTCAAGTTAA
 TAATCAGACAGGCACTAGTGTGGATGCTAATAATTTCTTCCAATGAGACAA
 GTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGCTGTAT
 AAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCTTT
 AGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAAGGGAAT
 ATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAGCC
 CCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCAAGT
 ATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTGGCG
 TACGTGATACGACGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAGAG
 ACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAGAA
 AATAGCAACGCAAGGAAATATACATTTTCAATATAAGTAGAAGTAAAAA
 ATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGAC
 AGAATTTTTACGACCAATACTAATTTGAAGGAAATCAGTGGTTATC
 TTATAAATCATTTCAATGGTGTTCGTCGTTTTGTTTGTCTAGGTAAAGCAT
 CTTCAAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCCAA
 GCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACCACTAC
 AGGTTTTGATATTTTAAATTACGAATATTAAAGATGATAACGGTATCGCTG
 CTGTTAAGGTACCGGTTTTGGACTGAACAAAGGAGGCAAGATGATATTA
 TGGTATACAGCTGTAACCTACTGGGGATGGCAACTACAAAGTAGCTGTATC
 ATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCAATTTACT
 ACCAAGAAGCTAGTGGGACACTTGTAGGTGTACAGGAACATAAGTGACA
 GTAGCTGGAACATAATTTCTCAAGAACCTATTGAAATGGTTTAGCAAA
 GACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAATGAAGCTA
 AAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATAAAT
 TATGATCAAGTATTGACAGCAGATGGTTACCAAGTGGATTCTTACAAATC
 TTATAGTGGTGTTCGTCGCTATATTCTGTGAAAAAGCTAACTACAAAGTA
 GTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTA
 CCTAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGAGTCA
 ACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAAAA
 TACATTATGATCAAGTGTAGTAGTAGATGGTCACTAGTGGATTTCATAC
 AAGAGTTATTCGGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8910

STRAIN 1169NT

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTC
 TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCA
 TAATGGTCAACAAGTCCTGTTTTTGGGATCAAACCTACATCGGTTCAAGTT
 AATAATCAGACAGGCACTAGTGTGGATGCTAATAATTTCTTCCAATGAGAC
 AAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGCTGTG
 ATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
 TTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAAGGAA
 TTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAG
 CCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCAA
 GTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGGTGG
 CGTACGTGATACGACGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAG

Table 89: Comparative Sequences relating to SAG1350

AGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTTATACATTTTCACATAAAGTAGAAGTAAA
 AAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTTGACAAAGGAG
 ACAGAATTTTTCAGACCAATATACTAATTTGAAGGAAATCAGTGGTTA
 TCTTATAAATCAATCAATGGTGTTCGTGTTTTGTTTTGCTAGGTAAAGC
 ATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCTCAACCAC
 AAGCCCGTATTACTAAACTGGTAGACTGACTATTTCTAACGAAACCACT
 ACAGGTTTTGATATTTAATTAACGAATATTAAGATGATAACGGTATCGC
 TGCTGTTAAGGTACCGGTTTTGGACTGAACAAGGAGGCAAGATGATATTA
 AATGGTATACAGCTGTAACACTGGGGATGGCAACTACAAAGTAGCTGTA
 TCATTTGCTGACCATAGAATGAGAAGGCTTTTATAATATTCATTTATA
 CTACCAAGAGCTAGTGGGACACTTGTAGGTGTAACAGGAATAAAGTGA
 CAGTAGCTGGAaCTAATTTCTCTCAAGAACCTATTGAAAAATGGTTTAGCA
 AAGACTGGTGTATTATAATATTCGGAAGTACTGAAGTAAAAATGAAGC
 TAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATAA
 ATTATGATCAAGTATTGACAGCAGATGGTTACCACTGGATTCTTTACAAA
 TCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAAG
 TAGTGA AAAAGCGAAGATGAGGCGACTAAACCGACTAGTTATCCCACT
 TACCTAAACAGGTACCTATACATTTACTAAAAGTGTAGATGTGAAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAA
 AATACATTTATGATCAAGTGTAGTAGTAGTGGTCATCAGTGGATTTCAT
 ACAAGAGTTATTCGGTATTCTGCTGCTATATTGAAATT

SEQ ID NO. 8911

STRAIN JM9130013

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
 CTCTACGTAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTC
 ATAATGGTCACAAGTCTGTTTTTTCGGGATCAAACTACATCGGTTCAAGT
 TAATAATCAGACAGGCACCTAGTGTGGATGCTAATAATTTCTTCAATGAGA
 CAAGTGCCTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 GATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
 TTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTTACCTGAACAAGGGA
 ATTATGTTTATAGCAAAAGAACCGAGGTGAAAAATACACCTTCAAATCA
 GCCCAGTAGCTTTCTATGCAAAAGAGGTGATAAAGTTTTCTATGACCA
 AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGTG
 GCGTACGTCGATACGAGCTATTGAGTCACTAGATCCATCAGGAGGTTC
 GAGACTAAAGCACCTACTCTCTGTAACAAATTCAGGAAGCAATAATCAAGA
 GAAATAGCAACGCAAGGAAATTTATACATTTTTCACATAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCCAACTCAATTTACATTTGGACAAAGGA
 GACAGAATTTTTCAGCAACAAATACTAATTTGAAGGAATCAGTGGTT
 ATCTTATAAATCATTCATGGTGTTCGTGTTTTGTTTTGCTAGGTAAAG
 CATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
 CAAGCCCGTATTACTAAAAGTGGTAGACTGACTATTTATAACGAAACCAAC
 TACAGGTTTTGATATTTAATTACGAATATAAAGATGATAACGGTATCG
 CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
 AAATGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTGT
 ATCATTTGCTGACCATAGAATGAGAAGGGCTTTTATAATATTCATTTAT
 ACTACCAAGAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAAGTG
 ACAGTAGCTGGAACTAATTTCTCTCAAGAACCTATTGAAAAATGGTTTAGC
 AAAGACTGGTGTTTATAATATTTATCGGAAGTACTGAAGTAAAAAATGAAG
 CTAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTTACCACTGGATTCTTTACAA
 ATCTTATAGTGGTGTTCGTGCTATATTCTCTGAAAAAGCTAACTACAA
 GTAGTGAAAAAGCGAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
 TTACCTAAAAACAGGTACCTATACATTTACTAAAAGTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAA
 AAATACATTTATGATCAAGTGTAGTAGTAGTGGTCATCAGTGGATTTC
 TACAAGAGTTATTCGGTATTCTGCTGCTATATTGAAATT

PRETTY of: /biotmp/msa255059.2{*} February 11, 2003 08:41 ..

| | | | |
|---------------------------|------------------|------------|----------------------------------|
| | 1 | | 50 |
| msa255059.2{91_M732} | ----- --CAAGTAAA | TGATACTAAG | CAATCTTACT CTCTACGTAA |
| msa255059.2{91_M781} | ---AAAAAAG | GACAAGTAAA | TGATACTAAG CAATCTTACT CTCTACGTAA |
| msa255059.2{91_COH1} | ---AAAAAAG | GACAAGTAAA | TGATACTAAG CAATCTTACT CTCTACGTAA |
| msa255059.2{91_18RS21} | ---AAAAAAG | GACAAGTAAA | TGATACTAAG CAATCTTACT CTCTACGTAA |
| msa255059.2{91_2603} | atgAAAAAAG | GACAAGTAAA | TGATACTAAG CAATCTTACT CTCTACGTAA |
| msa255059.2{91_1169NT} | ---AAAAAAG | GACAAGTAAA | TGATACTAAG CAATCTTACT CTCTACGTAA |
| msa255059.2{91_090} | ---AAAAAAG | GACAAGTAAA | TGATACTAAG CAATCTTACT CTCTACGTAA |
| msa255059.2{91_A909} | ---AAAAAAG | GACAAGTAAA | TGATACTAAG CAATCTTACT CTCTACGTAA |
| msa255059.2{91_CJB110} | ---AAAAAAG | GACAAGTAAA | TGATACTAAG CAATCTTACT CTCTACGTAA |
| msa255059.2{91_H36B} | ---AAAAAAG | GACAAGTAAA | TGATACTAAG CAATCTTACT CTCTACGTAA |
| msa255059.2{91_JM9130013} | ---AAAAAAG | GACAAGTAAA | TGATACTAAG CAATCTTACT CTCTACGTAA |
| Consensus | ***** | ***** | ***** |

| | | | |
|------------------------|------------|-----------|----------------------------------|
| | 51 | | 100 |
| msa255059.2{91_M732} | ATATAAATTT | GGTTAGCAT | CAGTAATTTT AGGGTCATTC ATAATGGTCA |
| msa255059.2{91_M781} | ATATAAATTT | GGTTAGCAT | CAGTAATTTT AGGGTCATTC ATAATGGTCA |
| msa255059.2{91_COH1} | ATATAAATTT | GGTTAGCAT | CAGTAATTTT AGGGTCATTC ATAATGGTCA |
| msa255059.2{91_18RS21} | ATATAAATTT | GGTTAGCAT | CAGTAATTTT AGGGTCATTC ATAATGGTCA |
| msa255059.2{91_2603} | ATATAAATTT | GGTTAGCAT | CAGTAATTTT AGGGTCATTC ATAATGGTCA |
| msa255059.2{91_1169NT} | ATATAAATTT | GGTTAGCAT | CAGTAATTTT AGGGTCATTC ATAATGGTCA |

Table 89: Comparative Sequences relating to SAG1350

| | | | | | |
|---------------------------|-------------|------------|------------|------------|------------|
| msa255059.2{91_090} | ATATAAATTT | GGTTTAGCAT | CAGTAATTTT | AGGGTCATTC | ATAATGGTCA |
| msa255059.2{91_A909} | ATATAAATTT | GGTTTAGCAT | CAGTAATTTT | AGGGTCATTC | ATAATGGTCA |
| msa255059.2{91_CJB110} | ATATAAATTT | GGTTTAGCAT | CAGTAATTTT | AGGGTCATTC | ATAATGGTCA |
| msa255059.2{91_H36B} | ATATAAATTT | GGTTTAGCAT | CAGTAATTTT | AGGGTCATTC | ATAATGGTCA |
| msa255059.2{91_JM9130013} | ATATAAATTT | GGTTTAGCAT | CAGTAATTTT | AGGGTCATTC | ATAATGGTCA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | CAAGTCCTGT | TTTTGCGGAT | CAAACTACAT | CGGTTCAAGT | TAATAATCAG |
| msa255059.2{91_M781} | CAAGTCCTGT | TTTTGCGGAT | CAAACTACAT | CGGTTCAAGT | TAATAATCAG |
| msa255059.2{91_COH1} | CAAGTCCTGT | TTTTGCGGAT | CAAACTACAT | CGGTTCAAGT | TAATAATCAG |
| msa255059.2{91_18RS21} | CAAGTCCTGT | TTTTGCGGAT | CAAACTACAT | CGGTTCAAGT | TAATAATCAG |
| msa255059.2{91_2603} | CAAGTCCTGT | TTTTGCGGAT | CAAACTACAT | CGGTTCAAGT | TAATAATCAG |
| msa255059.2{91_1169NT} | CAAGTCCTGT | TTTTGCGGAT | CAAACTACAT | CGGTTCAAGT | TAATAATCAG |
| msa255059.2{91_090} | CAAGTCCTGT | TTTTGCGGAT | CAAACTACAT | CGGTTCAAGT | TAATAATCAG |
| msa255059.2{91_A909} | CAAGTCCTGT | TTTTGCGGAT | CAAACTACAT | CGGTTCAAGT | TAATAATCAG |
| msa255059.2{91_CJB110} | CAAGTCCTGT | TTTTGCGGAT | CAAACTACAT | CGGTTCAAGT | TAATAATCAG |
| msa255059.2{91_H36B} | CAAGTCCTGT | TTTTGCGGAT | CAAACTACAT | CGGTTCAAGT | TAATAATCAG |
| msa255059.2{91_JM9130013} | CAAGTCCTGT | TTTTGCGGAT | CAAACTACAT | CGGTTCAAGT | TAATAATCAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | ACAGGCCACTA | GTGTGGATGc | TAATAATTCT | TCCAATGAGA | CAAGTGCCTC |
| msa255059.2{91_M781} | ACAGGCCACTA | GTGTGGATGc | TAATAATTCT | TCCAATGAGA | CAAGTGCCTC |
| msa255059.2{91_COH1} | ACAGGCCACTA | GTGTGGATGc | TAATAATTCT | TCCAATGAGA | CAAGTGCCTC |
| msa255059.2{91_18RS21} | ACAGGCCACTA | GTGTGGATGc | TAATAATTCT | TCCAATGAGA | CAAGTGCCTC |
| msa255059.2{91_2603} | ACAGGCCACTA | GTGTGGATGc | TAATAATTCT | TCCAATGAGA | CAAGTGCCTC |
| msa255059.2{91_1169NT} | ACAGGCCACTA | GTGTGGATGc | TAATAATTCT | TCCAATGAGA | CAAGTGCCTC |
| msa255059.2{91_090} | ACAGGCCACTA | GTGTGGATGc | TAATAATTCT | TCCAATGAGA | CAAGTGCCTC |
| msa255059.2{91_A909} | ACAGGCCACTA | GTGTGGATGc | TAATAATTCT | TCCAATGAGA | CAAGTGCCTC |
| msa255059.2{91_CJB110} | ACAGGCCACTA | GTGTGGATGc | TAATAATTCT | TCCAATGAGA | CAAGTGCCTC |
| msa255059.2{91_H36B} | ACAGGCCACTA | GTGTGGATGc | TAATAATTCT | TCCAATGAGA | CAAGTGCCTC |
| msa255059.2{91_JM9130013} | ACAGGCCACTA | GTGTGGATGc | TAATAATTCT | TCCAATGAGA | CAAGTGCCTC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | AAGTGTGATT | ACTTCCAATA | ATGATAGTGT | TCAAGCGTCT | GATAAAGTTG |
| msa255059.2{91_M781} | AAGTGTGATT | ACTTCCAATA | ATGATAGTGT | TCAAGCGTCT | GATAAAGTTG |
| msa255059.2{91_COH1} | AAGTGTGATT | ACTTCCAATA | ATGATAGTGT | TCAAGCGTCT | GATAAAGTTG |
| msa255059.2{91_18RS21} | AAGTGTGATT | ACTTCCAATA | ATGATAGTGT | TCAAGCGTCT | GATAAAGTTG |
| msa255059.2{91_2603} | AAGTGTGATT | ACTTCCAATA | ATGATAGTGT | TCAAGCGTCT | GATAAAGTTG |
| msa255059.2{91_1169NT} | AAGTGTGATT | ACTTCCAATA | ATGATAGTGT | TCAAGCGTCT | GATAAAGTTG |
| msa255059.2{91_090} | AAGTGTGATT | ACTTCCAATA | ATGATAGTGT | TCAAGCGTCT | GATAAAGTTG |
| msa255059.2{91_A909} | AAGTGTGATT | ACTTCCAATA | ATGATAGTGT | TCAAGCGTCT | GATAAAGTTG |
| msa255059.2{91_CJB110} | AAGTGTGATT | ACTTCCAATA | ATGATAGTGT | TCAAGCGTCT | GATAAAGTTG |
| msa255059.2{91_H36B} | AAGTGTGATT | ACTTCCAATA | ATGATAGTGT | TCAAGCGTCT | GATAAAGTTG |
| msa255059.2{91_JM9130013} | AAGTGTGATT | ACTTCCAATA | ATGATAGTGT | TCAAGCGTCT | GATAAAGTTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | TAAATAGTCA | AAATACGGCA | ACAAAGGACA | TTACTACTCC | TTTAGTAGAG |
| msa255059.2{91_M781} | TAAATAGTCA | AAATACGGCA | ACAAAGGACA | TTACTACTCC | TTTAGTAGAG |
| msa255059.2{91_COH1} | TAAATAGTCA | AAATACGGCA | ACAAAGGACA | TTACTACTCC | TTTAGTAGAG |
| msa255059.2{91_18RS21} | TAAATAGTCA | AAATACGGCA | ACAAAGGACA | TTACTACTCC | TTTAGTAGAG |
| msa255059.2{91_2603} | TAAATAGTCA | AAATACGGCA | ACAAAGGACA | TTACTACTCC | TTTAGTAGAG |
| msa255059.2{91_1169NT} | TAAATAGTCA | AAATACGGCA | ACAAAGGACA | TTACTACTCC | TTTAGTAGAG |
| msa255059.2{91_090} | TAAATAGTCA | AAATACGGCA | ACAAAGGACA | TTACTACTCC | TTTAGTAGAG |
| msa255059.2{91_A909} | TAAATAGTCA | AAATACGGCA | ACAAAGGACA | TTACTACTCC | TTTAGTAGAG |
| msa255059.2{91_CJB110} | TAAATAGTCA | AAATACGGCA | ACAAAGGACA | TTACTACTCC | TTTAGTAGAG |
| msa255059.2{91_H36B} | TAAATAGTCA | AAATACGGCA | ACAAAGGACA | TTACTACTCC | TTTAGTAGAG |
| msa255059.2{91_JM9130013} | TAAATAGTCA | AAATACGGCA | ACAAAGGACA | TTACTACTCC | TTTAGTAGAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | ACAAAGCCAA | TGGTGGAAAA | AACATTACCT | GAACAAGGGA | ATTATGTTTA |
| msa255059.2{91_M781} | ACAAAGCCAA | TGGTGGAAAA | AACATTACCT | GAACAAGGGA | ATTATGTTTA |
| msa255059.2{91_COH1} | ACAAAGCCAA | TGGTGGAAAA | AACATTACCT | GAACAAGGGA | ATTATGTTTA |
| msa255059.2{91_18RS21} | ACAAAGCCAA | TGGTGGAAAA | AACATTACCT | GAACAAGGGA | ATTATGTTTA |
| msa255059.2{91_2603} | ACAAAGCCAA | TGGTGGAAAA | AACATTACCT | GAACAAGGGA | ATTATGTTTA |
| msa255059.2{91_1169NT} | ACAAAGCCAA | TGGTGGAAAA | AACATTACCT | GAACAAGGGA | ATTATGTTTA |
| msa255059.2{91_090} | ACAAAGCCAA | TGGTGGAAAA | AACATTACCT | GAACAAGGGA | ATTATGTTTA |
| msa255059.2{91_A909} | ACAAAGCCAA | TGGTGGAAAA | AACATTACCT | GAACAAGGGA | ATTATGTTTA |
| msa255059.2{91_CJB110} | ACAAAGCCAA | TGGTGGAAAA | AACATTACCT | GAACAAGGGA | ATTATGTTTA |
| msa255059.2{91_H36B} | ACAAAGCCAA | TGGTGGAAAA | AACATTACCT | GAACAAGGGA | ATTATGTTTA |
| msa255059.2{91_JM9130013} | ACAAAGCCAA | TGGTGGAAAA | AACATTACCT | GAACAAGGGA | ATTATGTTTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | TAGCAAAGAA | ACCGAGGTGA | AAAATACACC | TTCAAATCA | GCCCCAGTAG |
| msa255059.2{91_M781} | TAGCAAAGAA | ACCGAGGTGA | AAAATACACC | TTCAAATCA | GCCCCAGTAG |
| msa255059.2{91_COH1} | TAGCAAAGAA | ACCGAGGTGA | AAAATACACC | TTCAAATCA | GCCCCAGTAG |
| msa255059.2{91_18RS21} | TAGCAAAGAA | ACCGAGGTGA | AAAATACACC | TTCAAATCA | GCCCCAGTAG |
| msa255059.2{91_2603} | TAGCAAAGAA | ACCGAGGTGA | AAAATACACC | TTCAAATCA | GCCCCAGTAG |

Table 89: Comparative Sequences relating to SAG1350

| | | | | | |
|---------------------------|------------|------------|------------|------------|-------------|
| msa255059.2{91_1169NT} | TAGCAAAGAA | ACCGAGGTGA | AAAATACACC | TTCAAATCA | GCCCCAGTAG |
| msa255059.2{91_090} | TAGCAAAGAA | ACCGAGGTGA | AAAATACACC | TTCAAATCA | GCCCCAGTAG |
| msa255059.2{91_A909} | TAGCAAAGAA | ACCGAGGTGA | AAAATACACC | TTCAAATCA | GCCCCAGTAG |
| msa255059.2{91_CJB110} | TAGCAAAGAA | ACCGAGGTGA | AAAATACACC | TTCAAATCA | GCCCCAGTAG |
| msa255059.2{91_H36B} | TAGCAAAGAA | ACCGAGGTGA | AAAATACACC | TTCAAATCA | GCCCCAGTAG |
| msa255059.2{91_JM9130013} | TAGCAAAGAA | ACCGAGGTGA | AAAATACACC | TTCAAATCA | GCCCCAGTAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 401 | | | | | |
| msa255059.2{91_M732} | CTTTCTATGC | AAAGAAAGGT | GATAAAGTTT | TCTATGACCA | AGTATTTAAT |
| msa255059.2{91_M781} | CTTTCTATGC | AAAGAAAGGT | GATAAAGTTT | TCTATGACCA | AGTATTTAAT |
| msa255059.2{91_COH1} | CTTTCTATGC | AAAGAAAGGT | GATAAAGTTT | TCTATGACCA | AGTATTTAAT |
| msa255059.2{91_18RS21} | CTTTCTATGC | AAAGAAAGGT | GATAAAGTTT | TCTATGACCA | AGTATTTAAT |
| msa255059.2{91_2603} | CTTTCTATGC | AAAGAAAGGT | GATAAAGTTT | TCTATGACCA | AGTATTTAAT |
| msa255059.2{91_1169NT} | CTTTCTATGC | AAAGAAAGGT | GATAAAGTTT | TCTATGACCA | AGTATTTAAT |
| msa255059.2{91_090} | CTTTCTATGC | AAAGAAAGGT | GATAAAGTTT | TCTATGACCA | AGTATTTAAT |
| msa255059.2{91_A909} | CTTTCTATGC | AAAGAAAGGT | GATAAAGTTT | TCTATGACCA | AGTATTTAAT |
| msa255059.2{91_CJB110} | CTTTCTATGC | AAAGAAAGGT | GATAAAGTTT | TCTATGACCA | AGTATTTAAT |
| msa255059.2{91_H36B} | CTTTCTATGC | AAAGAAAGGT | GATAAAGTTT | TCTATGACCA | AGTATTTAAT |
| msa255059.2{91_JM9130013} | CTTTCTATGC | AAAGAAAGGT | GATAAAGTTT | TCTATGACCA | AGTATTTAAT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 451 | | | | | |
| msa255059.2{91_M732} | AAAGATAATG | TgAAATGGAT | TTTATATAAG | TCTTTTgGTG | GCGTACGTCG |
| msa255059.2{91_M781} | AAAGATAATG | TgAAATGGAT | TTTATATAAG | TCTTTTgGTG | GCGTACGTCG |
| msa255059.2{91_COH1} | AAAGATAATG | TgAAATGGAT | TTTATATAAG | TCTTTTgGTG | GCGTACGTCG |
| msa255059.2{91_18RS21} | AAAGATAATG | TgAAATGGAT | TTTATATAAG | TCTTTTgGTG | GCGTACGTCG |
| msa255059.2{91_2603} | AAAGATAATG | TgAAATGGAT | TTTATATAAG | TCTTTTgGTG | GCGTACGTCG |
| msa255059.2{91_1169NT} | AAAGATAATG | TgAAATGGAT | TTTATATAAG | TCTTTTgGTG | GCGTACGTCG |
| msa255059.2{91_090} | AAAGATAATG | TgAAATGGAT | TTTATATAAG | TCTTTTgGTG | GCGTACGTCG |
| msa255059.2{91_A909} | AAAGATAATG | TgAAATGGAT | TTTATATAAG | TCTTTTgGTG | GCGTACGTCG |
| msa255059.2{91_CJB110} | AAAGATAATG | TgAAATGGAT | TTTATATAAG | TCTTTTgGTG | GCGTACGTCG |
| msa255059.2{91_H36B} | AAAGATAATG | TgAAATGGAT | TTTATATAAG | TCTTTTgGTG | GCGTACGTCG |
| msa255059.2{91_JM9130013} | AAAGATAATG | TgAAATGGAT | TTTATATAAG | TCTTTTgGTG | GCGTACGTCG |
| Consensus | ***** | *..***** | ***** | *****_*** | ***** |
| 501 | | | | | |
| msa255059.2{91_M732} | ATACGCAGCT | ATTGAGTCAC | TAGATCCATC | AGGAGGTTCA | GAGACTAAAG |
| msa255059.2{91_M781} | ATACGCAGCT | ATTGAGTCAC | TAGATCCATC | AGGAGGTTCA | GAGACTAAAG |
| msa255059.2{91_COH1} | ATACGCAGCT | ATTGAGTCAC | TAGATCCATC | AGGAGGTTCA | GAGACTAAAG |
| msa255059.2{91_18RS21} | ATACGCAGCT | ATTGAGTCAC | TAGATCCATC | AGGAGGTTCA | GAGACTAAAG |
| msa255059.2{91_2603} | ATACGCAGCT | ATTGAGTCAC | TAGATCCATC | AGGAGGTTCA | GAGACTAAAG |
| msa255059.2{91_1169NT} | ATACGCAGCT | ATTGAGTCAC | TAGATCCATC | AGGAGGTTCA | GAGACTAAAG |
| msa255059.2{91_090} | ATACGCAGCT | ATTGAGTCAC | TAGATCCATC | AGGAGGTTCA | GAGACTAAAG |
| msa255059.2{91_A909} | ATACGCAGCT | ATTGAGTCAC | TAGATCCATC | AGGAGGTTCA | GAGACTAAAG |
| msa255059.2{91_CJB110} | ATACGCAGCT | ATTGAGTCAC | TAGATCCATC | AGGAGGTTCA | GAGACTAAAG |
| msa255059.2{91_H36B} | ATACGCAGCT | ATTGAGTCAC | TAGATCCATC | AGGAGGTTCA | GAGACTAAAG |
| msa255059.2{91_JM9130013} | ATACGCAGCT | ATTGAGTCAC | TAGATCCATC | AGGAGGTTCA | GAGACTAAAG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 551 | | | | | |
| msa255059.2{91_M732} | CACCTACTCC | TGTAACAAAT | TCAGGAAGCA | ATAATCAAGA | GAAAAATAGCA |
| msa255059.2{91_M781} | CACCTACTCC | TGTAACAAAT | TCAGGAAGCA | ATAATCAAGA | GAAAAATAGCA |
| msa255059.2{91_COH1} | CACCTACTCC | TGTAACAAAT | TCAGGAAGCA | ATAATCAAGA | GAAAAATAGCA |
| msa255059.2{91_18RS21} | CACCTACTCC | TGTAACAAAT | TCAGGAAGCA | ATAATCAAGA | GAAAAATAGCA |
| msa255059.2{91_2603} | CACCTACTCC | TGTAACAAAT | TCAGGAAGCA | ATAATCAAGA | GAAAAATAGCA |
| msa255059.2{91_1169NT} | CACCTACTCC | TGTAACAAAT | TCAGGAAGCA | ATAATCAAGA | GAAAAATAGCA |
| msa255059.2{91_090} | CACCTACTCC | TGTAACAAAT | TCAGGAAGCA | ATAATCAAGA | GAAAAATAGCA |
| msa255059.2{91_A909} | CACCTACTCC | TGTAACAAAT | TCAGGAAGCA | ATAATCAAGA | GAAAAATAGCA |
| msa255059.2{91_CJB110} | CACCTACTCC | TGTAACAAAT | TCAGGAAGCA | ATAATCAAGA | GAAAAATAGCA |
| msa255059.2{91_H36B} | CACCTACTCC | TGTAACAAAT | TCAGGAAGCA | ATAATCAAGA | GAAAAATAGCA |
| msa255059.2{91_JM9130013} | CACCTACTCC | TGTAACAAAT | TCAGGAAGCA | ATAATCAAGA | GAAAAATAGCA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 601 | | | | | |
| msa255059.2{91_M732} | ACGCAAGGAA | ATTATACATT | TTTACATAAA | GTAGAAGTAA | AAAATGAAGC |
| msa255059.2{91_M781} | ACGCAAGGAA | ATTATACATT | TTTACATAAA | GTAGAAGTAA | AAAATGAAGC |
| msa255059.2{91_COH1} | ACGCAAGGAA | ATTATACATT | TTTACATAAA | GTAGAAGTAA | AAAATGAAGC |
| msa255059.2{91_18RS21} | ACGCAAGGAA | ATTATACATT | TTTACATAAA | GTAGAAGTAA | AAAATGAAGC |
| msa255059.2{91_2603} | ACGCAAGGAA | ATTATACATT | TTTACATAAA | GTAGAAGTAA | AAAATGAAGC |
| msa255059.2{91_1169NT} | ACGCAAGGAA | ATTATACATT | TTTACATAAA | GTAGAAGTAA | AAAATGAAGC |
| msa255059.2{91_090} | ACGCAAGGAA | ATTATACATT | TTTACATAAA | GTAGAAGTAA | AAAATGAAGC |
| msa255059.2{91_A909} | ACGCAAGGAA | ATTATACATT | TTTACATAAA | GTAGAAGTAA | AAAATGAAGC |
| msa255059.2{91_CJB110} | ACGCAAGGAA | ATTATACATT | TTTACATAAA | GTAGAAGTAA | AAAATGAAGC |
| msa255059.2{91_H36B} | ACGCAAGGAA | ATTATACATT | TTTACATAAA | GTAGAAGTAA | AAAATGAAGC |
| msa255059.2{91_JM9130013} | ACGCAAGGAA | ATTATACATT | TTTACATAAA | GTAGAAGTAA | AAAATGAAGC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| 651 | | | | | |
| msa255059.2{91_M732} | TAAGGTAGCG | AGTCCAATC | AATTTACATT | GGACAAAGGA | GACAGAATTT |
| msa255059.2{91_M781} | TAAGGTAGCG | AGTCCAATC | AATTTACATT | GGACAAAGGA | GACAGAATTT |
| msa255059.2{91_COH1} | TAAGGTAGCG | AGTCCAATC | AATTTACATT | GGACAAAGGA | GACAGAATTT |
| msa255059.2{91_18RS21} | TAAGGTAGCG | AGTCCAATC | AATTTACATT | GGACAAAGGA | GACAGAATTT |

Table 89: Comparative Sequences relating to SAG1350

| | | | | | |
|---------------------------|------------|-------------|------------|------------|------------|
| msa255059.2{91_2603} | TAAGGTAGCG | AGTCCAACCTC | AATTTACATT | GGACAAAGGA | GACAGAATTT |
| msa255059.2{91_1169NT} | TAAGGTAGCG | AGTCCAACCTC | AATTTACATT | GGACAAAGGA | GACAGAATTT |
| msa255059.2{91_090} | TAAGGTAGCG | AGTCCAACCTC | AATTTACATT | GGACAAAGGA | GACAGAATTT |
| msa255059.2{91_A909} | TAAGGTAGCG | AGTCCAACCTC | AATTTACATT | GGACAAAGGA | GACAGAATTT |
| msa255059.2{91_CJB110} | TAAGGTAGCG | AGTCCAACCTC | AATTTACATT | GGACAAAGGA | GACAGAATTT |
| msa255059.2{91_H36B} | TAAGGTAGCG | AGTCCAACCTC | AATTTACATT | GGACAAAGGA | GACAGAATTT |
| msa255059.2{91_JM9130013} | TAAGGTAGCG | AGTCCAACCTC | AATTTACATT | GGACAAAGGA | GACAGAATTT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | TTTACGACCA | AATACTAACT | ATTGAAGGAA | ATCAGTGGTT | ATCTTATAAA |
| msa255059.2{91_M781} | TTTACGACCA | AATACTAACT | ATTGAAGGAA | ATCAGTGGTT | ATCTTATAAA |
| msa255059.2{91_COH1} | TTTACGACCA | AATACTAACT | ATTGAAGGAA | ATCAGTGGTT | ATCTTATAAA |
| msa255059.2{91_18RS21} | TTTACGACCA | AATACTAACT | ATTGAAGGAA | ATCAGTGGTT | ATCTTATAAA |
| msa255059.2{91_2603} | TTTACGACCA | AATACTAACT | ATTGAAGGAA | ATCAGTGGTT | ATCTTATAAA |
| msa255059.2{91_1169NT} | TTTACGACCA | AATACTAACT | ATTGAAGGAA | ATCAGTGGTT | ATCTTATAAA |
| msa255059.2{91_090} | TTTACGACCA | AATACTAACT | ATTGAAGGAA | ATCAGTGGTT | ATCTTATAAA |
| msa255059.2{91_A909} | TTTACGACCA | AATACTAACT | ATTGAAGGAA | ATCAGTGGTT | ATCTTATAAA |
| msa255059.2{91_CJB110} | TTTACGACCA | AATACTAACT | ATTGAAGGAA | ATCAGTGGTT | ATCTTATAAA |
| msa255059.2{91_H36B} | TTTACGACCA | AATACTAACT | ATTGAAGGAA | ATCAGTGGTT | ATCTTATAAA |
| msa255059.2{91_JM9130013} | TTTACGACCA | AATACTAACT | ATTGAAGGAA | ATCAGTGGTT | ATCTTATAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | TCATTCAATG | GTGTTCTGTCG | TTTTGTTTTG | CTAGGTAAAG | CATCTTCAGT |
| msa255059.2{91_M781} | TCATTCAATG | GTGTTCTGTCG | TTTTGTTTTG | CTAGGTAAAG | CATCTTCAGT |
| msa255059.2{91_COH1} | TCATTCAATG | GTGTTCTGTCG | TTTTGTTTTG | CTAGGTAAAG | CATCTTCAGT |
| msa255059.2{91_18RS21} | TCATTCAATG | GTGTTCTGTCG | TTTTGTTTTG | CTAGGTAAAG | CATCTTCAGT |
| msa255059.2{91_2603} | TCATTCAATG | GTGTTCTGTCG | TTTTGTTTTG | CTAGGTAAAG | CATCTTCAGT |
| msa255059.2{91_1169NT} | TCATTCAATG | GTGTTCTGTCG | TTTTGTTTTG | CTAGGTAAAG | CATCTTCAGT |
| msa255059.2{91_090} | TCATTCAATG | GTGTTCTGTCG | TTTTGTTTTG | CTAGGTAAAG | CATCTTCAGT |
| msa255059.2{91_A909} | TCATTCAATG | GTGTTCTGTCG | TTTTGTTTTG | CTAGGTAAAG | CATCTTCAGT |
| msa255059.2{91_CJB110} | TCATTCAATG | GTGTTCTGTCG | TTTTGTTTTG | CTAGGTAAAG | CATCTTCAGT |
| msa255059.2{91_H36B} | TCATTCAATG | GTGTTCTGTCG | TTTTGTTTTG | CTAGGTAAAG | CATCTTCAGT |
| msa255059.2{91_JM9130013} | TCATTCAATG | GTGTTCTGTCG | TTTTGTTTTG | CTAGGTAAAG | CATCTTCAGT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | AGAAAAAAGT | GAAGATAAAG | AAAAAGTGTC | TCCTCAACCA | CAAGCCCCTA |
| msa255059.2{91_M781} | AGAAAAAAGT | GAAGATAAAG | AAAAAGTGTC | TCCTCAACCA | CAAGCCCCTA |
| msa255059.2{91_COH1} | AGAAAAAAGT | GAAGATAAAG | AAAAAGTGTC | TCCTCAACCA | CAAGCCCCTA |
| msa255059.2{91_18RS21} | AGAAAAAAGT | GAAGATAAAG | AAAAAGTGTC | TCCTCAACCA | CAAGCCCCTA |
| msa255059.2{91_2603} | AGAAAAAAGT | GAAGATAAAG | AAAAAGTGTC | TCCTCAACCA | CAAGCCCCTA |
| msa255059.2{91_1169NT} | AGAAAAAAGT | GAAGATAAAG | AAAAAGTGTC | TCCTCAACCA | CAAGCCCCTA |
| msa255059.2{91_090} | AGAAAAAAGT | GAAGATAAAG | AAAAAGTGTC | TCCTCAACCA | CAAGCCCCTA |
| msa255059.2{91_A909} | AGAAAAAAGT | GAAGATAAAG | AAAAAGTGTC | TCCTCAACCA | CAAGCCCCTA |
| msa255059.2{91_CJB110} | AGAAAAAAGT | GAAGATAAAG | AAAAAGTGTC | TCCTCAACCA | CAAGCCCCTA |
| msa255059.2{91_H36B} | AGAAAAAAGT | GAAGATAAAG | AAAAAGTGTC | TCCTCAACCA | CAAGCCCCTA |
| msa255059.2{91_JM9130013} | AGAAAAAAGT | GAAGATAAAG | AAAAAGTGTC | TCCTCAACCA | CAAGCCCCTA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | TTACTAAAAC | TGGTAGACTG | ACTATTTCtA | ACGAAACAAC | TACAGGTTTT |
| msa255059.2{91_M781} | TTACTAAAAC | TGGTAGACTG | ACTATTTCtA | ACGAAACAAC | TACAGGTTTT |
| msa255059.2{91_COH1} | TTACTAAAAC | TGGTAGACTG | ACTATTTCtA | ACGAAACAAC | TACAGGTTTT |
| msa255059.2{91_18RS21} | TTACTAAAAC | TGGTAGACTG | ACTATTTCtA | ACGAAACAAC | TACAGGTTTT |
| msa255059.2{91_2603} | TTACTAAAAC | TGGTAGACTG | ACTATTTCtA | ACGAAACAAC | TACAGGTTTT |
| msa255059.2{91_1169NT} | TTACTAAAAC | TGGTAGACTG | ACTATTTCtA | ACGAAACAAC | TACAGGTTTT |
| msa255059.2{91_090} | TTACTAAAAC | TGGTAGACTG | ACTATTTCtA | ACGAAACAAC | TACAGGTTTT |
| msa255059.2{91_A909} | TTACTAAAAC | TGGTAGACTG | ACTATTTCtA | ACGAAACAAC | TACAGGTTTT |
| msa255059.2{91_CJB110} | TTACTAAAAC | TGGTAGACTG | ACTATTTCtA | ACGAAACAAC | TACAGGTTTT |
| msa255059.2{91_H36B} | TTACTAAAAC | TGGTAGACTG | ACTATTTCtA | ACGAAACAAC | TACAGGTTTT |
| msa255059.2{91_JM9130013} | TTACTAAAAC | TGGTAGACTG | ACTATTTCtA | ACGAAACAAC | TACAGGTTTT |
| Consensus | ***** | ***** | *****-* | ***** | ***** |
| msa255059.2{91_M732} | GATATTTTAA | TTACGAATAT | TAAAGATGAT | AACGGTATCG | CTGCTGTTAA |
| msa255059.2{91_M781} | GATATTTTAA | TTACGAATAT | TAAAGATGAT | AACGGTATCG | CTGCTGTTAA |
| msa255059.2{91_COH1} | GATATTTTAA | TTACGAATAT | TAAAGATGAT | AACGGTATCG | CTGCTGTTAA |
| msa255059.2{91_18RS21} | GATATTTTAA | TTACGAATAT | TAAAGATGAT | AACGGTATCG | CTGCTGTTAA |
| msa255059.2{91_2603} | GATATTTTAA | TTACGAATAT | TAAAGATGAT | AACGGTATCG | CTGCTGTTAA |
| msa255059.2{91_1169NT} | GATATTTTAA | TTACGAATAT | TAAAGATGAT | AACGGTATCG | CTGCTGTTAA |
| msa255059.2{91_090} | GATATTTTAA | TTACGAATAT | TAAAGATGAT | AACGGTATCG | CTGCTGTTAA |
| msa255059.2{91_A909} | GATATTTTAA | TTACGAATAT | TAAAGATGAT | AACGGTATCG | CTGCTGTTAA |
| msa255059.2{91_CJB110} | GATATTTTAA | TTACGAATAT | TAAAGATGAT | AACGGTATCG | CTGCTGTTAA |
| msa255059.2{91_H36B} | GATATTTTAA | TTACGAATAT | TAAAGATGAT | AACGGTATCG | CTGCTGTTAA |
| msa255059.2{91_JM9130013} | GATATTTTAA | TTACGAATAT | TAAAGATGAT | AACGGTATCG | CTGCTGTTAA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | GGTACCGGTT | TGGACTGAAC | AAGGAGGGCA | AGATGATATT | AAATGGTATA |
| msa255059.2{91_M781} | GGTACCGGTT | TGGACTGAAC | AAGGAGGGCA | AGATGATATT | AAATGGTATA |
| msa255059.2{91_COH1} | GGTACCGGTT | TGGACTGAAC | AAGGAGGGCA | AGATGATATT | AAATGGTATA |

Table 89: Comparative Sequences relating to SAG1350

| | | | | | |
|---------------------------|------------|------------|------------|------------|------------|
| msa255059.2{91_18RS21} | GGTACCGGTT | TGGACTGAAC | AAGGAGGGCA | AGATGATATT | AAATGGTATA |
| msa255059.2{91_2603} | GGTACCGGTT | TGGACTGAAC | AAGGAGGGCA | AGATGATATT | AAATGGTATA |
| msa255059.2{91_1169NT} | GGTACCGGTT | TGGACTGAAC | AAGGAGGGCA | AGATGATATT | AAATGGTATA |
| msa255059.2{91_090} | GGTACCGGTT | TGGACTGAAC | AAGGAGGGCA | AGATGATATT | AAATGGTATA |
| msa255059.2{91_A909} | GGTACCGGTT | TGGACTGAAC | AAGGAGGGCA | AGATGATATT | AAATGGTATA |
| msa255059.2{91_CJB110} | GGTACCGGTT | TGGACTGAAC | AAGGAGGGCA | AGATGATATT | AAATGGTATA |
| msa255059.2{91_H36B} | GGTACCGGTT | TGGACTGAAC | AAGGAGGGCA | AGATGATATT | AAATGGTATA |
| msa255059.2{91_JM9130013} | GGTACCGGTT | TGGACTGAAC | AAGGAGGGCA | AGATGATATT | AAATGGTATA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | CAGCTGTAAC | TACTGGGGAT | GGCAACTACA | AAGTAGCTGT | ATCATTTGCT |
| msa255059.2{91_M781} | CAGCTGTAAC | TACTGGGGAT | GGCAACTACA | AAGTAGCTGT | ATCATTTGCT |
| msa255059.2{91_COH1} | CAGCTGTAAC | TACTGGGGAT | GGCAACTACA | AAGTAGCTGT | ATCATTTGCT |
| msa255059.2{91_18RS21} | CAGCTGTAAC | TACTGGGGAT | GGCAACTACA | AAGTAGCTGT | ATCATTTGCT |
| msa255059.2{91_2603} | CAGCTGTAAC | TACTGGGGAT | GGCAACTACA | AAGTAGCTGT | ATCATTTGCT |
| msa255059.2{91_1169NT} | CAGCTGTAAC | TACTGGGGAT | GGCAACTACA | AAGTAGCTGT | ATCATTTGCT |
| msa255059.2{91_090} | CAGCTGTAAC | TACTGGGGAT | GGCAACTACA | AAGTAGCTGT | ATCATTTGCT |
| msa255059.2{91_A909} | CAGCTGTAAC | TACTGGGGAT | GGCAACTACA | AAGTAGCTGT | ATCATTTGCT |
| msa255059.2{91_CJB110} | CAGCTGTAAC | TACTGGGGAT | GGCAACTACA | AAGTAGCTGT | ATCATTTGCT |
| msa255059.2{91_H36B} | CAGCTGTAAC | TACTGGGGAT | GGCAACTACA | AAGTAGCTGT | ATCATTTGCT |
| msa255059.2{91_JM9130013} | CAGCTGTAAC | TACTGGGGAT | GGCAACTACA | AAGTAGCTGT | ATCATTTGCT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | GACCATAAGA | ATGAGAAGGG | TCITTATAAT | ATTCAATTAT | ACTACCAAGA |
| msa255059.2{91_M781} | GACCATAAGA | ATGAGAAGGG | TCITTATAAT | ATTCAATTAT | ACTACCAAGA |
| msa255059.2{91_COH1} | GACCATAAGA | ATGAGAAGGG | TCITTATAAT | ATTCAATTAT | ACTACCAAGA |
| msa255059.2{91_18RS21} | GACCATAAGA | ATGAGAAGGG | TCITTATAAT | ATTCAATTAT | ACTACCAAGA |
| msa255059.2{91_2603} | GACCATAAGA | ATGAGAAGGG | TCITTATAAT | ATTCAATTAT | ACTACCAAGA |
| msa255059.2{91_1169NT} | GACCATAAGA | ATGAGAAGGG | TCITTATAAT | ATTCAATTAT | ACTACCAAGA |
| msa255059.2{91_090} | GACCATAAGA | ATGAGAAGGG | TCITTATAAT | ATTCAATTAT | ACTACCAAGA |
| msa255059.2{91_A909} | GACCATAAGA | ATGAGAAGGG | TCITTATAAT | ATTCAATTAT | ACTACCAAGA |
| msa255059.2{91_CJB110} | GACCATAAGA | ATGAGAAGGG | TCITTATAAT | ATTCAATTAT | ACTACCAAGA |
| msa255059.2{91_H36B} | GACCATAAGA | ATGAGAAGGG | TCITTATAAT | ATTCAATTAT | ACTACCAAGA |
| msa255059.2{91_JM9130013} | GACCATAAGA | ATGAGAAGGG | TCITTATAAT | ATTCAATTAT | ACTACCAAGA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | AGCTAGTGGG | ACACTTGTAG | GTGTAACAGG | AACTAAAGTG | ACAGTAGCTG |
| msa255059.2{91_M781} | AGCTAGTGGG | ACACTTGTAG | GTGTAACAGG | AACTAAAGTG | ACAGTAGCTG |
| msa255059.2{91_COH1} | AGCTAGTGGG | ACACTTGTAG | GTGTAACAGG | AACTAAAGTG | ACAGTAGCTG |
| msa255059.2{91_18RS21} | AGCTAGTGGG | ACACTTGTAG | GTGTAACAGG | AACTAAAGTG | ACAGTAGCTG |
| msa255059.2{91_2603} | AGCTAGTGGG | ACACTTGTAG | GTGTAACAGG | AACTAAAGTG | ACAGTAGCTG |
| msa255059.2{91_1169NT} | AGCTAGTGGG | ACACTTGTAG | GTGTAACAGG | AACTAAAGTG | ACAGTAGCTG |
| msa255059.2{91_090} | AGCTAGTGGG | ACACTTGTAG | GTGTAACAGG | AACTAAAGTG | ACAGTAGCTG |
| msa255059.2{91_A909} | AGCTAGTGGG | ACACTTGTAG | GTGTAACAGG | AACTAAAGTG | ACAGTAGCTG |
| msa255059.2{91_CJB110} | AGCTAGTGGG | ACACTTGTAG | GTGTAACAGG | AACTAAAGTG | ACAGTAGCTG |
| msa255059.2{91_H36B} | AGCTAGTGGG | ACACTTGTAG | GTGTAACAGG | AACTAAAGTG | ACAGTAGCTG |
| msa255059.2{91_JM9130013} | AGCTAGTGGG | ACACTTGTAG | GTGTAACAGG | AACTAAAGTG | ACAGTAGCTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | GAACTAATTC | TTCTCAAGAA | CCTATTGAAA | ATGGTTTAgC | AAAGACTGGT |
| msa255059.2{91_M781} | GAACTAATTC | TTCTCAAGAA | CCTATTGAAA | ATGGTTTAgC | AAAGACTGGT |
| msa255059.2{91_COH1} | GAACTAATTC | TTCTCAAGAA | CCTATTGAAA | ATGGTTTAgC | AAAGACTGGT |
| msa255059.2{91_18RS21} | GAACTAATTC | TTCTCAAGAA | CCTATTGAAA | ATGGTTTAgC | AAAGACTGGT |
| msa255059.2{91_2603} | GAACTAATTC | TTCTCAAGAA | CCTATTGAAA | ATGGTTTAgC | AAAGACTGGT |
| msa255059.2{91_1169NT} | GAACTAATTC | TTCTCAAGAA | CCTATTGAAA | ATGGTTTAgC | AAAGACTGGT |
| msa255059.2{91_090} | GAACTAATTC | TTCTCAAGAA | CCTATTGAAA | ATGGTTTAgC | AAAGACTGGT |
| msa255059.2{91_A909} | GAACTAATTC | TTCTCAAGAA | CCTATTGAAA | ATGGTTTAgC | AAAGACTGGT |
| msa255059.2{91_CJB110} | GAACTAATTC | TTCTCAAGAA | CCTATTGAAA | ATGGTTTAgC | AAAGACTGGT |
| msa255059.2{91_H36B} | GAACTAATTC | TTCTCAAGAA | CCTATTGAAA | ATGGTTTAgC | AAAGACTGGT |
| msa255059.2{91_JM9130013} | GAACTAATTC | TTCTCAAGAA | CCTATTGAAA | ATGGTTTAgC | AAAGACTGGT |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | GTTTATAATA | TTATCGGAAG | TACTGAAGTA | AAAAATGAAG | CTAAAATATC |
| msa255059.2{91_M781} | GTTTATAATA | TTATCGGAAG | TACTGAAGTA | AAAAATGAAG | CTAAAATATC |
| msa255059.2{91_COH1} | GTTTATAATA | TTATCGGAAG | TACTGAAGTA | AAAAATGAAG | CTAAAATATC |
| msa255059.2{91_18RS21} | GTTTATAATA | TTATCGGAAG | TACTGAAGTA | AAAAATGAAG | CTAAAATATC |
| msa255059.2{91_2603} | GTTTATAATA | TTATCGGAAG | TACTGAAGTA | AAAAATGAAG | CTAAAATATC |
| msa255059.2{91_1169NT} | GTTTATAATA | TTATCGGAAG | TACTGAAGTA | AAAAATGAAG | CTAAAATATC |
| msa255059.2{91_090} | GTTTATAATA | TTATCGGAAG | TACTGAAGTA | AAAAATGAAG | CTAAAATATC |
| msa255059.2{91_A909} | GTTTATAATA | TTATCGGAAG | TACTGAAGTA | AAAAATGAAG | CTAAAATATC |
| msa255059.2{91_CJB110} | GTTTATAATA | TTATCGGAAG | TACTGAAGTA | AAAAATGAAG | CTAAAATATC |
| msa255059.2{91_H36B} | GTTTATAATA | TTATCGGAAG | TACTGAAGTA | AAAAATGAAG | CTAAAATATC |
| msa255059.2{91_JM9130013} | GTTTATAATA | TTATCGGAAG | TACTGAAGTA | AAAAATGAAG | CTAAAATATC |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | AAGTCAGACC | CAATTTACTT | TAGAAAAAGG | TGACAAAATA | AATTATGATC |
| msa255059.2{91_M781} | AAGTCAGACC | CAATTTACTT | TAGAAAAAGG | TGACAAAATA | AATTATGATC |

| | | | | | | |
|---------------------------|-------------|-------------|-------------|-------------|------------|------------|
| msa255059.2{91_COH1} | AAGTCAGACC | CAATTTACTT | TAGAAAAAGG | TGACAAAATA | AATTATGATC | |
| msa255059.2{91_18RS21} | AAGTCAGACC | CAATTTACTT | TAGAAAAAGG | TGACAAAATA | AATTATGATC | |
| msa255059.2{91_2603} | AAGTCAGACC | CAATTTACTT | TAGAAAAAGG | TGACAAAATA | AATTATGATC | |
| msa255059.2{91_1169NT} | AAGTCAGACC | CAATTTACTT | TAGAAAAAGG | TGACAAAATA | AATTATGATC | |
| msa255059.2{91_A909} | AAGTCAGACC | CAATTTACTT | TAGAAAAAGG | TGACAAAATA | AATTATGATC | |
| msa255059.2{91_CJB110} | AAGTCAGACC | CAATTTACTT | TAGAAAAAGG | TGACAAAATA | AATTATGATC | |
| msa255059.2{91_H36B} | AAGTCAGACC | CAATTTACTT | TAGAAAAAGG | TGACAAAATA | AATTATGATC | |
| msa255059.2{91_JM9130013} | AAGTCAGACC | CAATTTACTT | TAGAAAAAGG | TGACAAAATA | AATTATGATC | |
| Consensus | ***** | ***** | ***** | ***** | ***** | |
| msa255059.2{91_M732} | 1301 | AAGTATTGAC | AGCAGATGGT | TACCAGTGGG | TTTCTTACAA | ATCTTATAGT |
| msa255059.2{91_M781} | AAGTATTGAC | AGCAGATGGT | TACCAGTGGG | TACCAGTGGG | TTTCTTACAA | ATCTTATAGT |
| msa255059.2{91_COH1} | AAGTATTGAC | AGCAGATGGT | TACCAGTGGG | TACCAGTGGG | TTTCTTACAA | ATCTTATAGT |
| msa255059.2{91_18RS21} | AAGTATTGAC | AGCAGATGGT | TACCAGTGGG | TACCAGTGGG | TTTCTTACAA | ATCTTATAGT |
| msa255059.2{91_2603} | AAGTATTGAC | AGCAGATGGT | TACCAGTGGG | TACCAGTGGG | TTTCTTACAA | ATCTTATAGT |
| msa255059.2{91_1169NT} | AAGTATTGAC | AGCAGATGGT | TACCAGTGGG | TACCAGTGGG | TTTCTTACAA | ATCTTATAGT |
| msa255059.2{91_A909} | AAGTATTGAC | AGCAGATGGT | TACCAGTGGG | TACCAGTGGG | TTTCTTACAA | ATCTTATAGT |
| msa255059.2{91_CJB110} | AAGTATTGAC | AGCAGATGGT | TACCAGTGGG | TACCAGTGGG | TTTCTTACAA | ATCTTATAGT |
| msa255059.2{91_H36B} | AAGTATTGAC | AGCAGATGGT | TACCAGTGGG | TACCAGTGGG | TTTCTTACAA | ATCTTATAGT |
| msa255059.2{91_JM9130013} | AAGTATTGAC | AGCAGATGGT | TACCAGTGGG | TACCAGTGGG | TTTCTTACAA | ATCTTATAGT |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | 1351 | GGTGTTTCGTC | GCTATATTCC | TGTGAAAAAG | CTAACTACAA | GTAGTGAAAA |
| msa255059.2{91_M781} | GGTGTTTCGTC | GCTATATTCC | TGTGAAAAAG | CTAACTACAA | GTAGTGAAAA | GTAGTGAAAA |
| msa255059.2{91_COH1} | GGTGTTTCGTC | GCTATATTCC | TGTGAAAAAG | CTAACTACAA | GTAGTGAAAA | GTAGTGAAAA |
| msa255059.2{91_18RS21} | GGTGTTTCGTC | GCTATATTCC | TGTGAAAAAG | CTAACTACAA | GTAGTGAAAA | GTAGTGAAAA |
| msa255059.2{91_2603} | GGTGTTTCGTC | GCTATATTCC | TGTGAAAAAG | CTAACTACAA | GTAGTGAAAA | GTAGTGAAAA |
| msa255059.2{91_1169NT} | GGTGTTTCGTC | GCTATATTCC | TGTGAAAAAG | CTAACTACAA | GTAGTGAAAA | GTAGTGAAAA |
| msa255059.2{91_A909} | GGTGTTTCGTC | GCTATATTCC | TGTGAAAAAG | CTAACTACAA | GTAGTGAAAA | GTAGTGAAAA |
| msa255059.2{91_CJB110} | GGTGTTTCGTC | GCTATATTCC | TGTGAAAAAG | CTAACTACAA | GTAGTGAAAA | GTAGTGAAAA |
| msa255059.2{91_H36B} | GGTGTTTCGTC | GCTATATTCC | TGTGAAAAAG | CTAACTACAA | GTAGTGAAAA | GTAGTGAAAA |
| msa255059.2{91_JM9130013} | GGTGTTTCGTC | GCTATATTCC | TGTGAAAAAG | CTAACTACAA | GTAGTGAAAA | GTAGTGAAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | 1401 | AGCGAAAGAT | GAGGCGACTA | AACCGACTAG | TTATCCCAAC | TTACCTAAAA |
| msa255059.2{91_M781} | AGCGAAAGAT | GAGGCGACTA | AACCGACTAG | AACCGACTAG | TTATCCCAAC | TTACCTAAAA |
| msa255059.2{91_COH1} | AGCGAAAGAT | GAGGCGACTA | AACCGACTAG | AACCGACTAG | TTATCCCAAC | TTACCTAAAA |
| msa255059.2{91_18RS21} | AGCGAAAGAT | GAGGCGACTA | AACCGACTAG | AACCGACTAG | TTATCCCAAC | TTACCTAAAA |
| msa255059.2{91_2603} | AGCGAAAGAT | GAGGCGACTA | AACCGACTAG | AACCGACTAG | TTATCCCAAC | TTACCTAAAA |
| msa255059.2{91_1169NT} | AGCGAAAGAT | GAGGCGACTA | AACCGACTAG | AACCGACTAG | TTATCCCAAC | TTACCTAAAA |
| msa255059.2{91_A909} | AGCGAAAGAT | GAGGCGACTA | AACCGACTAG | AACCGACTAG | TTATCCCAAC | TTACCTAAAA |
| msa255059.2{91_CJB110} | AGCGAAAGAT | GAGGCGACTA | AACCGACTAG | AACCGACTAG | TTATCCCAAC | TTACCTAAAA |
| msa255059.2{91_H36B} | AGCGAAAGAT | GAGGCGACTA | AACCGACTAG | AACCGACTAG | TTATCCCAAC | TTACCTAAAA |
| msa255059.2{91_JM9130013} | AGCGAAAGAT | GAGGCGACTA | AACCGACTAG | AACCGACTAG | TTATCCCAAC | TTACCTAAAA |
| Consensus | ***** | ***** | ***** | ***** | ***** | ***** |
| msa255059.2{91_M732} | 1451 | CAGGTACCTA | TACATTTACT | AAAACCTGTAG | ATGTGAAaAG | TCAACCTAAA |
| msa255059.2{91_M781} | CAGGTACCTA | TACATTTACT | AAAACCTGTAG | AAAACCTGTAG | ATGTGAAaAG | TCAACCTAAA |
| msa255059.2{91_COH1} | CAGGTACCTA | TACATTTACT | AAAACCTGTAG | AAAACCTGTAG | ATGTGAAaAG | TCAACCTAAA |
| msa255059.2{91_18RS21} | CAGGTACCTA | TACATTTACT | AAAACCTGTAG | AAAACCTGTAG | ATGTGAAaAG | TCAACCTAAA |
| msa255059.2{91_2603} | CAGGTACCTA | TACATTTACT | AAAACCTGTAG | AAAACCTGTAG | ATGTGAAaAG | TCAACCTAAA |
| msa255059.2{91_1169NT} | CAGGTACCTA | TACATTTACT | AAAACCTGTAG | AAAACCTGTAG | ATGTGAAaAG | TCAACCTAAA |
| msa255059.2{91_A909} | CAGGTACCTA | TACATTTACT | AAAACCTGTAG | AAAACCTGTAG | ATGTGAAaAG | TCAACCTAAA |
| msa255059.2{91_CJB110} | CAGGTACCTA | TAC | | | | |

Table 89: Comparative Sequences relating to SAG1350

| | | | | | |
|---------------------------|------------|------------|------------|-----------|------------|
| msa255059.2{91_M781} | TGATCAAGTG | TTAGTAGTAG | ATGGTCATCA | GTGGATTTC | TACAAGAGTT |
| msa255059.2{91_COH1} | TGATCAAGTG | TTAGTAGTAG | ATGGTCATCA | GTGGATTTC | TACAAGAGTT |
| msa255059.2{91_18RS21} | TGATCAAGTG | TTAGTAGTAG | ATGGTCATCA | GTGGATTTC | TACAAGAGTT |
| msa255059.2{91_2603} | TGATCAAGTG | TTAGTAGTAG | ATGGTCATCA | GTGGATTTC | TACAAGAGTT |
| msa255059.2{91_1169NT} | TGATCAAGTG | TTAGTAGTAG | ATGGTCATCA | GTGGATTTC | TACAAGAGTT |
| msa255059.2{91_090} | TGATCAAGTG | TTAGTAGTAG | ATGGTCATCA | GTGGATTTC | TACAAGAGTT |
| msa255059.2{91_A909} | TGATCAAGTG | TTAGTAGTAG | ATGGTCATCA | GTGGATTTC | TACAAGAGTT |
| msa255059.2{91_CJB110} | TGATCAAGTG | TTAGTAGTAG | ATGGTCATCA | GTGGATTTC | TACAAGAGTT |
| msa255059.2{91_H36B} | TGATCAAGTG | TTAGTAGTAG | ATGGTCATCA | GTGGATTTC | TACAAGAGTT |
| msa255059.2{91_JM9130013} | TGATCAAGTG | TTAGTAGTAG | ATGGTCATCA | GTGGATTTC | TACAAGAGTT |
| Consensus | ***** | ***** | ***** | ***** | ***** |

| | | | |
|---------------------------|------------|------------|-----------|
| | 1601 | | 1629 |
| msa255059.2{91_M732} | ATTCCGGTAT | TCGTCGCTAT | ATTGAAATT |
| msa255059.2{91_M781} | ATTCCGGTAT | TCGTCGCTAT | ATTGAAATT |
| msa255059.2{91_COH1} | ATTCCGGTAT | TCGTCGCTAT | ATTGAAATT |
| msa255059.2{91_18RS21} | ATTCCGGTAT | TCGTCGCTAT | ATTGAAATT |
| msa255059.2{91_2603} | ATTCCGGTAT | TCGTCGCTAT | ATTGAAATT |
| msa255059.2{91_1169NT} | ATTCCGGTAT | TCGTCGCTAT | ATTGAAATT |
| msa255059.2{91_090} | ATTCCGGTAT | TCGTCGCTAT | ATTGAAATT |
| msa255059.2{91_A909} | ATTCCGGTAT | TCGTCGCTAT | ATTGAAATT |
| msa255059.2{91_CJB110} | ATTCCGGTAT | TCGTCGCTAT | ATTGAAATT |
| msa255059.2{91_H36B} | ATTCCGGTAT | TCGTCGCTAT | ATTGAAATT |
| msa255059.2{91_JM9130013} | ATTCCGGTAT | TCGTCGCTAT | ATTGAAATT |
| Consensus | ***** | ***** | ***** |

SEQ ID NO. 8912

STRAIN 2603 frame: 1

MKKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQGTGTSVDANNSS
 SNETSASSVITSNNDSVQASDKVNVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKE
 TEVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVNWISYKSFQGVRRYAAIESLDPSGGSS
 ETKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGTDGNYKVAVSFADHKNEKGLYNI
 HLYYQEAAGTLVGVTGKVTGVTAGTNSQEP IENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLADGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8913

STRAIN 090 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQGTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVNVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET
 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVNWISYKSFQGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGTDGNYKVAVSFADHKNEKGLYNI
 HLYYQEAAGTLVGVTGKVTGVTAGTNSQEP IENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLADGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8914

STRAIN A909 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQGTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVNVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET
 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVNWISYKSFQGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGTDGNYKVAVSFADHKNEKGLYNI
 HLYYQEAAGTLVGVTGKVTGVTAGTNSQEP IENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLADGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8915

STRAIN H36B frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQGTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVNVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET
 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVNWISYKSFQGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGTDGNYKVAVSFADHKNEKGLYNI
 HLYYQEAAGTLVGVTGKVTGVTAGTNSQEP IENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLADGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8916

STRAIN 18RS21 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQGTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVNVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET

Table 89: Comparative Sequences relating to SAG1350

EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHWISYKSYSGIRRYI
EI

SEQ ID NO. 8917

STRAIN M732 frame: 1

QVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSSNET
SASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKETEVK
NTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLPKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHWISYKSYSGIRRYI
EI

SEQ ID NO. 8918

STRAIN COH1 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLPKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHWISYKSYSGIRRYI
EI

SEQ ID NO. 8919

STRAIN M781 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLPKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHWISYKSYSGIRRYI
EI

SEQ ID NO. 8920

STRAIN CJB110 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLPKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHWISYKSYSGIRRYI
EI

SEQ ID NO. 8921

STRAIN 1169NT frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHWISYKSYSGIRRYI
EI

SEQ ID NO. 8922

STRAIN JM9130013 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGVYNIIGSTEVKNEAKISSQTQ

Table 89: Comparative Sequences relating to SAG1350

FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDKVSKQPKVSSPFVEFNFQKGEKIHYDQVLVVDGHWISYKSYSGIRRYI
EI

PRETTY of: /biotmp/msa255178.2{*} February 11, 2003 08:51 ..

| | | | | | |
|---------------------------|------------|------------|------------|------------|-------------|
| | 1 | | | | 50 |
| msa255178.2{91_090} | -kkgQVNDTK | QSYSLRKYKF | GLASVILGSF | IMVTSVPFAD | QTTSVQVNNQ |
| msa255178.2{91_18RS21} | -kkgQVNDTK | QSYSLRKYKF | GLASVILGSF | IMVTSVPFAD | QTTSVQVNNQ |
| msa255178.2{91_2603} | -kkgQVNDTK | QSYSLRKYKF | GLASVILGSF | IMVTSVPFAD | QTTSVQVNNQ |
| msa255178.2{91_A909} | -kkgQVNDTK | QSYSLRKYKF | GLASVILGSF | IMVTSVPFAD | QTTSVQVNNQ |
| msa255178.2{91_CJB110} | -kkgQVNDTK | QSYSLRKYKF | GLASVILGSF | IMVTSVPFAD | QTTSVQVNNQ |
| msa255178.2{91_H36B} | -kkgQVNDTK | QSYSLRKYKF | GLASVILGSF | IMVTSVPFAD | QTTSVQVNNQ |
| msa255178.2{91_JM9130013} | -kkgQVNDTK | QSYSLRKYKF | GLASVILGSF | IMVTSVPFAD | QTTSVQVNNQ |
| msa255178.2{91_COH1} | -kkgQVNDTK | QSYSLRKYKF | GLASVILGSF | IMVTSVPFAD | QTTSVQVNNQ |
| msa255178.2{91_M781} | -kkgQVNDTK | QSYSLRKYKF | GLASVILGSF | IMVTSVPFAD | QTTSVQVNNQ |
| msa255178.2{91_M732} | ----QVNDTK | QSYSLRKYKF | GLASVILGSF | IMVTSVPFAD | QTTSVQVNNQ |
| msa255178.2{91_1169NT} | -kkgQVNDTK | QSYSLRKYKF | GLASVILGSF | IMVTSVPFAD | QTTSVQVNNQ |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 51 | | | | 100 |
| msa255178.2{91_090} | TGTSVDaNNs | SNETSASSVI | TSNNDsVQAS | DKVVNSQNTA | TKDITTPPLVE |
| msa255178.2{91_18RS21} | TGTSVDaNNs | SNETSASSVI | TSNNDsVQAS | DKVVNSQNTA | TKDITTPPLVE |
| msa255178.2{91_2603} | TGTSVDaNNs | SNETSASSVI | TSNNDsVQAS | DKVVNSQNTA | TKDITTPPLVE |
| msa255178.2{91_A909} | TGTSVDaNNs | SNETSASSVI | TSNNDsVQAS | DKVVNSQNTA | TKDITTPPLVE |
| msa255178.2{91_CJB110} | TGTSVDaNNs | SNETSASSVI | TSNNDsVQAS | DKVVNSQNTA | TKDITTPPLVE |
| msa255178.2{91_H36B} | TGTSVDaNNs | SNETSASSVI | TSNNDsVQAS | DKVVNSQNTA | TKDITTPPLVE |
| msa255178.2{91_JM9130013} | TGTSVDaNNs | SNETSASSVI | TSNNDsVQAS | DKVVNSQNTA | TKDITTPPLVE |
| msa255178.2{91_COH1} | TGTSVDaNNs | SNETSASSVI | TSNNDsVQAS | DKVVNSQNTA | TKDITTPPLVE |
| msa255178.2{91_M781} | TGTSVDaNNs | SNETSASSVI | TSNNDsVQAS | DKVVNSQNTA | TKDITTPPLVE |
| msa255178.2{91_M732} | TGTSVDaNNs | SNETSASSVI | TSNNDsVQAS | DKVVNSQNTA | TKDITTPPLVE |
| msa255178.2{91_1169NT} | TGTSVDaNNs | SNETSASSVI | TSNNDsVQAS | DKVVNSQNTA | TKDITTPPLVE |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 101 | | | | 150 |
| msa255178.2{91_090} | TKPMVEKTLp | EQGNYVYSKE | TEVKNTPSKS | APVAFYAKKG | DKVFYDQVFN |
| msa255178.2{91_18RS21} | TKPMVEKTLp | EQGNYVYSKE | TEVKNTPSKS | APVAFYAKKG | DKVFYDQVFN |
| msa255178.2{91_2603} | TKPMVEKTLp | EQGNYVYSKE | TEVKNTPSKS | APVAFYAKKG | DKVFYDQVFN |
| msa255178.2{91_A909} | TKPMVEKTLp | EQGNYVYSKE | TEVKNTPSKS | APVAFYAKKG | DKVFYDQVFN |
| msa255178.2{91_CJB110} | TKPMVEKTLp | EQGNYVYSKE | TEVKNTPSKS | APVAFYAKKG | DKVFYDQVFN |
| msa255178.2{91_H36B} | TKPMVEKTLp | EQGNYVYSKE | TEVKNTPSKS | APVAFYAKKG | DKVFYDQVFN |
| msa255178.2{91_JM9130013} | TKPMVEKTLp | EQGNYVYSKE | TEVKNTPSKS | APVAFYAKKG | DKVFYDQVFN |
| msa255178.2{91_COH1} | TKPMVEKTLp | EQGNYVYSKE | TEVKNTPSKS | APVAFYAKKG | DKVFYDQVFN |
| msa255178.2{91_M781} | TKPMVEKTLp | EQGNYVYSKE | TEVKNTPSKS | APVAFYAKKG | DKVFYDQVFN |
| msa255178.2{91_M732} | TKPMVEKTLp | EQGNYVYSKE | TEVKNTPSKS | APVAFYAKKG | DKVFYDQVFN |
| msa255178.2{91_1169NT} | TKPMVEKTLp | EQGNYVYSKE | TEVKNTPSKS | APVAFYAKKG | DKVFYDQVFN |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 151 | | | | 200 |
| msa255178.2{91_090} | KDNVkwISYK | SfcGVRRYAA | IESLDPSGGS | ETKAPTPTN | SGSNNQEKIA |
| msa255178.2{91_18RS21} | KDNVkwISYK | SfcGVRRYAA | IESLDPSGGS | ETKAPTPTN | SGSNNQEKIA |
| msa255178.2{91_2603} | KDNVkwISYK | SfcGVRRYAA | IESLDPSGGS | ETKAPTPTN | SGSNNQEKIA |
| msa255178.2{91_A909} | KDNVkwISYK | SfcGVRRYAA | IESLDPSGGS | ETKAPTPTN | SGSNNQEKIA |
| msa255178.2{91_CJB110} | KDNVkwISYK | SfcGVRRYAA | IESLDPSGGS | ETKAPTPTN | SGSNNQEKIA |
| msa255178.2{91_H36B} | KDNVkwISYK | SfcGVRRYAA | IESLDPSGGS | ETKAPTPTN | SGSNNQEKIA |
| msa255178.2{91_JM9130013} | KDNVkwISYK | SfcGVRRYAA | IESLDPSGGS | ETKAPTPTN | SGSNNQEKIA |
| msa255178.2{91_COH1} | KDNVkwISYK | SfcGVRRYAA | IESLDPSGGS | ETKAPTPTN | SGSNNQEKIA |
| msa255178.2{91_M781} | KDNVkwISYK | SfcGVRRYAA | IESLDPSGGS | ETKAPTPTN | SGSNNQEKIA |
| msa255178.2{91_M732} | KDNVkwISYK | SfcGVRRYAA | IESLDPSGGS | ETKAPTPTN | SGSNNQEKIA |
| msa255178.2{91_1169NT} | KDNVkwISYK | SfcGVRRYAA | IESLDPSGGS | ETKAPTPTN | SGSNNQEKIA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 201 | | | | 250 |
| msa255178.2{91_090} | TQGNyTFSHK | VEVKNEAKVA | SPTQFTLDKG | DRIFYDQILT | IEGNQWLSYK |
| msa255178.2{91_18RS21} | TQGNyTFSHK | VEVKNEAKVA | SPTQFTLDKG | DRIFYDQILT | IEGNQWLSYK |
| msa255178.2{91_2603} | TQGNyTFSHK | VEVKNEAKVA | SPTQFTLDKG | DRIFYDQILT | IEGNQWLSYK |
| msa255178.2{91_A909} | TQGNyTFSHK | VEVKNEAKVA | SPTQFTLDKG | DRIFYDQILT | IEGNQWLSYK |
| msa255178.2{91_CJB110} | TQGNyTFSHK | VEVKNEAKVA | SPTQFTLDKG | DRIFYDQILT | IEGNQWLSYK |
| msa255178.2{91_H36B} | TQGNyTFSHK | VEVKNEAKVA | SPTQFTLDKG | DRIFYDQILT | IEGNQWLSYK |
| msa255178.2{91_JM9130013} | TQGNyTFSHK | VEVKNEAKVA | SPTQFTLDKG | DRIFYDQILT | IEGNQWLSYK |
| msa255178.2{91_COH1} | TQGNyTFSHK | VEVKNEAKVA | SPTQFTLDKG | DRIFYDQILT | IEGNQWLSYK |
| msa255178.2{91_M781} | TQGNyTFSHK | VEVKNEAKVA | SPTQFTLDKG | DRIFYDQILT | IEGNQWLSYK |
| msa255178.2{91_M732} | TQGNyTFSHK | VEVKNEAKVA | SPTQFTLDKG | DRIFYDQILT | IEGNQWLSYK |
| msa255178.2{91_1169NT} | TQGNyTFSHK | VEVKNEAKVA | SPTQFTLDKG | DRIFYDQILT | IEGNQWLSYK |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| | 251 | | | | 300 |
| msa255178.2{91_090} | SFNGVRRFVL | LGKASSVEKT | EDKEKVSPQP | QARITKTGRL | TiSNETTTGF |
| msa255178.2{91_18RS21} | SFNGVRRFVL | LGKASSVEKT | EDKEKVSPQP | QARITKTGRL | TiSNETTTGF |
| msa255178.2{91_2603} | SFNGVRRFVL | LGKASSVEKT | EDKEKVSPQP | QARITKTGRL | TiSNETTTGF |
| msa255178.2{91_A909} | SFNGVRRFVL | LGKASSVEKT | EDKEKVSPQP | QARITKTGRL | TiSNETTTGF |
| msa255178.2{91_CJB110} | SFNGVRRFVL | LGKASSVEKT | EDKEKVSPQP | QARITKTGRL | TiSNETTTGF |

Table 89: Comparative Sequences relating to SAG1350

| | | | | | |
|---------------------------|------------|-------------|------------|------------|------------|
| msa255178.2{91_H36B} | SFNGVRRFVL | LGKASSVEKT | EDKEKVSPQP | QARITKTGRL | TISNETTTGF |
| msa255178.2{91_JM9130013} | SFNGVRRFVL | LGKASSVEKT | EDKEKVSPQP | QARITKTGRL | TISNETTTGF |
| msa255178.2{91_COH1} | SFNGVRRFVL | LGKASSVEKT | EDKEKVSPQP | QARITKTGRL | TISNETTTGF |
| msa255178.2{91_M781} | SFNGVRRFVL | LGKASSVEKT | EDKEKVSPQP | QARITKTGRL | TISNETTTGF |
| msa255178.2{91_M732} | SFNGVRRFVL | LGKASSVEKT | EDKEKVSPQP | QARITKTGRL | TISNETTTGF |
| msa255178.2{91_1169NT} | SFNGVRRFVL | LGKASSVEKT | EDKEKVSPQP | QARITKTGRL | TISNETTTGF |
| Consensus | ***** | ***** | ***** | ***** | *-***** |
| msa255178.2{91_090} | DILITNIKDD | NGIAAVKVPV | WTEQGGQDDI | KWYTAVTTGD | GNKQVAVSFA |
| msa255178.2{91_18RS21} | DILITNIKDD | NGIAAVKVPV | WTEQGGQDDI | KWYTAVTTGD | GNKQVAVSFA |
| msa255178.2{91_2603} | DILITNIKDD | NGIAAVKVPV | WTEQGGQDDI | KWYTAVTTGD | GNKQVAVSFA |
| msa255178.2{91_A909} | DILITNIKDD | NGIAAVKVPV | WTEQGGQDDI | KWYTAVTTGD | GNKQVAVSFA |
| msa255178.2{91_CJB110} | DILITNIKDD | NGIAAVKVPV | WTEQGGQDDI | KWYTAVTTGD | GNKQVAVSFA |
| msa255178.2{91_H36B} | DILITNIKDD | NGIAAVKVPV | WTEQGGQDDI | KWYTAVTTGD | GNKQVAVSFA |
| msa255178.2{91_JM9130013} | DILITNIKDD | NGIAAVKVPV | WTEQGGQDDI | KWYTAVTTGD | GNKQVAVSFA |
| msa255178.2{91_COH1} | DILITNIKDD | NGIAAVKVPV | WTEQGGQDDI | KWYTAVTTGD | GNKQVAVSFA |
| msa255178.2{91_M781} | DILITNIKDD | NGIAAVKVPV | WTEQGGQDDI | KWYTAVTTGD | GNKQVAVSFA |
| msa255178.2{91_M732} | DILITNIKDD | NGIAAVKVPV | WTEQGGQDDI | KWYTAVTTGD | GNKQVAVSFA |
| msa255178.2{91_1169NT} | DILITNIKDD | NGIAAVKVPV | WTEQGGQDDI | KWYTAVTTGD | GNKQVAVSFA |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255178.2{91_090} | DHKNEKGLYN | IHLYYQEASG | TLVGVTGTV | TVAGTNSSQE | PIENGLAKTG |
| msa255178.2{91_18RS21} | DHKNEKGLYN | IHLYYQEASG | TLVGVTGTV | TVAGTNSSQE | PIENGLAKTG |
| msa255178.2{91_2603} | DHKNEKGLYN | IHLYYQEASG | TLVGVTGTV | TVAGTNSSQE | PIENGLAKTG |
| msa255178.2{91_A909} | DHKNEKGLYN | IHLYYQEASG | TLVGVTGTV | TVAGTNSSQE | PIENGLAKTG |
| msa255178.2{91_CJB110} | DHKNEKGLYN | IHLYYQEASG | TLVGVTGTV | TVAGTNSSQE | PIENGLAKTG |
| msa255178.2{91_H36B} | DHKNEKGLYN | IHLYYQEASG | TLVGVTGTV | TVAGTNSSQE | PIENGLAKTG |
| msa255178.2{91_JM9130013} | DHKNEKGLYN | IHLYYQEASG | TLVGVTGTV | TVAGTNSSQE | PIENGLAKTG |
| msa255178.2{91_COH1} | DHKNEKGLYN | IHLYYQEASG | TLVGVTGTV | TVAGTNSSQE | PIENGLAKTG |
| msa255178.2{91_M781} | DHKNEKGLYN | IHLYYQEASG | TLVGVTGTV | TVAGTNSSQE | PIENGLAKTG |
| msa255178.2{91_M732} | DHKNEKGLYN | IHLYYQEASG | TLVGVTGTV | TVAGTNSSQE | PIENGLAKTG |
| msa255178.2{91_1169NT} | DHKNEKGLYN | IHLYYQEASG | TLVGVTGTV | TVAGTNSSQE | PIENGLAKTG |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255178.2{91_090} | VYNIIGSTEV | KNEAKISSQT | QFTLEKGDKI | NYDQVLTADG | YQWISYKSYS |
| msa255178.2{91_18RS21} | VYNIIGSTEV | KNEAKISSQT | QFTLEKGDKI | NYDQVLTADG | YQWISYKSYS |
| msa255178.2{91_2603} | VYNIIGSTEV | KNEAKISSQT | QFTLEKGDKI | NYDQVLTADG | YQWISYKSYS |
| msa255178.2{91_A909} | VYNIIGSTEV | KNEAKISSQT | QFTLEKGDKI | NYDQVLTADG | YQWISYKSYS |
| msa255178.2{91_CJB110} | VYNIIGSTEV | KNEAKISSQT | QFTLEKGDKI | NYDQVLTADG | YQWISYKSYS |
| msa255178.2{91_H36B} | VYNIIGSTEV | KNEAKISSQT | QFTLEKGDKI | NYDQVLTADG | YQWISYKSYS |
| msa255178.2{91_JM9130013} | VYNIIGSTEV | KNEAKISSQT | QFTLEKGDKI | NYDQVLTADG | YQWISYKSYS |
| msa255178.2{91_COH1} | VYNIIGSTEV | KNEAKISSQT | QFTLEKGDKI | NYDQVLTADG | YQWISYKSYS |
| msa255178.2{91_M781} | VYNIIGSTEV | KNEAKISSQT | QFTLEKGDKI | NYDQVLTADG | YQWISYKSYS |
| msa255178.2{91_M732} | VYNIIGSTEV | KNEAKISSQT | QFTLEKGDKI | NYDQVLTADG | YQWISYKSYS |
| msa255178.2{91_1169NT} | VYNIIGSTEV | KNEAKISSQT | QFTLEKGDKI | NYDQVLTADG | YQWISYKSYS |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255178.2{91_090} | GVRRIIPVKK | LTTSSSEKAKD | EATKPTSYPN | LPKGTGYTFT | KTVDVKSQPK |
| msa255178.2{91_18RS21} | GVRRIIPVKK | LTTSSSEKAKD | EATKPTSYPN | LPKGTGYTFT | KTVDVKSQPK |
| msa255178.2{91_2603} | GVRRIIPVKK | LTTSSSEKAKD | EATKPTSYPN | LPKGTGYTFT | KTVDVKSQPK |
| msa255178.2{91_A909} | GVRRIIPVKK | LTTSSSEKAKD | EATKPTSYPN | LPKGTGYTFT | KTVDVKSQPK |
| msa255178.2{91_CJB110} | GVRRIIPVKK | LTTSSSEKAKD | EATKPTSYPN | LPKGTGYTFT | KTVDVKSQPK |
| msa255178.2{91_H36B} | GVRRIIPVKK | LTTSSSEKAKD | EATKPTSYPN | LPKGTGYTFT | KTVDVKSQPK |
| msa255178.2{91_JM9130013} | GVRRIIPVKK | LTTSSSEKAKD | EATKPTSYPN | LPKGTGYTFT | KTVDVKSQPK |
| msa255178.2{91_COH1} | GVRRIIPVKK | LTTSSSEKAKD | EATKPTSYPN | LPKGTGYTFT | KTVDVKSQPK |
| msa255178.2{91_M781} | GVRRIIPVKK | LTTSSSEKAKD | EATKPTSYPN | LPKGTGYTFT | KTVDVKSQPK |
| msa255178.2{91_M732} | GVRRIIPVKK | LTTSSSEKAKD | EATKPTSYPN | LPKGTGYTFT | KTVDVKSQPK |
| msa255178.2{91_1169NT} | GVRRIIPVKK | LTTSSSEKAKD | EATKPTSYPN | LPKGTGYTFT | KTVDVKSQPK |
| Consensus | ***** | ***** | ***** | ***** | ***** |
| msa255178.2{91_090} | VSSPVEFNQ | KGEKIHVDQV | LVVDGHWIS | YKSYSGIRRY | IEI |
| msa255178.2{91_18RS21} | VSSPVEFNQ | KGEKIHVDQV | LVVDGHWIS | YKSYSGIRRY | IEI |
| msa255178.2{91_2603} | VSSPVEFNQ | KGEKIHVDQV | LVVDGHWIS | YKSYSGIRRY | IEI |
| msa255178.2{91_A909} | VSSPVEFNQ | KGEKIHVDQV | LVVDGHWIS | YKSYSGIRRY | IEI |
| msa255178.2{91_CJB110} | VSSPVEFNQ | KGEKIHVDQV | LVVDGHWIS | YKSYSGIRRY | IEI |
| msa255178.2{91_H36B} | VSSPVEFNQ | KGEKIHVDQV | LVVDGHWIS | YKSYSGIRRY | IEI |
| msa255178.2{91_JM9130013} | VSSPVEFNQ | KGEKIHVDQV | LVVDGHWIS | YKSYSGIRRY | IEI |
| msa255178.2{91_COH1} | VSSPVEFNQ | KGEKIHVDQV | LVVDGHWIS | YKSYSGIRRY | IEI |
| msa255178.2{91_M781} | VSSPVEFNQ | KGEKIHVDQV | LVVDGHWIS | YKSYSGIRRY | IEI |
| msa255178.2{91_M732} | VSSPVEFNQ | KGEKIHVDQV | LVVDGHWIS | YKSYSGIRRY | IEI |
| msa255178.2{91_1169NT} | VSSPVEFNQ | KGEKIHVDQV | LVVDGHWIS | YKSYSGIRRY | IEI |
| Consensus | ***** | ***** | ***** | ***** | *** |

CLAIMS:

1. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is
5 encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of both GAS and *Streptococcus pneumoniae*.
2. The immunogenic composition of claim 1, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 1.
3. An immunogenic composition comprising a combination of GBS polypeptides, said
10 combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of GAS.
4. The immunogenic composition of claim 3, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 2.
- 15 5. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of *Streptococcus pneumoniae*.
6. The immunogenic composition of claim 5, wherein said GBS polypeptides are encoded
20 by GBS polynucleotide sequences selected from GBS Subset 3.
7. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS serotype polynucleotide sequence which is homologous to at least one other GBS serotype.
- 25 8. The immunogenic composition of claim 2, 4 or 6, wherein one or more of the GBS polypeptides are encoded by GBS serotype polynucleotide sequences which are homologous to at least one other GBS serotype.
9. An immunogenic composition comprising a fusion protein, wherein said fusion protein comprises a first polypeptide sequence which is encoded by a GBS serotype polynucleotide
30 which is conserved across one or more GBS serotypes.
10. A polynucleotide sequence, or a fragment comprising at least 10 contiguous polynucleotides, selected from the sequences set forth on Tables 13 – 31 and 40 – 89.
11. The polynucleotide fragment of claim 10, wherein said fragment is derived from a GBS serotype polynucleotide sequence and is homologous to at least one additional GBS serotype
35 polynucleotide sequence.

Figure 1

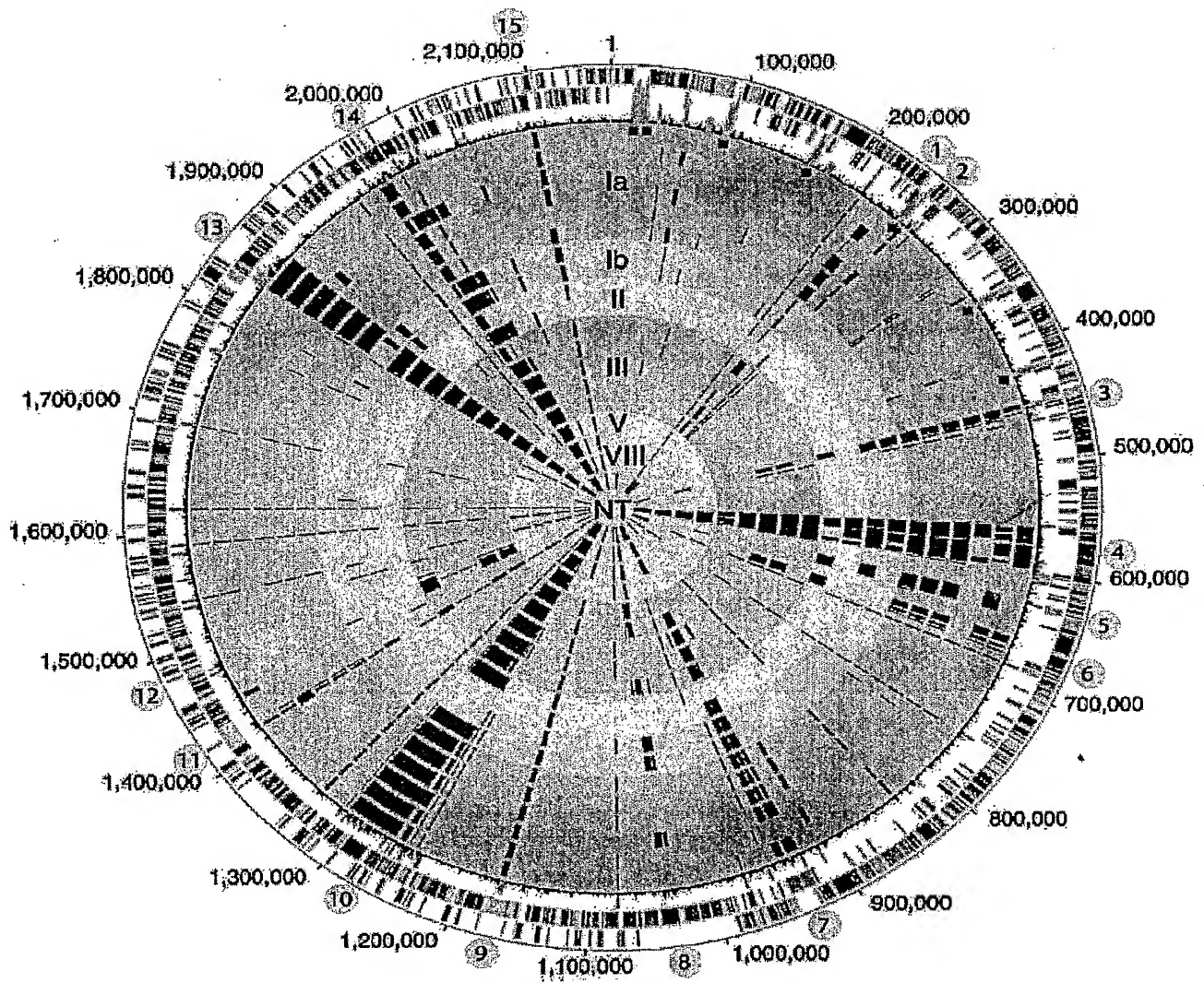


Figure 2

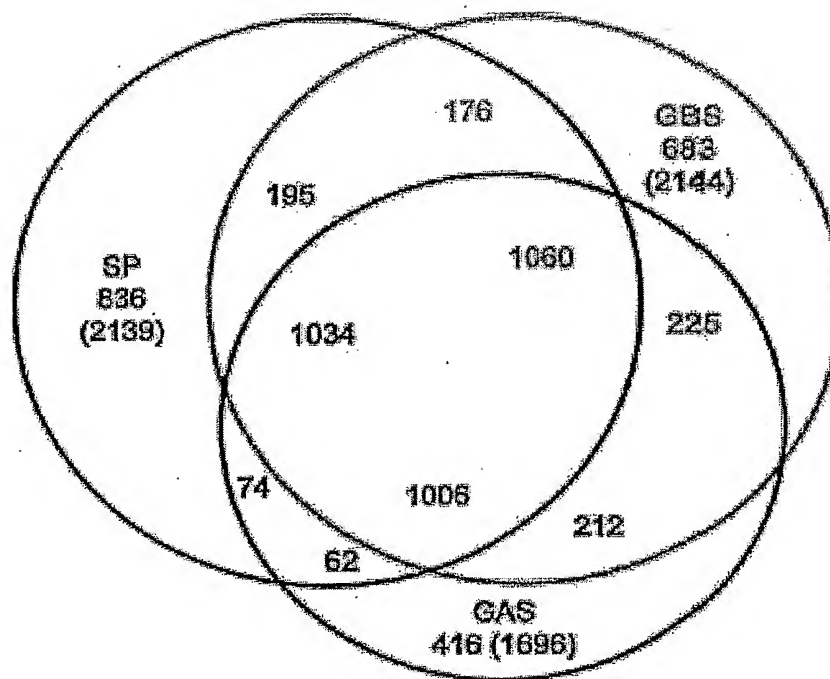
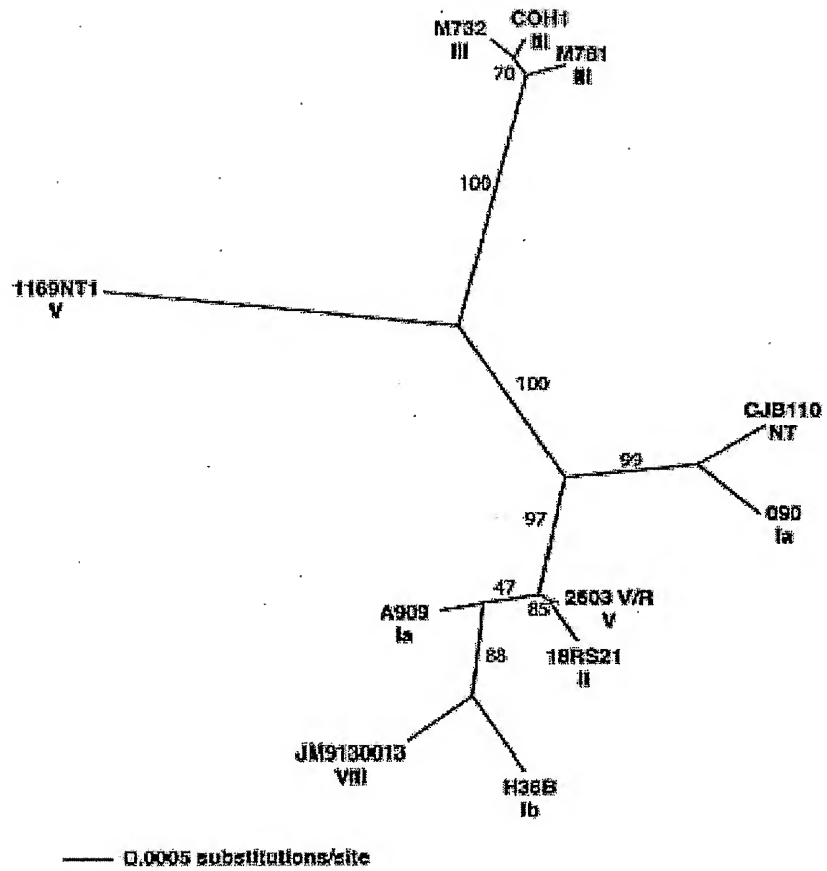


Figure 3



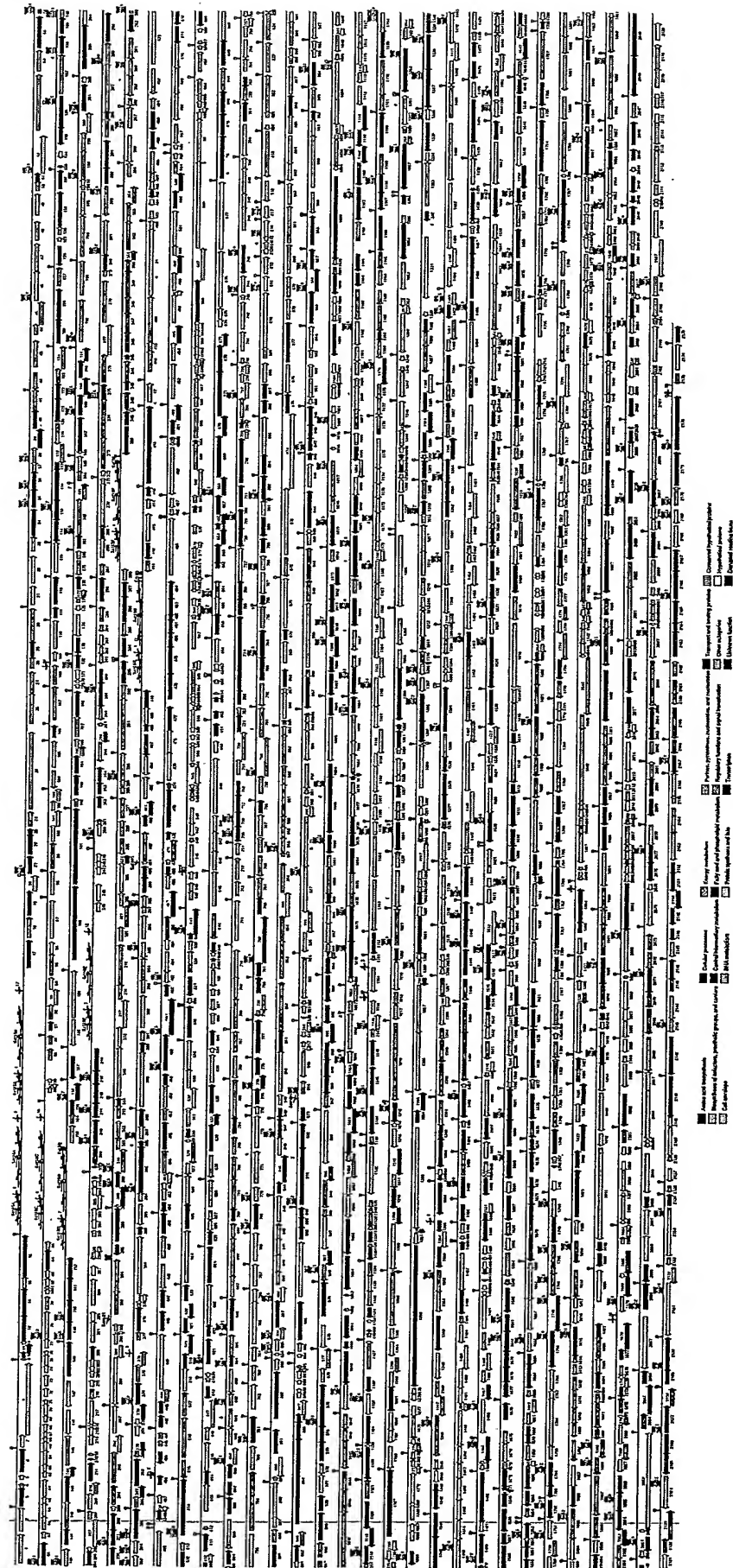


FIGURE 4

